

STIC Search Report Biotech-Chem Library

STIC Database Tracking London

TO: Nita M Minnifield

Location: REM-3C01/3C18

Art Unit: 1645

Thursday, June 30, 2005

Case Serial Number: 08/170344

From: Paul Schulwitz

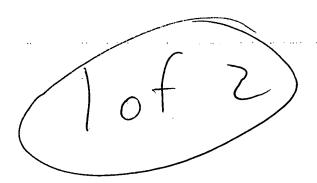
Location: Biotech-Chem Library

REM-1A65

Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Searda Notes





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hemLib

· . -
STIC-Biotech/C
From: Sent: To: Cc: Subject:
Dear STIC,
Please sear
Thomas

Pak, Michael Thursday, June 23, 2005 9:18 AM

STIC-Biotech/ChemLib

Minnifield, Nita

FW: sequence search approval--08/170344

ch the multiple sequence search set forth below.

Thanks,

Mike Pak

----Original Message-----

From: Sent:

Minnifield, Nita

To:

Wednesday, June 22, 2005 11:17 AM

Subject:

Pak, Michael sequence search approval--08/170344

Michael,

08/170344

This case has been ABN since 01/97; however Applicants petitioned to have it revived and of course it was revived. There are 74 short peptide sequences in the claims that it appears I have examined in the past. However, I don't see any sequence search results in the eDAN file. I need a commercial and interference search done. Please approve so I can get this case moved.

STIC

Please do commercial and interference sequence search on SEQ ID NO: 1-75 (all aa sequences) of this application.

Please provide a paper copy of all results.

Thanks, Minnifield, 71976 Art Unit 1645 Office REM-3C01 Mailbox REM-3C18 571-272-0860

*****	**********	***********
STAFF USE ONLY	Type of Search	Vendors and cost where applicable
		STN:
Searcher:	NA#: AA#:	DIALOG:
Searcher Phone: 2-	Interference: SPDI:	QUESTEL/ORBIT:
Date Searcher Picked up:	S/L: Oligomer:	LEXIS/NEXIS:
Date Completed:	Encode/Transl:	SEQUENCE SYSTEM:
Searcher Prep/Rev. Time:	Structure#: Text:	WWW/Internet:
Online Time:	Inventor: Litigation:	Other(Specify):

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

June 28, 2005, 18:23:48 ; Search time 11.2 Seconds (without alignments) 77.317 Million cell updates/sec Run on:

To Sold

US-08-170-344-9 52 1 CVYCKQQLL 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
i: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein E6 - human	E6 protein - human		E6 protein - human			E6 protein - human	E6 protein - human	E6 protein - human	hypothetical prote		ORF MSV251 hypothe	protein T27A1.5 [i	E6 protein - human	astB/chuR-related	hypothetical 32.7K	phenylalanine-tRNA	phenylalanine-tRNA	conserved hypothet	astB/chuR-related	E6 protein - human	E6 protein - human	hypothetical prote	unknown protein en	conserved hypothet	polyol dehydrogena	homeotic protein l	aromatic amino aci	aromatic amino aci
SUMMARIES	ID	M6WLHS	W6WL35	W6WL31	W6WL51	836503	W6WL56	A44890	WGWLPR	S36515	S57108	S36544	T28412	H88022	S15621	A72267	200060	E71863	C64570	C64416	G72269	W6WL43	836561	H90816	D85676	C69444	AF1783	159360	AE0521	QRECAA
	DB	7	Ч	7	7	~	-	~	Н	7	~	7	7	~	-	7	7	~	~	-	~	-	~			~			~	Т
	Length	158	149	149	151	153	155	155	158	148	954	150	329	449	153	454	291	328	328	381	442	155	158	185	210	274	343	400	456	457
مين	Query Match	100.0	86.5	78.8	78.8	78.8	78.8	•	78.8	76.9	76.9	75.0	75.0	75.0	73.1	73.1	71.2	•	71.2	71.2	71.2	69.2	69.2	•		•	69.2	69.2	٠	69.2
	Score	52	45	41	41	41	41	41	41	40	40	39	39	39	38	38	37	37	37	37	37	36	36	36	36	36	36	36	36	36
	Result No.	н	7	м	4	ī.	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

37 CVYCKQQLL 45

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1 CVYCKOOLL

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ine orige pitemore	amino	aromatic amino aci	hypothetical prote	insulin receptor -	E6 protein - human	probable NADH-plas	co-induced hydroge	E6 protein - human	E6 protein - human	E6 protein - human	polyol dehydrogena	homeotic protein 1	homeotic protein 1	surface antigen -	transposase [impor
D85494	D90643	AG0415	T10634	A56081	156705	C71018	H75114	W6WL18	W6WL39	S36497	AF1407	150376	S38821	B44418	T45520
c	10	~	~	Н	~	N	~	-	н	N	N		н	~	N
457	457	465	870	2148	57	136	138	158	158	159	343	395	395	412	429
69	69.2	69.5	69.5	69.2	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3
3,6	36	36	36	36	35	35	32	35	35	32	35	32	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

W6WLHS protein E6 - human papillomavirus type 16 protein E6 - human papillomavirus type 16 C;Species: human papillomavirus type 16 C;Species: human papillomavirus type 16 C;Accession: A03682; T10427 R;Scedorf, K.; Krammer, G; Durst, M.; Suhai, S.; Rowekamp, W.G. N;Itle: Human papillomavirus type 16 DNA sequence. A;Reference number: A22355; MUD:85246220; PMID:2990099
A;Accession: A03682 A;Molecule type: DNA A;Residues: 1-158 <see> A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303 R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B. J. Virol. 65, 2033-2097, 1991</see>
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the lev A; Reference number: 217014; MUID: 91162763; PMID: 1848319 A; Accession: T10427 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-158 < KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032 C;Genetics: C;Genetics: C;Super:Emaily: papillomavirus E6 protein C;Superfamily: papillomavirus E7 protein; C;Keywords: DNA binding; early protein; zinc finger F;37-73/Region: zinc finger CCCC motif F;110-146/Region: zinc finger CCCC motif
Query Match Best Local Similarity 100.0%; Score 52; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.095; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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A; Cross-references: UNIPROT: P26554; GB: M62877
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A,Accession: 836579
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-155 <DEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                          CVYCKKEL 37
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                                                                                                                                                                                                                                                                                                                                                                     1 CVYCKQQL 8
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A; Residues: 1-153 < DEL>
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                       EG protein - human papillomavirus type 51
A; Species: human papillomavirus type 51
A; Note: host Homo sapiens (man)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
D; Jule 100 C; Jule 100 C;
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C,Superfearintly: papillomavirus Bs protein
C,Reywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rigoldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
Virology 171, 306-311, 1989
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
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C;Species: human papillomavirus type 31
A;Note: host Homo sapilens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Molecule type: DNA
A;Residues: 1-151 <LUN>
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Best Local Similarity 8،۰۰۰
ابم 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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Be protein - human papillomavirus type 56

C;Species: human papillomavirus type 56

C;Species: human papillomavirus type 56

C;Species: 1-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: A33377; 836579

C;Accession: A33377; B36579

J; Gen. Virol. 70, 3099-3104, 1989

A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers.

A;Reference number: A33377; MUID:90063558; PMID:2555440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deposite: human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36639
Bubmitted to the EMBL Data Library, August 1993
A;Bescription: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Reference: S36503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross.references: EMBL:X74483; NID:9397053; PIDN:CAA52596.1; PID:9397054
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA binding; early protein; transforming protein; zinc finger
F; 33-69/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                            Gaps
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A; Residues: 1-155 < LOE>
A; Cross-references: UNIPROT: P24836
R; Cross-references: UNIPROT: P24836
B; Delius; H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A; Description: Primer-directed sequencing of human papillomavirus types.
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                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                         Indels
C;Superfamily: papillomavirus E6 protein
S;Reywords: DNA binding; early protein; zinc finger
F;30-6(Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                         DB 1;
                                                                                                                                                                     78.8%; Score 41; DB 1
75.0%; Pred. No. 6.3;
iive 2; Mismatches
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                                                                                                                                                                     Query Match 78.8
Best Local Similarity 75.0
Matches 6; Conservative
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nes 6; Conservative
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A,Accession: S36515
A,Molecule type: DNA
A,Molecule: 1-148 <DEL>
A,Cross-references: UNIPROT: P36811; EMBL: X74476; NID: 9396989; PIDN: CAA52555.1; PID: 9396
C,Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-594 «MAN»
A; Cross-rences: 1-594 «MAN»
A; Cross-rences: 101PROT: P47134; EMBL: Z49589; NID:g1015781; PIDN: CAA89616.1; PID:g10
R; Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.
Yeast 12, 869-875, 1996
A; Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frame
A; Reference number: S71676; MUID:96437976; PMID:8840504
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A,Residues: 1-150 <DEL>
A,Cross-references: UNIPROT:P36807; EMBL:X74472; NID:g396956; PIDN:CAA52530.1; PID:g396
C,Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-594 «HUD:
A;Ccosa-references: EMBL:147993; NID:g1019675; PIDN:AAB39312.1; PID:g1019708
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nypothetical protein YJR089w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein J1880
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul.-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57108; S71708
R;Manus, V.; Huang, M.E.; Galibert, F.
A;Reference number: S57085
A;Reference number: S57085
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C.Species: human papillomavirus type 26
C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Accession: S36544
R.Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A.Description: Primer-directed sequencing of human papillomavirus types.
A.Reference number: S36469
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                          Query Match 75.0%; Score 40; DB 2; Length 148; Best Local Similarity 75.0%; Pred. No. 9.1; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.9%; Score 40; DB 2; 75.0%; Pred. No. 37; tive 1; Mismatches
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B6 protein - human papillomavirus type 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: early protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0003849
A;Map position: 10R
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Best Local Similarity 75.0
Pest Local 6; Conservative
        A; Reference number: S36469
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A;Gene: SGD:BIR1
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C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
E;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5569, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A;Reference number: A40509; MUID:91374616; PMID:1716694
                                                                                                                                                                                                                                                                                                                                                               66 from an invasive carcinoma of
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E6 protein - human papillomavirus type 66
C; Species: human papillomavirus type 66
C; Species: human papillomavirus type 66
C; Date: 31.Mar-1993 #sequence_revision 31.Mar-1993 #text_change 09-Jul-2004
C; Accession: A44890
R; Tawheed, A.R; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A; Title: Characterization of human papillomavirus type 66 from an invasive car A; Recence number: A44890; MUD:92129556; PMID:1663515
A; Recence number: A44890
A; Molecule type: DNA
A; Residues: 1-155 <-TANA
A; Residues: 1-155 <-TANA
A; Residues: 1-155 <-TANA
A; Residues: UNIPROT: Q80955
A; Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:78638)
C; Superfamily: papillomavirus E6 protein
C; Keyworde: Sind finger CCCC motif
F; 33-69/Region: zinc finger CCCC motif
F; 106-142/Region: zinc finger CCCC motif
                                                                                                                                                                                  procein - human papillomavirus type 66
Species: human papillomavirus type 66
Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
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C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36515
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submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
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A;Molecule type: DNA
A;Residues: 1-158 «REU-
A;Cross-references: UNIPROT:P27862; GB:M73258
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;32-68/Fegion: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
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Pred. No. 6.5;
2; Mismatches
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75.0%;
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Similarity 75.0%;
6; Conservative 2
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Best Local Similarity 75.0
Matches 6; Conservative
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CVYCKKEL 40
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CVYCRRQL 39
CVYCKOOL 8
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Best Local Similarity
Matches 6; Conserv
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R; Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A; Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A; Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A; Reference number: S15614; MUID:91188699; PMID:1964523
A; Molecule type: DNA
A; Mesidues: 1-153 cHIR>
A; Residues: 1-153 cHIR>
A; Residues: 1-153 cHIR>
A; Cross-references: UNIPROT: P22158; EMBL: X55965; NID: G60882; PIDN: CAA39430.1; PID: G6088
C; Superfamily: papillomavirus E6 procein
C; Superfamily: papillomavirus E7 protein; transforming protein; zinc finger
F; 29-65/Region: zinc finger CCCC motif
F; 102-118/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A72267
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.M.

Ajure 399, 323-329, 1999

Ajtile: Evidence for lateral gene transfer between Archaea and Bacteria from genome se Ajrile: Evidence for lateral gene transfer between Archaea and Bacteria from genome se Ajreference number: A72200; MUID:99287316; PMID:10360571

Ajactession: A72267

Ajacteus: preliminary

Ajmolecule type: DNA

Ajresidues: 1-454 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9X148; GB:AE001787; GB:AE000512; NID:g4981882; PIDN:AAD363
A;Experimental source: strain MSB8
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                          73.1%; Score 38; DB 1; Length 153; 75.0%; Pred. No. 20; tive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             astB/chuR-related protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.1%; Score 38; DB 66.7%; Pred. No. 46; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: June 28, 2005, 19:23:23 Job time : 12.2 secs
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Best Local Similarity 75.04
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Best Local Similarity 66.7
Matches 6; Conservative
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A78000; MUID:99069613; PMID:9851916
A;Note: see websites genome, wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Accession: H88022
A;Accession: H88022
A;Accession: preliminary
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A;Cross.references: UNIPROT:017275; GB:chr_II; PIDN:AB71045.1; PID:g2429516; GSPDB:GN00q
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9YVJ1; EMBL:AF063866; NID:g4049647; PIDN:AAC97727.1; PID:g4
C;Genetics:
A;Note: MSV251
                                                                                                                                                                                                                                                                        ORF MSV251 hypothetical protein containing C3H2C3 RING finger - Melanoplus sanguinipes
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E6 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15621
                                                                                                                                                                                                                                                                                                  C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                            Gaps
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                                                                                                                                                                                                                                                                                                                  C;Accession: T28412
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, B.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28412
A;Accession: T28412
A;Molecule type: DNA
A;Residues: 1-329 AFC>
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                                         Indels
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A;Map position: 2
C;Superfamily: Arabidopsis amino acid transport protein I
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Pred. No. 24;
1; Mismatches
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Pred. No. 31;
3; Mismatches
               Pred. No. 13;
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MEDILIPE-21846-229; PubMed=11857370;
MEDILIPE-21846-229; PubMed=11857370;
WALTE K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
servical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404704; AAL01365-11.
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C0919B2;
C010B2;
C1 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
T1 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
T2 01-DEC-2003 (TEMBLrel. 25, Last annotation update)
T3 Human papillomavirus type 16.
T4 Wiruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
T4 NOTE TAXID=10581;
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Shippy R., Siwkowski A., Hampel A.;
Shippy R., Siwkowski A., Hampel A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL. 10599001 AAB03505.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNB binding; IEA.
InterPro; IRRO01334; E6.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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VE6_HPV16
Q8JMU8
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Q8QHPS
Q8QHTO
Q8QRDS
Q8QRD6
Q8QRD7
           Q9WMP2
O9WMP3
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                         June 28, 2005, 17:44:26 ; Search time 55.3 Seconds (without alignments) 83.340 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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    protein search, using sw model

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EMBL; AF404703; AAL01363.1; -..
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
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MEDLINE=21846.229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
"Sequence 97:868 874 (2002).

Int. J. Cancer 97:868 874 (2002).

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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MATER K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Mater K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 99:868=874(2002).
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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                                                            Query Match 100.0%; Score 52; DB 2; Length 130; Best Local Similarity 100.0%; Pred. No. 0.091; Matches 9; Conservative 0; Mismatches 0; Indels
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GETAI, PF00518; E6; 1.
NON TER.
SEQÜENCE 130 AA; 15779 MW; 26D0147D39
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404694; AAL01345.1; -.
EMBL; AF404694; Chost cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Wattes K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL; AR404702; AAL01361.1; -.

EMG); GO:0042025; C:host cell nucleus; IEA.

GO; GO:0040577; F:DNA binding; IEA.
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Indels
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01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-DEC-2003 (TYEMBLrel. 25, Last annotation update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Yiruses, dapna viruses, no RNA stage; Papillomaviridae,
Papillomavirus
NCBI_TAXID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment 19, Last annotation update)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae,
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0; Mismatches
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9; Conservative
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Les 9; Conservative
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Les 9; Conservative
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NCBI_TaxID=10581;
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SEQUENCE
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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         100.0%; Score 52; DB 2; Length 130; 100.0%; Pred. No. 0.091; ive 0; Mismatches 0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 0.091;
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SEQUENCE FROM N.A.
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NCBI_TaxID=10581;
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NCBI_TaxID=10566;
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Beth-Giraldo E., Giraldo G.;

Beth-Giraldo E., Giraldo G.;

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Beth-Giraldo E., Giraldo G.;

J. Gen. Virol. 78:2199-2208(1997).

EMBL. AR03015; AAB70732.1;

GO: GO: 0042025; C:host cell nucleus; IEA.

GO: GO: 0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment 19, Pression 1
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EMBL, AF404698, AALO1353.1, -
GQ; GO:00432025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

Pfam, PF00518; B6; 1.

NON TER

SEQÜENCE 143 AA; 17274 MW; SFB0F7EIEC6DBA82 CRC64;
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SEQUENCE 151 Aa; 18238 MW; BEF32A8B016CC88B CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches 9; Conservative
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Matches 9; Conservative
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CVYCKQQLL 30
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MEDINES-97474; PubMed=9292007;

MEDINES-97474; PubMed=9292007;

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Tornesello M.L., Giraldo G.;

"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";

D. Gen. Virol. 78:2199-2208(1997).

EMBL, AF003016; AAB70733.1; -.

GO, GO:0042025; C.Host cell nucleus; IEA.

InterPro; IPR001334; E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last an
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EMBL; U34125; AAA91672.1; -.
EMBL; U34131; AAA91678.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IFR001334; E6.
Fram; PPG0518; E6; 1.
SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
                                                                                                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Sequence 3, Application US/10484063
; Sequence 3, Application US/10484063
; Publication No. US2005048467A1
; GENERAL INFORMATION:
    APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLEN, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:56002
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
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US-10-25-115-3150-0

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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-47-390-6

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US-10-17-390-6

US-10-884-063-20

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - protein search, using sw model
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seq length: 200000000
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Match Length
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Result No.

sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 23, Appl Sequence 21, Appl Sequence 21069, A Sequence 21069, A Sequence 229548, Sequence 6, Appli Sequence 6, Appli Sequence 19640, Sequence 19640, Sequence 19519, A Sequence 185751, Sequence 185751,

Minimum DB Maximum DB

Database

Searched:

10, Appl 6, Appl 6, Appl 6, Appl 14, Appl 10, Appl 11, Ap

Sequence 10, 1 Sequence 10, 1 Sequence 6, Ap

Sequence

Sequence 1 Sequence 1 Sequence 1

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US-10-476-570-10
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LENGTH: 21
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: BOUNGLLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLI
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
APPL
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100.0%; Score 52; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 9; Conservative 0; Mismatches 0; Indels
                                       S-10-476-570-24
Sequence 24, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
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LENGTH: 15
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LENGTH: 15
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6.14-45
US-10-476-570-9
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: ONGRITH NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLERE, Bernard

APPLICANT: BOUNGAULLE-MORATILLE

APPLICANT: BOUNGAULLE-MORATILLE

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived

FILE REFERENCE: 45636-571-US

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT PILING DATE: 2003-11-04

PRIOR PILING DATE: 2003-11-04

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 9

LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: MAKURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: Depillomavirus proteins and uses thereof
TITLE OF INVENTION: DADILOMAVIRUS LOGALICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
FRIOR FILING DATE: 2003-11-04
FRIOR FILING DATE: 2002-05-03
FRIOR PLING DATE: 2002-05-03
FRIOR PRIOR GENERAL SECONDAL SE
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                                                                                                                                                                                                                                                                  ; Sequence 10, Application US/10476570; Publication No. US20040170644A1; GENERAL INFORMATION:
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ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
CVYCKOOLL 10
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US-10-484-063-27

US-10-484-063-27

Sequence 27, Application US/10484063

Publication No. US20050048467A1

GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: POLLEN, MICHELE

TITLE OF INVENTION: PRE-CANCEROUS GROWTHS, INCLUDING CIN

TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REPERENCE: 1204-01-16

CURRENT FILING DATE: 2002-07-19

PRIOR FILING DATE: 2002-07-19

PRIOR FILING DATE: 2002-07-19

PRIOR FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 27

SEQ ID NO 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Human papillomavirus type 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                         30 CVYCKQQLL
                                                                                                                           US-10-484-063-20
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Sequence 6, Application US/1017390
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: Schuler, Gerold
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polymucleotides by Electroporation
TITLE REFERENCE: 021505w0/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT MAILLERE, BETNARG
APPLICANT: MAILLERE, BETNARG
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GINVENTION: MAXUNE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXUNE of peptides derived from E6 and/or E7
TITLE OF INVENTION: DATE: 2003-11-04
FILE REPERRACE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
FRIOR PELIAGO DATE: 2003-05-03
FRIOR FILING DATE: 2002-05-03
FRIOR FILING DATE: 2002-05-03
FRIOR FILING DATE: 2002-05-04
NUMBER OF EQ ID NOS: 63
SOFTWARE: PATENTIN VEY: 2.1
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100.0%; Score 52; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels (
             Query Match 100.0%; Score 52; DB 16; Length 32; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 52; DB 16; Length 33; 100.0%; Pred. No. 0.16; artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                           Sequence 19, Application US/10476570 Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                              24 CVYCKQQLL 32
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                                                                                                    1 CVYCKOOLL 9
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LENGTH: 33
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Gaps

Gaps

Page

us-08-170-344-9.rapb

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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 CVYCKQQLL 50
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                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 171
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US-10-000-903-4
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                                                             APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: DARTICULARLY IN VACCINATION
TITLE OF INVENTION: DARTICULARLY IN VACCINATION
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-02
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 2
LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same;
FILE REFERENCE: 21402-559;
CURRENT APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2003-02-14
PRIOR PRIOR PILING DATE: 2002-02-14
NUMBER: OF SEQ ID NOS: 198
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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Pred. No. (
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; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
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Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
Sequence 2, Application US/10858384 Publication No. US20050033025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-367-057-16
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US-10-472-724-2
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APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT PILING DATE: 2003-09-17
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
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Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels C
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APPLICANT: MACFARLAN, RODERICK I.
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
TITLE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEX: 2.1
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Fublication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ghislaine
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                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Synthetic Construct US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-367-309A-1

Sequence 1, Application US/09367309A

; Publication No. US20020081329A1

; GENERAL INFORMATION:
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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899, 771
CURRENT FILING DATE: 2004-07-27
PRIOR PILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastsEQ for Windows Version 3.0
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OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type; OTHER INFORMATION: 16)

US-10-899-771-4
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Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. 1; Length 273;
Matches 9; Conservative 0; Mismatches 0; Indels (
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SERVATH: 273
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Publication No. US20050031638A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 CVYCKQQLL 151
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                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapien
US-10-000-903-4
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US-10-899-771-4
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4537, Ap 1, Appli

Sequence Sequence Sequence

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Sequence:

Searched:

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Sequence 575, Application US/08159339A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: HLA Binding peptides and Their
MUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
            US-09-485-885-21
US-09-485-885-23
US-09-138-27-4537
US-09-138-27-7C-1
US-08-159-339A-226
US-08-159-339A-238
US-08-159-339A-570
US-08-159-339A-570
US-08-159-339A-176
US-08-159-339A-176
US-08-159-339A-176
US-08-159-339A-176
US-09-270-767-60607
US-09-270-767-60607
US-09-270-767-60607
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US-09-270-767-60607
US-09-270-767-60607
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: DISKETE CORE SOFTWARE: FASESE (for Windows Version 2.0 SOFTWARE: FASESE (for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-804-1992
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-804-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 31,762
REFERENCE/DOCKET NUMBER: 32,762
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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US-08-159-339A-575
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STATE: CA
COUNTRY:
Sequence 6, Appli
Sequence 14, Appl
Sequence 31270, A
Sequence 24285, A
Sequence 24285, A
Sequence 5935, Ap
Sequence 5935, Ap
Sequence 5935, Ap
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9659, Ap
12427, A
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-316-239A-2

US-08-316-239B-3

US-08-316-239B-4

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US-09-28-796A-24285
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US-08-767-942A-19
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US-09-270-767-39036
US-09-270-767-54253
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                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                             US-08-170-344-9
52
1 CVYCKQQLL 9
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Match Length DB
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100.0
100.0
100.0
100.0
92.3
78.8
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                                                                                                                                                                              Title:
Perfect score:
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RESULT 4
US-08-316-239B-3
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                                                             100.0%; Score 52; DB 3; Length 10; 100.0%; Pred. No. 0.0064;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCRMATION:
APPLICANT: DILLINER, JOAKIM
APPLICANT: DILLINER, LENA
APPLICANT: DILLINER, HENA
APPLICANT: CHENG, HWRE-MING
TITLE OF INVENTION: SYNTHERIC PEPTIDES OF HUMAN
TITLE OF INVENTION: SYNTHERIC PEPTIDES OF HUMAN
TITLE OF INVENTION: USFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: ASSOCIATES, P.A.
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FORDING
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IAM PC COMPACTED
MEDIUM TYPE: Floppy disk
COMPUTER: AND COMPACTE WINGOWS 3.0
SOFTWARE: MICROSOFT WOR 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE:
ATTOMEY, ASSOCIATES
ATTOMEY, ASSOCIATES
ATTOMEY, ASSOCIATES
ATTOMEY, ASSOCIATES
ATTOMEY APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTOMEY, ASSOCIATED
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                                                                                                                             0; Mismatches
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Patent No. 5932412
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US-09-980-523A-2
Sequence 2, Application US/09980523A
Parent No. 6783763
GENERAL INFORMATION:
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REGISTRATION NUMBER: 37,13:
REFERENCE/DOCKET NUMBER: 19,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                           Query Match
Best Local Similarity 100...
9; Conservative
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Matches 9; Conservative
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MOLECULE TYPE: peptide
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US-08-159-339A-575
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US-08-934-915-160
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US-09-159-182-14

US-09-159-182-14

Sequence 14, Application US/09359382

Patent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARNS, Stirling John
APPLICANT: EDWARNS, Siziling John
APPLICANT: EDWARNS, Siziling John
APPLICANT: ERAER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
CURRENT APPLICATION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPRENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
FARLIER APPLICATION NUMBER: PCT/AU95/00868
FARLIER APPLICATION NUMBER: PCT/AU95/00868
FARLIER PILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 27

SEGUTARRE: PatentIn Ver: 2.0
                   APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEALEN, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT APPLICATION NUMBER: US/08/660,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 14
LENTH: 172
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ORGANISM: Human papillomavirus type 16
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Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: BOUYENEL], Michael E.
APPLICANT: Inglis, Stephen C.
                                                                                                                                                                                                                                                                                                                             TYPE: PRT . ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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US-08-117-083-10
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
TITLE OF INVENTION: Cervical Cancer
TOWNEST OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Jagtiani & Associates
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                                                                                    100.0%; Score 52; DB 1; Length 162; 100.0%; Pred. No. 0.084; tive 0; Mismatches 0; Indel8
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ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.,
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: 35,205
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1970-9453
TELERPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6126 Rocky Way Court CITY: Centreville STREET VA
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                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
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LENGTH: 162 amino acids
TYPE: amino acid
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Best Local Similarity 100...
9, Conservative
                                                                                  Query Match
Best Local Similarity 100.
Matches 9, Conservative
  protein
NO
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                                                                                                                                                                                                                  37 CVYCKQQLL 45
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HYPOTHETICAL: US-08-316-239B-3
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
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APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEB, John Cooper
APPLICANT: WEB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 01722/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT APPLICATION NUMBER: US/09/25
EARLIER APPLICATION NUMBER: US/09/25
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1994-12-20
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Sequence 1, Application US/09367309A

Patent No. 642807

GENERAL INFORMATION:

APPLICANT: MACIPALEAN, RODERICK I.

APPLICANT: MALLIANS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR PILING DATE: 1999-02-19

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO I

LENTH: 266
                                                                                                                                                                             Query Match 100.0%; Score 52; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
18-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
       ORGANISM: Artificial Sequence
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Matches 9; Conservative
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Fatent No. 6004557
GENERAL INFORMATION
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. 11227/130
TITLE REFERENCE: 17227/130
CURRENT PILING DATE: 1997-09-22
FARLIER REPERICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 1894-12-20
NUMBER OF SEQ ID NOS: 1005
NUMBER OF SEQ ID NOS: 2.0
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APPLICANT: Munro, Alan J.

TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins

TUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:
ADDRESSEB: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco
STRET: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 52; DB 1; Length 182;
100.0%; Pred. No. 0.093;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Xaa refers to stop codon in
the open reading frame."
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: EN PE COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/117,083
FILING DATE: 10-SEP-1993
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: A-58783
TELEPAOKE: 415-1989
TELEPAOKE: 415-398-3249
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CRARACTERISTICS:
LENGTH: 182 amino acids
TTPE: A mino aci
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1.182
OTHER INFORMATION: V
US-08-117-083-10
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111
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100.0%; Score 52; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 52; DB 3; Length 371; 100.0%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Combardo Bennehikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR PELICATION NUMBER: PCT/FEP98/05285
FRIOR PELICATION NUMBER: GB 9717953.5
FRIOR PELLOTION NUMBER: GB 9717953.5
FRIOR PELLOTION NUMBER: GB 9717953.5
FRIOR PELLOTION NUMBER: GB 9717953.5
SPIOR FILING DATE: 1999-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Varein: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-2
NUMBER: FS COLD NOS: 23
SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/09485885
; Patent No. 6342224
                                                                                                                                                                                    ; Sequence 6, Application US/09485885; Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 9; Conservative
                                                           162 CVYCKQQLL 170
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVYCKQQLL 9
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                              1 CVYCKQQLL
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US-09-485-885-14
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US-09-485-885-6
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LENGTH: 390
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LENGTH: 371
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100.0%; Score 52; DB 4; Length 266; 100.0%; Pred. No. 0.13; 1. Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 52; DB 3; Length 273; 100.0%; Pred. No. 0.14; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEC ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Catherine Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE OF INVENTION: Vaccine
FILE OF INVENTION: Vaccine
FILE OF INVENTION: ASCINGATE, 2000-02-18
FILE APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/09485885
Patent No. 6342224
                                                                                                                                                                                                                                                    Sequence 4, Application US/09485885
Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                               Conservative
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                                                                                                                                       37 CVYCKQQLL 45
                                                                                            1 CVYCKQQLL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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US-09-485-885-10
                                                                                                                                                                                                                                   US-09-485-885-4
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Search completed: June 28, 2005, 19:29:12 Job time : 18.15 secs

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June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                               Run on:
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283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-170-344-80 51 1 AYIDNYNKF 9 Title: Perfect score: Sequence: Scoring table: Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	tubulin gamma chai	qamma	tubulin gamma-2 ch	tubulin gamma-1 ch	glutathione transf	superoxide dismuta	hypothetical prote	cal		Zn-binding lipopro	യ	hypothetical prote	probable membrane	ACMNPV orf117 - Bo	hypothetical prote	superoxide dismuta	iron superoxide di	superoxide dismuta	superoxide dismuta	superoxide dismuta	hypothetical prote	glycosyl transfera	raffinose-raffinos	hypothetical prote	probable serine/th	traB protein - Esc	adherence factor T	ORF MSV250 hypothe	adenylate kinase (
SUMMARIES	S44193			T47957		T50831							B71621			AC3120	AC2173	A39267	JC4611	D98167	T10549	F95158	F98024	S14924	837998	179267	D81702	œ	A35235
Length DB	469 2		474 2		218 2										136 2	•••	•••				320 2							441 2	194 2
% Query Match	76.5	76.5	76.5	76.5	•	74.5	4	4	n	72.5	72.5		72.5	0	9.07	9.07	9.04	9.07	9.07	9.06	9.07	9.07			9.04	9.04	70.6	9.69	9.89
Score	39	39	39	39	38	38	38	38	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36		35
Result No.	1	7	m	4	S	9	7	60	σ	10	11	12	13	14	15		17	18	19	20	21	22	23	24	25	56	27	28	29

ferrochelatase - D	hypothetical prote	flagellar hook-ass	hypothetical prote	NADH2 dehydrogenas	sulfite reductase	hypothetical prote	otnG protein - Vib	probable membrane	rhoptry complex po	hypothetical prote	hypothetical prote	hypothetical prote				c
B75435	T20811	D84102	A36813	S59143	F84979	T44313	S70954	866769	A45554	T18451	T01908	T08945	T04204	E59106	H72663	OHMENWOT 14
~	~	~	~	~	N	~	N	~	0	~	~	~	~	7	0	
316	389	395	435	545	601	730	730	196	895	911	1392	1415	1515	125	135	
68.6	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	9.89	66.7	66.7	
35	35	32	32	32	32	32	32	32	32	35	35	35	32	34	34	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
tubulin gamma chain - maize

C; Species : Zea mays (maize)

C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C; Date: 13-Jan-1995 #scoppin, V.; Endle, M.C.; Lambert, A.M.

C; Accession: S44193

A; Reference number: S44193

A; Reference number: S44193

A; Accession: S44193

A; Accession: S44193

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-469 < CAN>

A; Coss-references: UNIPROT: Q41808; EMBL: X78891; NID: G474405; PIDN: CAAS55488.1; PID: G474

C; Superfamily: tubulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.5
Best Local Similarity 66.7
Matches 6; Conservative
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superoxide dismuta	tubulin gamma chain - fern (Anemia phyllitidis)
hypothetical prote	C;Species: Anemia phyllitidis
hypothetical prote	C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 09-Jul-2004
probable superoxid	C;Accession: S39553
Zn-binding lipopro	R;Fuchs, U.; Moepps, B.; Maucher, H.P.; Schraudolf, H.
serine-type carbox	Plant Mol. Biol. 23, 595-603, 1993
hypothetical prote	A; Title: Isolation, characterization and sequence of a cDNA encoding gamma-tubulin prot
probable membrane	A; Reference number: S39553; MUID: 94033338; PMID: 8219092
AcMNPV orf117 - Bo	A;Accession: S39553
hypothetical prote	A;Status: preliminary
superoxide dismuta	A; Molecule type: mRNA
iron superoxide di	A;Residues: 1-472 <fuc></fuc>
superoxide dismuta	A;Cross-references: UNIPROT:P34785; EMBL:X69188; NID:9429150; PIDN:CAA48932.1; PID:9429
superoxide dismuta	C;Superfamily: tubulin
superoxide dismuta	
hypothetical prote	Query Match 76.5%; Score 39; DB 2; Length 472;
glycosyl transfera	Best Local Similarity 66.7%; Pred. No. 30;
raffinose-raffinos	Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
hypothetical prote	

|::||| || 406 AFLDNYRKF 414

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1 AYIDNYNKF 9

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glutathione transferase (EC 2.5.1.18) (clone PM239x14) - Arabidopsis thaliana Gispecies: Arabidopsis thaliana (mouse-ear cress) (cjspecies: Arabidopsis thaliana (mouse-ear cress) (cjspecies: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004 (cjaccession: 836835, 831968 (mouse-ear cress) (cjaccession: 836835, 831968 (mouse-ear cress) (cjaccession: 836835, 831968 (mouse-peroxidase activity from Arabidop A, Reference number: 836835, MUD:93387310; PMID:8375395 (mouse-ear creation: 836835) (mouse-ear course-ear creation: 836835) (mouse-ear creation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T08G3.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24707
R;Lloyd, C.
R;Lloyd, C.
R;Lloyd, C.
A;Reference number: Z19926
A;Reference number: Z19926
A;Accession: T24707
A;Reference number: J19926
A;Accession: T24707
A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T50831
R;Lino-Neto, T.; Tavares, R.M.; Palme, K.; Pais, M.S.S.
submitted to the EMBL Data Library, September 1998
A;Description: Expression of superoxide dismutases during senescence and regreening of A;Reference number: Z25250
A;Accession: T50831
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F;64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 74.5%; Score 38; DB 2; Length 218; Local Similarity 66.7%; Pred. No. 20; 1; Indels es 6; Conservative 2; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-240 <LIN>
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45 AYLDNYHPF 53
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Best Local S
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47857; T5559
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
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A; Residues: 1-474 < DBH>
A; Residues: 1-474 < DBH>
A; Cross-references: UNIPROT: P38557; EMBL: AL132959
A; Experimental source: cultivar Columbia; BAC clone F15G16
B; Liu, B.; Joshi, H.C.; Wilson, T.J.; Silflow, C.D.; Palevitz, B.A.; Snustad, D.P.
Blant Cell 6, 303-314, 1994
A; Title: gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and immunofluorescence
A; Reference number: Z22994; MUD: 8148650; PMID: 8148650
A; Accession: T50559
                                                                                                                                                                                                                                                                                     immunoblot, and immunofluorescence
                                                                                                                                                           Filiu, B.; Joshi, H.C.; Wilson, T.J.; Silflow, C.D.; Palevitz, B.A.; Snustad, D.P. Plant Cell 6, 303-314, 1994

A;Title: gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and immunofluores A;Reference number: Z22994; MUID:8148650; PMID:8148650
A;Accession: T50558
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule rype: DNA
A;Residues: 1-474 <LIU>
A;Ross-references: UNIPROT:P38558; EMBL:U03990; PIDN:AAA20654.1
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                                           C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
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A;Introns: 43/3; 148/1; 281/3; 299/3; 334/3; 359/3; 374/3; 417/3; 452/3
A;Note: F15G16.40
C;Superfamily: tubulin
C;Keywords: microtubule
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tubulin gamma-2 chain [imported] - Arabidopsis thaliana
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A;Molecule type: DNA
A;Residues: 1-474 <-LIU->
A;Cross-references: EMBL:U02069; PIDN:AAA20653.1
A;Experimental source: Columbia
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30;
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Pred. No. 30;
2; Mismatches
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Pred. No.
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405 AFLDNYRKF 413
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405 AFLDNYRKF 413
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Matches 6; Conserv
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Best Local Similarity
Matches 6; Conser
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                                                                                                                                        Accession: T50558
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Zn-binding lipoprotein related (surface adhesin A), ADHS [imported] - Clostridium aceto C;Species: Clostridium acetobutylicum (C;Species: L4-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Cacesion: E97096 E;Accession: E97096 E;Accession: E97096 E;Accession: E97096 E;Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. 3. Bacteriol. 183, 4823-4838, 2001 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1 A;Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sering carboxypeptidase like protein - Arabidopsis thaliana
N.Alternate names: protein F4F15.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-0un-2000 #sequence_revision 02-0un-2000 #text_change 09-Jul-2004
C;Accession: T49979
R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, K. submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25015
A;Accession: T49979
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-298 <KUR>
A;Cross-references: UNIPROT:Q971P7; GB:AE001437; PIDN:AAK79560.1; PID:g15024548; GSPDB:
A;Experimental source: Clostridium acetobutylicum ATCC824
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A;Cross-references: UNIPROT:Q9SV04; EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.110
A;Experimental source: cultivar Columbia; BAC clone F4F15
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C;Species: Caenorhabditis elegans
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03872
R;Bradshaw, H.; Graves, T.; Fronick, W.
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A,Introns: 116/1; 151/1
C,Superfamily: serine carboxypeptidase
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165 YYDNYDKF 172
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58 AYVTNYNK 65
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268 MDNYNKF 274
         1 AYIDNYNK 8
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A;Gene: CAC1593
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C; Superfamily: manganese; metalloprotein; oxidoreductase
F; 51, 99, 188, 192/Binding site: manganese (His, His, Asp, His) #status predicted
                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C'Species: Drosophila melanogaster
C'Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C'Accession: T12681
R'Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
submitted to the RMBL Data Library, January 1998
A'Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A'Reference number: Z17572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 -LIN>
A;Residues: ULIN>
A;Cross-references: UNIPROT:Q42672; EMBL:L77078; NID:g1369764; PID:g1369765
A;Experimental source: cultivar Tainong 2; callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable superoxide dismutase (EC 1.15.1.1) (Mn) - papaya
N.Alternate names: manganese superoxide dismutase
C;Species: Carica papaya (papaya)
C;Date: 16-Jul.1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                               Gaps
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A;Gene: CESP:T08G3.7
A;Map position: 5
A;Introns: 48(3; 302/2; 342/3; 480/1; 605/3; 644/1; 719/1; 850/1; 896/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F36D3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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A;Molecule type: DNA
A;Residues: 1-1102 <PER>
A;Cross-references: UNIPROT:Q9WE53; EMBL:AL021106; PIDN:CAA15938.1
A;Experimental source: clone cosmid 63B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 63B12.9 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1102;
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                                                                                                                                                     Length 943;
                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 107/2; 301/1
A;Note: 63B12.9
C;Superfamily: fruit fly hypothetical protein 63B12.9
                                                                                                                                               Score 38; DB 2;
Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.5%; Score 38; DB 2; Best Local Similarity 75.0%; Pred. No. 1e+02; Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T09788
R;Lin, C.T.; Lin, M.T.
submitted to the EMBL Data Library, June 1996
AREference number: Z16854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: FlyBase: FBgn0000117
                                                                                                                                                     74.5%;
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Best Local Similarity 75.01
Matches 6; Conservative
                                                                                                                                                  Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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637 AYINAYNKF 645
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Cipecies: Borrella burgdorferi (Lyme disease spirochete)
Cipate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Cipate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Cipate: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Cipate: 18-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
Ribrares 18-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit son, D.; Peterson, J.; Rerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
Nature 390, 580-586, 1997
A;Authors: Smith H.O.; Venter, J.C.
A;Authors: Smith H.O.; Venter, J.C.
A;Atitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUD:98065943; PMID:9403685
A;Accession: E70182
A;Accession: E70182
A;Accession: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-136 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:O51606; GB:AE001167; GB:AE000783; NID:g2688585; PIDN:AAC670
A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.6%; Score 36; DB 2; Length 136; Best Local Similarity 75.0%; Pred. No. 28; Matches 6; Conservative 1; Mismatches 1; Indels
              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein BB0662 - Lyme disease spirochete
              2; Mismatches
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                  5; Conservative
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                                                                                                       3 IDNYNKP 9
                  Matches
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                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Redidues: 1-611 <MIL>
A;Cross-references: UNIPROT:O16229; EMBL:AF016418; NID:g2291147; PIDN:AAB65284.1; PID:g2
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A;Reaidues: 1-225 cGRP>
A;Cross-references: UNIPROT:Q9TV98; GB:AE001379; GB:AE001362; NID:g3845118; PIDN:AAC7182
A;Experimental source: clone 3D7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C;Accession: B71621
C;Accession: B71621
R;Gardner, M.J; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUD:99021743; PMID:9804551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane associated protein PFB0190c - malaria parasite (Plasmodium falciparum)
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C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41855
R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-95 <AMAN>A;Residues: 1-95 <AMAN
A;Residues: 1-95 <AMAN>A;Residues: 1-95 <AMAN>A;Res
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A;Introns: 32/3; 109/3; 141/1; 264/3; 303/1; 378/1; 411/3; 517/1; 563/3
A;Note: C49G7.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C49G7.
A;Reference number: Z16068
A;Accession: T03872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 72.5%; Score 37; DB 2;
Best Local Similarity 66.7%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches
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A, Note: Orf_96
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity
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A;Gene: PFB0190c
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SEQUENCE FROM N.A.

STRAIN=HDD100 / DSM 50701 / ATCC 15356 / NCIB 9529;

PubMed=14752164; DOI=10.1126/science.1093027;

Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

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Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

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Rendullic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

Rendullic S., Jagtap P., Rosinus R.J., Rosinus R.J.,

Rendullic S., Jagtap P., Rosinus R.J., Rosinus R.J.,

Rendullic S., Jagtap P., Rosinus R.J., Rosinus R.J.,

Rendullic S., Jagtap P., Rosinus R.J.,

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                                               feline cord
plasmodium
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Bdellovibrionacae; Bdellovibrio.
NCBL_TaxID=959;
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EMBL. amally.

HSSP; P04179; 1AP6.

GO; GO:00046872; F:metal ion binding; IEA.

GO; GO:0004784; F:superoxide dismutase activity; IEA.

GO; GO:0004784; F:superoxide metabolism; IEA.

GO; GO:0004784; F:superoxide metabolism; IEA.

InterPro; IPR001189; SODismutase.

Pfam; PF02777; Sod Fe_C; 1.

PRINTS; PR01703; MNSODISMTASE.

PFODM: PFO000415; SODIsmutase; 1.

PROSITE; PS00088; SOD MN; 1.

PROSITE; PS00088; SOD MN; 1.

COMPLETE PS00088; SOD MN; 1.

SEQUENCE 206 AA; 23077 MW; 80A93190CAFE37D7 CRC64;
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Last annotation update)
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Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SodB protein (BC 1.15.1.1).
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84.958 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                           1612378 seqs, 512079187 residues
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TBG2 MAIZE
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Q7RD59
TKT BUCBP
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Q972B2
Q8A9I1
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Q94165
Q660K8
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Q6MDS4
Q8A3L3
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Gapop 10.0 , Gapext 0.5
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2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Score

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Minimum DB s Maximum DB s

Title: Perfect score:

Seguence:

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Run on:

Scoring table:

Searched:

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SEQUENCE FROM N.A.

STRAIN=VPI-5482 / ATCC 29148;

STRAIN=VPI-5482 / ATCC 29148;

STRAIN=22550868; PubMed=12663928; DOI=10.1126/science.1080029;

Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";

Science 299:2074-2076(2003).

ENBL, AE016829; AA07541.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

InterPro; IRRO05495; YjgP_YjgQ.

Fam; PF03139; YjgP_YjgQ.

Fam; PF03139; YjgP_YjgQ.

Fam; PF03139; AygP_YjgQ.

SEQUENCE 365 AA; 42000 MW; A9B40726B279AB46 CRC64;
InterPro; IPR005739; Topol_arch.
InterPro; IPR006171; Toprim_dom.
InterPro; IPR006171; Toprim_dom.
InterPro; IPR006154; Toprim_sub.
Pfam; PF01151; Toprim; I.
Pfam; PF01751; Toprim; I.
Pfam; PR00417; PRTPISMASBI.
SWART; SW00437; TOPRE; I.
SWART; SW00439; TOPRE; I.
TIGRFAMB; TGR81067; TopA_arch; I.
TIGRFAMB; TGR81067; TopA_arch; I.
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Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similarities with sp|P31377 Saccharomyces cerevisiae YAL014c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%; Score 42; DB 2; Length 664; 75.0%; Pred. No. 41; ive 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      664 AA; 76602 MW; 051FF24D876C5A7B CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity 75...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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DNA Res. 8:123-140(2001).
-!- FUNCTION: The reaction catalyzed by topoisomerases leads to the conversion of one topological isomer of DNA to another (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eimilarity)
--- CATALYITC ACTIVITY: ATP-independent breakage of single-stranded DNA, followed by passage and rejoining.
--- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
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Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017234; AAS04400.1;
InterPro; IPR007621; DUF477.
Fram, PP04535; DUF477.
Fram, PP04535; DUF477; I.
Complete protecome.
                                                                                                                                                                                      Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 82.4%; Score 42; DB 2; Length 304; Best Local Similarity 75.0%; Pred. No. 19; Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005694; C:chtromosome; IEA.
GO; GO:0005917; F:DNA topoisomerase type I activity; IEA.
GO; GO:0006304; P:DNA dopoisomerase type I activity; IEA.
GO; GO:0006265; P:DNA topological change; IEA.
GO; GO:0006268; P:DNA unwinding; IEA.
InterPro; IPR003601; DNAtopl_APP bind.
InterPro; IPR003602; DNAtopl_DNA_bind.
InterPro; IPR003602; DNA_tpisomrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0972B2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
664aa long hypothetical DNA topoisomerase.
OrderedLocusNames=ST1216;
                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=JCM 10545 / 7;
MEDLINE=21456156; PubMed=11572479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP000985; BAB66257.1; -.
HSSP; 029238; 1GL9.
                                                                                                                                                                     OrderedLocusNames=MAP2083c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||:|||
70 YVDNFNKF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 YIDNYNKF 9
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                        76.5%; Score 39; DB 2; Length 399; 75.0%; Pred. No. 87; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 39; DB 1; Length 421; 66.7%; Pred. No. 92;
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Prodom; PD000007; Clg_helix; 2.
SEQUENCE 399 AA; 46196 MW; 7D0284B08E13F6E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47541 MW; 7C2BC3B91EC77523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-DUL-2004 (Rel. 44, Last annotation update)
Tubulin gamma-3 chain (Gamma-3 tubulin) (Fragment)
Name=TUBG3; Synonyms=TUBC, TUBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002454; Gamma_tubulin.
InterPro; IPR002459; Tub_Frs2_C.
InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin.
InterPro; IPR003008; Tubulin_Frs2.
Pfam; PF00091; Tubulin; 1.
Pfam; PF03953; Tubulin C; 1.
PRINTS; PR0161; TUBULIN.
PR05TTE; P800127; TUBULIN; 1.
RTP-binding; Microtubule; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                       421 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                       Query Match
Beet Local Similarity 75.00,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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357 AFLDNYRKF 365
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                                                                                                                                                                                                        2 YIDNYNKF 9
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                                                                                                                                                                                                                                                                                                                                                                                                 TBG3 MAIZE
Q41874;
                                SEQUENCE
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Q75M06
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A Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
A Borsons L., Fabre E., Fairhead C., Confanioleri F., de Daruvar A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Rachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennen D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
Nature 430:35-44(2004)
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MEDILINE=21223405; PubMed=11322826; DOI=10.1006/plas.2000.1501;
Tu A.H.T., Voelker L.L., Shen X., Dybvig K.;
"Complete nucleotide sequence of the mycoplasma virus Pl genome.";
Plasmid 45:122-126(2001).
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MEDLINE=95273474; PubMed=7753907; DOI=10.1006/plas.1995.1005;
Zou N., Park K., Dybvig K.;
"Mycoplasma virus Pl has a linear, double-stranded DNA genome with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasma virus Pl.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
NCBI_TaxID=35238;
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PROSITE, PS50192, T SNARE, 1.
SEQUENCE 275 AA; 31113 MW; E9A225E6BE766CFE CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.5%; Score 39; DB
87.5%; Pred. No. 59;
iive 0; Mismatches
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Plasmid 33:41-49(1995).
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01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2003 (TrEMBLrel. 24,
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les 7; Conservative
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  NCBI_TaxID=284593;
                                                          SEQUENCE FROM N.A.
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SO TIME SO SET THE SO 
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Chow T.-Y., Haing Y.-I.C., Chen S.-J., Chen H.-H., Liu S.-M.,
Chow T.-Y., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-X.,
A Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Lee M.-C., Leu H.-L.,
A Haiao S.-H., Haiung J.-N., Hau C.-H., Kau P.-I., Lee M.-C., Leu H.-L.,
A Wu H.-P., Shaw J.-F.;
A Li X.-F., Lin X.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
A Li X.-F., Shaw J.-F.;
Cheng C.-H., Chung G.-H., Tan B.-B.,
C.-I. SIMILARITY: Belongs to the tubulin family.
C.-I. SIMILARITY: Belongs to the tubulin family.
C.-I. SIMILARITY: Belongs to the tubulin family.
C.-I. SIMILARITY: Belongs activity. IEA.
C.-I. SIMILARITY: Belongs to the tubulin family.
C.-I. SIMILARITY: Belongs to the tubulin. IEA.
C.-I. SIMILARITY: Belongs to the tubulin.
C.-I. SIMILARITY: PRO10174; Tubulin.
C.-I. S. M. C.-Y., Yu S.-M.,
C.-Y., Yu
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STRAIN=cv. Black Mexican Sweet;
MEDLINE=95175624; PubMed=7870837; DOI=10.1104/pp.107.1.309;
Lopez I., Khan S., Sevik M., Cande W.Z., Hussey P.J.;
"Isolation of a full-length cDNA encoding Zea mays gamma-tubulin.";
Plant Physiol. 107:309-310(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Zea mays (maize).
Eukaryota, Viridlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative tubulin gamma-2 chain (Gamma-2 tubulin).
Name=P0676G05.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEG1 MAIZE STANDARD; PRT; 469 AA. 041807; Q41873; 16-OCT-2001 (Rel. 40, Last sequence update) 05-ULL-2004 (Rel. 40, Last sequence update) Tubulin gamma-1 chain (Gamma-1 tubulin).
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STRAIN=cv. Black Mexican Sweet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTP-binding, Microtubule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAINscv. Black Mexican Sweet;
Canaday J., Stoppin V., Endle M.C., Lambert A.M.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Tubulin is the major constituent of microtubules. Gamma tubulin is found at microtubule organizing centers (MTOC) such as the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
-- SIMILARITY: Belongs to the tubulin family.
Canaday J., Stoppin V., Endle M.C., Lambert A.M.;
"Identification of two maize CDNAs encoding gamma-tubulin.";
"Johnitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Tubulin is the major constituent of microtubules. Gamma-tubulin is found at microtubule organizing centers (WTOC) such as the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
-!- SIMILARITY: Belongs to the tubulin family.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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A Pfam; PP003051; Tubulin; 1.

R Pfam; PR0161; Tubulin; 2.

DR PROSITE; PS00227; Tubulin).

KW GTP-binding; Microtubule; Multigene family.

TRD 142 148 GTP (Potential).

TRD 152 352 Y -> D (in Ref. 2).

Trongth 469
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01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Name=TUBG2; Synonyms=TUBC, TUBG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002454; Gamma_tubulin.
InterPro; IPR008280; Tub_Frsz_C.
InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin_Frsz.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X83695; CAA58670.1; -.
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Les 6; Conservative
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405 AFLDNYRKF 413
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Q41808;
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us-08-170-344-80.rup

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Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
NCBI_TaxID=4513;
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                                                                                                                                                76.5%; Score 39; DB 1; Length 469; 66.7%; Pred. No. 1e+02; Live 2; Mismatches 1; Indels
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66.7%; Pred. No. 1e+02;
iive 2; Mismatches 1; Indels
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GO; GO: 004529; C: tubulin; IEA.

GO; GO: 000525; F: GTP binding; IEA.

GO; GO: 000324; F: GTPs activity; IEA.

GO; GO: 000129; F: GTPs activity; IEA.

GO; GO: 000129; F: structural molecule activity; IEA.

GO; GO: 00046785; P: microtubule polymerization; IEA.

GO; GO: 0007189; P: microtubule based movement; IEA.

R InterPro; IPR002454; Gamma tubulin.

R InterPro; IPR002404; Gamma tubulin.

R InterPro; IPR0032009; Tubulin.

R InterPro; IPR0032009; Tubulin, I.

R Pfam; PF00391; Tubulin, I.

R Pfam; PF00391; Tubulin, I.

R PRINTS; PR01164; GAMMATUBULIN.

R PRNSTS; RR01164; GAMMATUBULIN.

R PRNSTS; RR01164; TUBULIN.

R PRNSTS; RR01164; GAMMATUBULIN.
   PROSITE; PS00227; TUBULIN; 1.
GTP-binding; Microcubule; Multigene family.
NP BIND 142 GTP (Pocential).
SEQUENCE 469 AA; 52870 MW; 4BDES98F64D69655 CRC64;
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SEQUENCE 469 AA; 52775 MW; 6FF014015160AFAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Thesis (2000), Pachbereich Biologie der Johannes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gutenberg-Universitaet Mainz, Germany.
-!- SIMILARITY: Belongs to the tubulin family.
BMBL; AJ772313; CAB76380.1; -.
HSRSP; P02554; ITUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tubulin gamma chain (Gamma tubulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9M421;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2004 (TrEMBLrel. 26,
Gamma tubulin.
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Best Local Similarity 66.77,
Best G; Conservative
                                                                                                                        Query Match
Best Local Similarity 66.7
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405 AFLDNYRKF 413
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405 AFLDNYRKF 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TBG_ANEPH
P34785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=gtub;
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Q9M421
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ID TBG_A
AC P3478
DT 01-FE
DT 05-UU
DE TUDU1
GN Name=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of a cDNA (OstubG2) encoding a gamma-tubulin in the rice plant (Oryza sativa).";

(er) Plant Gene Register PGR99-186

-!- PUNCTION: Tubulin is the major constituent of microtubules. Gamma tubulin is found at microtubule organizing centers (MTOC) such the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
-!- SIMILARITY: Belongs to the tubulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 46, Last annotation update)
Tubulin gamma-2 chain (Gamma-2 tubulin).
Name=TUBG2; Synonyms=TUBC;
Oryza sativa (Rice).
Eukaryota; Virighlantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Japonica / Yeongnambyeo;
Kim Y.-K., Cha Y.-K., Jun H.-Y., Kim J.-D., Choi J.-S., Kim H.-R.,
Han I.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.5%; Score 39; DB 1; Length 469; 66.7%; Pred. No. 1e+02; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP BIND 142 148 GTP (Potential).
SEQUENCE 469 AA, 52841 MW; 3F06E5848FA2B5D1 CRC64;
                                                                            PIRSP, 544193; S44193; S44193;
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or send an email to license@isb-sib.ch).
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Gramene; 049068; ...
InterPro; IPR002454; Gamma_tubulin.
InterPro; IPR00217; Tubulin.
InterPro; IPR003008; Tubulin.
Ffam; PF00091; Tubulin; 1.
Ffam; PF00391; Tubulin; 1.
Ffam; PF03933; Tubulin C.
Fran; PF03933; Tubulin C.
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                                                             EMBL; X78891; CAA55488.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6, Conservative
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405 AFLDNYRKF 413
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ID TBG2_ORYSA
AC 049068;
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RESULT 11

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Astronombat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Bartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
A belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
A wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
A wurbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
A widelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
A Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
A Martis A., Argiriou A., Flores M., Liguori R., Vitale D.,
A Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Wewes H.-W.,
A Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
10-JUL-2004 (Rel. 44, Last annotation update)
Name=TUBG1; OrderedLocusNames=At3g61650; ORFNames=F15G16.40;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
GO; GO:0000930; C:gamma-tubulin complex; ISS.

GO; GO:000520; F:protein binding; ISS.

GO; GO:000520; F:protein binding; ISS.

R GO; GO:000520; F:errotein binding; ISS.

R GO; GO:0000212; P:meiotic spindle assembly; ISS.

R GO; GO:0007020; P:microtubule nucleation; ISS.

R GO; GO:0007022; P:microtubule nucleation; ISS.

R GO; GO:0007052; P:microtubule nucleation; ISS.

R GO; GO:0007052; P:microtubule nucleation; ISS.

R GO; GO:0007052; P:microtubule nucleation; ISS.

R GO; GO:0007058; P:microtubule nucleation; ISS.

R GO; GO:0007058; P:microtubule nucleation; ISS.

R InterPro; IPR00201; Tubulin.

R InterPro; IPR003208; Tubulin. FtsZ.

InterPro; IPR00388; Tubulin. C; 1.

R Ffam; PF00091; Tubulin. C; 1.

DR PRINTS; PR01164; TUBULIN.

R PRINTS; PR01164; TUBULIN.

DR PRNSTE; PS00227; TUBULIN. UNKNOWN_1.
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STRIN-cv. Columbia;
MEDLINE=94198600; PubMed=8148650;
Liu B., Joshi H.C., Wilson T.J., Silflow C.D., Palevitz B.A.,
Snustad D.P.;
"Gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.5%; Score 39; DB 2; Length 472; 66.7%; Pred. No. 1e+02; ive 2; Mismatches 1; Indels
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STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 AA; 53183 MW; 968965CF9870844B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunofluorescence studies.";
Plant Cell 6:303-314(1994).
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Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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405 AFLDNYRKF 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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TBG1_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                             MEDLINE=9403338; PubMed=8219092; Muchs U., Moepps B., Maucher H.P., Schraudolf H.; Puchs U., Moepps B., Maucher H.P., Schraudolf H.; Fuchs U., Moepps B., Maucher H.P., Schraudolf H.; Moepps B., Maucher H.P., Schraudolf H.; Sw."; Plant Mol. Biol. 23:595-603(1993).

-! FUNCTION: Tubulin is the major constituent of microtubules. Gamma-tubulin is found at microtubule organizing centers (WTOC) such as the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Fabales, Fabaceae, Papilionoideae, Genisteae, Lupinus.
       Anemia phyllitidis (Fern).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Moniliformopses, Filicophyta, Filicopsida, Filicales, Schizaeaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Salbo N.J.M., Van Der Straeten D., Rodrigues-Pousada C.;
Subint-ted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the tubulin family.
EMBL; AF376053; AAN87551.1; -.
HSSP; 902554; ITUB.
GO; GO:000513; C:centrosome; ISS.
GO; GO:000794; C:condensed nuclear chromosome; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP (Potential).
F1E76F51BCC2DA09 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P02554; IFFX.
InterPro; IPR002454; Gamma tubulin.
InterPro; IPR0010380; Tub_FtsZ_C.
InterPro; IPR0010317; Tubulin.
InterPro; IPR001030; Tubulin.
FtsZ.
Ffam; PP00101; Tubulin, FtsZ.
Pfam; PP03953; Tubulin, C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1161; TUBULIN.
PROSITE; PS00227; TUBULIN; 1.
GTP-binding; Microtubule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lupinus albus (White lupine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X69188; CAA48932.1; -.
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                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                         NCBI_TaxID=12940;
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Q8GZT0
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Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Framer C.M., Kaneko T., Nakamura Y., Sato S.L., White O., Venter J.C., Sasamoto S., Kimura T., Ideeswa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watunda M., Yasuda M., Tabata S., Saguence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                          Nature 408:820-822(2000).

-!- FUNCTION: Tubulin is the major constituent of microtubules. Gamma tubulin is found at microtubule organizing centers (MTOC) such as the spindle poles or the centrosome, suggesting that it is involved in the minus-end nucleation of microtubule assembly.
-!- SIMILARITY: Belongs to the tubulin family.
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474 AA; 53246 MW; EE7636FF6277209D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTP-binding; Microtubule; Multigene family NP BIND 142 148 GTP (Potentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U02069; AAA20653.1; --
EMBL; AL132959; CAB71095.1; --
PIR; T47957; T47957.
HSSP; P02554; IFFX.
INTERPRO; IPR002454; Gamma_tubulin.
INTERPRO; IPR008280; Tub FESZ_C.
INTERPRO; IPR008217; Tubulin.
INTERPRO; IPR003008; Tubulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00091; Tubulin; 1.
Pfam; PF03953; Tubulin C; 1.
PRINTS; PR01161; TUBULIN.
PROSITE; PS00227; TUBULIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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Matches 6: Conser
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Search completed: June 29, 2005, 01:35:01 Job time : 56.2473 secs

|::||| || 405 AFLDNYRKF 413 1 AYIDNYNKF 9

ð 셤 TOPE BLONK (USDA)

Sequence 57, Appl Sequence 57, Appl Sequence 57, Appl Sequence 36, Appl Sequence 115148, Sequence 249348, Sequence 249348, Sequence 219923, Sequence 2109923, Sequence 2109923, Sequence 2109923, Sequence 2109923, Sequence 216, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 32, Appl Sequence 30, Appl Sequence 513, Appl Sequence 30, A

US-09-765-272-202 US-09-765-744A-48 5 US-10-282-1224-7430 US-10-472-928-2766 5 US-10-618-581-31 5 US-10-618-581-31 5 US-10-282-122A-53134 US-09-071-035-32

US-10-282-122A-57209 US-10-912-362-30 US-10-369-493-569

ALIGNMENTS

US-10-206-576-30

US-10-912-362-32 US-09-071-035-30 US-10-206-576-32

US-10-270-786-57 US-10-270-710-57 US-10-270-856-57 US-10-270-846-57 US-10-270-876-36 US-10-270-786-36 US-10-270-710-36 US-10-270-710-36 US-10-270-710-36 US-10-270-86-36 US-10-270-86-36 US-10-270-86-36 US-10-270-86-36 US-10-270-86-36 US-10-270-86-36 US-10-270-86-36 US-10-425-115-249334 US-10-425-115-249334 US-10-425-115-249350 US-10-425-115-249350 US-10-425-115-34360

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APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HIA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Flopped disk

MEDIUM TYPE: Flopped disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: BATENTIN Release #1.0, Version #1.25

SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824

FILING DATE: 23-NOV-1994

CLASSIFICATION NUMBER: US 08/278,634

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34,774

REPERENCE/POCKET NUMBER: 14137-80-1

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08344824 Publication No. US20030152580A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
US-08-344-824-13
 RESULT 1
Sequence 13, Appl
Sequence 4201, Ap
Sequence 4357, Ap
Sequence 2297, Ap
Sequence 4201, Ap
Sequence 4501, Ap
Sequence 4357, Ap
Sequence 2492, Ap
Sequence 211, App
Sequence 57, Appl
Sequence 57, Appl
                                                                                               June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds (without alignments) 64.268 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-149-138-4201
US-10-149-138-4357
US-10-149-135-2188
US-10-149-135-2297
US-10-149-138-4201
US-10-654-601-2492
US-10-654-601-2492
US-10-751-845-121
US-10-751-845-121
US-10-270-878-57
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                                                                                                                                                                                                                                                                  1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Recaph, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2006.013001
CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT APPLICATION NUMBER: US 09/458,298
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-10-0
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-06-04
            HER2/neu Using Peptide and Nucleic Acid Compositions
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100.0%; Score 51; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
TITLE OF INVENTION: HELK, .....

FILE REFERENCE: 2060.0140001

CURRENT APPLICATION NUMBER: US/10/149,138

CURRENT PILING DATE: 2002-66-10

PRIOR APPLICATION NUMBER: PCT/US00/33591

PRIOR FILING DATE: 2000-12-11

PRIOR PILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SOFTWARE: Patentin version 3.1

SEQ ID NO 4357

LENGTH: 9
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US-10-149-135-2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Artificial Peptide US-10-149-138-4357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-149-135-2188
Sequence 2188, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Stdney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Reogh, Elissa
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, John
APPLICANT: Stathwood, Scott
APPLICANT: Suthwood, Scott
APPLICANT: Chesnut, Robert
APPLICANTON: HERZ/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2000-0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2000-12-11
FRIOR FILING DATE: 2000-12-11
FRIOR FILING DATE: 1999-12-11
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APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 8; I 100.0%; Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-149-138-4357; Sequence 4357, Application US/10149138; Publication No. US20040018971A1; GENERAL INFORMATION:
APPLICANT: Fikes, John; APPLICANT: Sette, Alessandro; APPLICANT: Sidney, John; APPLICANT: Southwood, Scott; APPLICANT: Chesnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4201, Application US/10149138 Publication No. US20040018971A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ,
0
         TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Best Local Similarity 10v..
--- 9; Conservative
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                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide
US-08-344-824-13
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Matches 9; Conserv
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sotte, Alessandro
APPLICANT: Suthwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Control of the Region Cellular Immune Responses to
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2000-104001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2000-12-10
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 1999-12-11
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
       PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SSCTWARE: PatentIn version 3.1
SEQ ID NO 4201
LENGTH: 9
                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4357, Application US/10149138; Publication No. US20040121946A9; GENERAL INFORMATION:
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph T.
                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Sequence 4201, Application US/2004012194649

Fublication No. US2004012194649

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Chesnut, Robert

APPLICANT: Chesnut, Robert

APPLICANT: Chesnut, Robert

APPLICANT: Chesnut, Regen

TITLE OF INVENTION: Inducing Cellular Immune Responses to

TITLE OF INVENTION: Inducing Cellular Immune Responses to

TITLE OF INVENTION: USING Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060-014001

CURRENT APPLICATION NUMBER: VS/10/149,138

CURRENT FILING DATE: 2002-06-10

PRIOR FILING DATE: 2000-12-11
                                                                                                                                                                                         Sequence 2297, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fixes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Chesnut, Robert
APPLICATION NUMBER: US 09/189, 702
FRIOR PILING DATE: 1999-12-10
FRIOR PILING DATE: 1999-11-20
FRIOR PILING DATE: 1999-11-20
FRIOR PILING DATE: 1999-11-20
FRIOR PILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-04
FRIOR FILING DATE: 1999-03-05
FRIOR FILING DATE: 1990-03-05
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100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
1 AYIDNYNKF 9
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Length 9;

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100.0%; Score 51; DB 17; 100.0%; Pred. No. 1.6e+06;
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; ORGANISM: Bacteriophage RM378
US-10-270-878-57
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US-10-270-875-57
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Best Local Similarity 7/...
7; Conservative
           Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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118 AHIDNFNKF 126
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1 AYIDNYNKF 9
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Best Local Similarity
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APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Office of the constant of the
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Sequence 121, Application No. US20050100928A1

Sebrication No. US20050100928A1

Sebrication No. US20050100928A1

Sebrication No. US20050100928A1

APPLICANT: Hedley, Mary Lynne

APPLICANT: Urban, Robert G.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPTIDES

FILE REFERENCE: 08191-01301

CURRENT APPLICATION NUMBER: US/10/564,225

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09
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NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-654-601-2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; DB 17; Length 9; 100.0%; Pred. No. 1.6e+06; ative 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 121
LENGTH: 9
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-751-845-121
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Sequence 57, Application US/10270878

Publication No. US20030082790A1

GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggyidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
CURRENT APPLICANT: US/10.01
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT FILING DATE: 2000-10-11
PRIOR PLLING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 349
                                                                                                                                                                                                                                    US-LU-4.7-84.5-7,
Sequence 57, Application US/10270875
Fublication No. US20030082741A1
GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
CURRENT APPLICANT: US/09/585,858
FILE REFERRINGE: 2799-1001
CURRENT FILING DATE: 2000-12-18
FRIOR PILING DATE: 2000-12-18
FRIOR PILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.4%; Score 42; DB 14; Length 349; 77.8%; Pred. No. 35; cive 2; Mismatches 0; Indels
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Pred. No. 35;
0; Indels
0; Mismatches
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                                                                                                                                                                                Sequence 57, Application US/10270859
; Publication No. US20030092134A1
; GENERAL INFORMATION:
    APPLICANT: Sigridur Hjorleifsdotter
; APPLICANT: Gudmundur O. Hreggyidsson
    APPLICANT: Olafur H. Fridjonsson
    APPLICANT: Olafur H. Fridjonsson
    APPLICANT: Arthor Aevarsson
    APPLICANT: Jakob K. Kristjansson
    TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
    TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
    TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
    CURRENT FILING DATE: 2000-10-11
    CURRENT FILING DATE: 2000-10-11
    PRIOR APPLICATION NUMBER: US/10/270,859
    PRIOR FILING DATE: 2000-12-18
    PRIOR FILING DATE: 2000-12-18
    PRIOR FILING DATE: 1000-12-18
    PRIOR SEQ ID NOS: 73
    SOFTWARE: FastSEQ for Windows Version 4.0
    LENGTH- 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 57, Application US/10270846
; bublication No. US2003012972A1
; GENERAL INFORMATION:
    APPLICANT: Sigridur Hjorleifsdotter
; APPLICANT: Gudmundur O. Hreggvidsson
    APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
    TITLE OF INVENTION: Bacteriophage
; TITLE OF INVENTION: Bacteriophage
; TITLE OF INVENTION: Bacteriophage
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION WUMBER: US/10/270,846
; CURRENT FILING DATE: 2000-10-11
; PRIOR FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-06-02
; MIMBER: Ol/37,120
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Pred. No. 35;
2; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.4%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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; ORGANISM: Bacteriophage RM378
US-10-270-846-57
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US-10-270-859-57
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118 AHIDNFNKF 126
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118 AHIDNFNKF 126
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US-10-270-846-57
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US-10-270-859-57
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GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gladundur O. Hreggvidsson
APPLICANT: Gladur H. Fridjonsson
APPLICANT: Olatur H. Fridjonsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001.
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US/09/585,858
PRIOR PLING DATE: 2000-12-18
PRIOR PLING DATE: 2000-12-18
PRIOR PELING DATE: 2000-12-18
PRIOR PELING DATE: 1009-06.02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FRESEQ for Windows Version 4.0
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  Indels
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APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Host Organism
TITLE OF INVENTION: Host Organism
CURRENT APPLICATION NUMBER: US/10/270,786
CURRENT FILING DATE: 2002-10-11
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  Mismatches
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PRIOR FILING DATE: 2000-12-18
PRIOR PLILING DATE: 1999-06-02
PRIOR FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
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Pred. No.
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Publication No. US20030092128A1
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Best Local Similarity 77.8%;
Matches 7; Conservative 5
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US-10-270-786-57
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US-10-270-710-57
7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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118 AHIDNFNKF 126
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1 AYIDNYNKF 9 |:|||:||| 118 AHIDNFNKF 126

Search completed: June 29, 2005, 05:48:18 Job time: 53.8517 secs

49, Appl 462, Appl 462, Appl 7086, Ap 3, Appli 2, Appli 4919, Appli 14919, Ap

Sequence Sequence Sequence Sequence

Sequence Seq Sequence Sequence Sequence

Sequence

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Sequence 128, Application US/08159339A; Patent No. 6037135; Patent No. 6037135; Patent No. 6037135; Application US/08159339A; Patent No. 6037135; APPLICANT: Kubo, Ralph T. APPLICANT: Sette, Alessandro APPLICANT: Cells, Esteban; TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: Uses; NUMBER OF SEQUENCES: 1254; CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Townsend and Townsend and Crew LLP; STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
           US-09-144-925-5
US-09-144-925-5
US-10-270-858-49
US-09-107-532A-4629
US-09-949-016-7086
US-09-949-016-7086
US-08-015-986A-3
US-08-446-33-3
US-08-446-363-3
US-08-446-363-2
US-09-270-767-49194
US-09-270-767-49194
US-09-248-796A-5309
US-09-248-796A-194
US-09-248-796A-194
US-09-248-796A-14879
US-09-248-796A-2761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: 'USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COPERATING SYSTEM: DOS
SOFTWARE: FastERG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339A
FILING DATE: 07-824
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-84G-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-84G-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-84G-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
·USA
                                                                                                                                                                                                                                                                                                                                                                         US-08-159-339A-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
 STATE:
Sequence 128, App
Sequence 249. App
Sequence 57, Appl
Sequence 57, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 1551, A
Sequence 202, App
Sequence 202, App
Sequence 127, App
Sequence 354, Ap
Sequence 3294, Ap
Sequence 3294, Ap
Sequence 3294, Ap
Sequence 48165, Appl
Sequence 30, Appl
Sequence 3294, Ap
Sequence 3194, Appl
Sequence 3194, Appl
Sequence 3194, Appl
Sequence 3194, Appl
Sequence 6137, Appl
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Sequence 18009, A
Sequence 8, Appli
Sequence 8, Appli
                                                                                                June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-159-339A-128

US-09-543-608A-48

US-09-539-0410-2492

US-09-585-858-57

US-10-270-878-57

US-09-585-883-36

US-09-248-796A-15551

US-09-248-796A-15551

US-09-248-796A-15551

US-09-248-796A-15551

US-09-248-796A-15551

US-09-107-433-4710

US-09-107-532A-4734

US-09-107-532A-4734

US-09-107-532A-4334

US-09-107-532A-4334

US-09-107-532A-4334

US-09-107-532A-1334

US-09-107-532A-1334

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US-09-107-532A-1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-248-796A-18
US-08-015-985-8
US-09-280-597-8
                                                                                                                                                                                                                                                                            513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                                                 US-08-170-344-80
51
1 AYIDNYNKF 9
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Match Length DB
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                                                                                                                                                                  Title:
Perfect score:
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Maximum DB
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                                                                                                        Run on:
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Query Match
Best Local Similarity
Matches 7; Conserv
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APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Chemut, Robert
APPLICANT: Chemut, Robert
APPLICANT: Chemut, Robert
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Uning Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0060007
CURRENT PEPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-10
PRIOR PLING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: US 08/820,360
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APPLICANT: Sette, Alessandro
APPLICANT: Satte, John D.
APPLICANT: Standary, John
APPLICANT: Southwood, Scott
APPLICANT: Clais, Esteban
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Epimenut, Robert
APPLICANT: Epimenut, Robert
APPLICANT: Epimenut Inc.
TITLE OF INVENTION: HIA Class I A2 Tumor Associated Antigen
TITLE OF INVENTION: Peptides and Vaccine Compositions
FILE REFERENCE: 018623-015710US
CURRENT APPLICATION NUMBER: US/09/543,608A
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
                                           100.0%; Score 51; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
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                                                                                        0; Mismatches
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US-09-543-608A-48
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; Sequence 2492, Application US/09239043D
sequence 2492, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                            US-09-543-608A-48
; Sequence 48, Application US/09543608A
; Patent No. 6602510
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Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D.
Celis, Esteban
Kubo, Ralph T.
Grey, Howard M.
Chesnut, Robert
Epimmune Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                   Query Match
Best Local Similarity 100...
9, Conservative
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Best Local Similarity luv...
9; Conservative
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1 AYIDNYNKF 9
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US-08-159-339A-128
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PRIOR FILING DATE: 1997-03-12
PRIOR PLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1994-12-01
PRIOR PLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR PLICATION NUMBER: US 08/347,824
PRIOR PLICATION NUMBER: US 08/348
PRIOR PLICATION NUMBER: US 08/278,634
PRIOR PLICATION NUMBER: US 08/278,634
PRIOR PLILING DATE: 1994-07-21
PRIOR PLILING DATE: 1994-07-21
PRIOR PLILING DATE: 1994-02-06
PRIOR PLICATION NUMBER: US 08/197,484
PRIOR PLILING DATE: 1994-02-16
PRIOR PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-02-16
PRIOR PLING DATE: 1994-02-16
PRIOR PLING DATE: 1994-02-16
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
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Patent No. 6493161

GENERAL INFORMATION:
APPLICANT: Gudmundur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Jakob K. Kristjansson
APPLICANT: Jakob K. Kristjansson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/09/585,858
CURRENT APPLICATION NUMBER: 05/0137,120

PRIOR FILING DATE: 1999-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Standard peptide that binds to HLA A*2401
US-09-239-043D-2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.4%; Score 42; DB 4; Length 349; 77.8%; Pred. No. 12; tive 2; Mismatches 0; Indels
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100.0%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 57, Application US/10270878
; Patent No. 6818425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Bacteriophage RM378
US-09-585-858-57
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118 AHIDNFNKF 126
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US-00-248-796A-15551

Sequence 15551, Application US/09248796A

Sequence 15551, Application US/09248796A

Sequence 15551, Application US/09248796A

Taren No. 674713V

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC;

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196,132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-08-13

PRIOR FILING DATE: 1999-08-13

MUMBER OF SEQ ID NOS: 28208

LENGTH: 300
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Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Kaith Weinstock et al

APPLICANT: Kaith Weinstock et al

APPLICANT: Kaith Weinstock et al

APPLICANT: Routh Weinstock et al

APPLICANT: Routh Weinstock et al

APPLICANT: Routh Weinstock et al

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: VOWER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 27542
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Pred. No. 30;
2; Mismatches 0; Indels
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            TITLE OF INVENTION: Bacceriophage RM378 of a Thermophilic TITLE OF INVENTION: Bacceriophage RM378 of a Thermophilic TITLE OF INVENTION: Host Organism FILE REFERENCE: 2739-1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT FILING DATE: 2002-10-11
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: EastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 871
Jakob K. Kristjansson
                                                                                                                                                                                                                                                                                                                                                                                    82.4%;
                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-878-36
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Best Local Similarity 75.0°
"--rhes 6; Conservative
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118 AHIDNFNKF 126
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104 YLDNYGKF 111
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Best Local Similarity
Tr Conserva
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Fatent No. 6492161
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Arnthor Averasson
APPLICANT: Arnthor Averasson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
CURRENT APPLICATION UNDERS: US/09/585,858
CURRENT APPLICATION NUMBER: US/09/585,858
FILE REFERENCE: 2799.1001-001
CURRENT FILING DATE: 1999-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 871
         APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739.1001-001
CURRENT APPLICATION NUMBER: US/10/270,878
CURRENT APPLICATION NUMBER: US/99/585,858
PRIOR FILING DATE: 2002-10-11
PRIOR FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.4%; Score 42; DB 4; Length 871; Best Local Similarity 77.8%; Pred. No. 30; Matches 7; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.4%; Score 42; DB 4; Length 349; 77.8%; Pred. No. 12; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 349
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Patent No. 6818425
GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Bacteriophage RM378
US-10-270-878-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Bacteriophage RM378
US-09-585-858-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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118 AHIDNFNKF 126
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us-08-170-344-80.rai

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RESULT 12
US-09-583-110-3554
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Sequence 202, Application US/09536784

Setent No. 6573082

GENERAL INFORMATION:

APPLICAMT: Choi et. al.

TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                      Sequence 202, Application US/08961083

Batent No. 6159469

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                     ö
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                                                                                                     Score 36; DB 4; Length 250;
Pred. No. 90;
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFTCATION 1915
CLASSIFTCATION 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: BACOKES, A. Anders
REGISTRATION NUMBER: 95373
REFERENCE/DOCKET NUMBER: PB340P2
TELEFAN: (301) 309-8504
TELEFAN: (301) 309-8512
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acids
                                                                                                            70.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.6%;
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27542
                                                                                        Query Match
Best Local Similarity 85.7-
اتمه 6، Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 AYIDIYOKF 208
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186 IDNFNKF 192
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US-08-961-083-202
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Sequence 3554, Application US/09583110

| Sequence 3554, Application US/09583110
| Patent No. 6699703
| Ganeral Invokation
| Title Company | Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
| TITLE OF INVENTION: WINDER: US/09/583,110
| CURRENT APPLICATION NUMBER: US/09/583,110
| PRIOR PILING DATE: 1998-06-30
| PRIOR PILING DATE: 1998-06-30
| PRIOR PILING DATE: 1998-05-12
| PRIOR APPLICATION NUMBER: US/00/051,553
| PRIOR PILING DATE: 1998-05-12
| PRIOR SEQ ID NOS: 5322
| SEQ ID NO 3554
| LENGTH: 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.6%; Score 36; DB 4; Length 303; 77.8%; Pred. No. 1.1e+02; Live 0; Mismatches 2; Indels
                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MACHELLE S. MACKE
REGISTRATION NUMBER: 41,971
REPERBENCE/DOCKET NUMBER: PB340P3
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

NOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 202:
US-09-536-784-202
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; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 70.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                   CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AYIDIYQKF 208
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32948
LENGTH: 153
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                 APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                           COUNTER READABLE FORM:

MEDIUM TYPE: Diskette Compatible COMPUTER: Diskette Compatible COMPUTER: IBM Compatible COPERATING SYSTEM: DOS SOFTWARE: FastESE for Windows Version 2.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 00/926,666
FILING DATE: 07-AUG-1992
CLASSIFICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-AMG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/FORDE: 1815) 576-0300
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; Sequence 32948, Application US/09270767
; Patent No. 6703491
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Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8
Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                STREET: TWO EMETTY: San Francisco
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                                                                                                                                                                                   Sequence 4710, Application US/09107433
Patent No. 680074
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: CLANDANA
COMPUTER: CLANDANA
OPERATING SYSTEM: «UNKNOWN)
SOFTWARE: «UNKNOWN)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-0Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/05153
FILING DATE: MAY 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
TELEFRONEY (781)893-5007
TELEFRONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...331; SEQUENCE DESCRIPTION; SEQ ID NO: 4710: US-09-107-433-4710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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US-08-159-339A-127
; Sequence 127, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 4710:
SEQUENCE CHARACTERISTICS:
LENGTH: 331 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLGGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                            225 AYIDIYOKF 233
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                    1 AYIDNYNKF
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Matches
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0; Gaps
                                             0; Indels
Query Match 68.6%; Score 35; DB 4; Length 153; Best Local Similarity 71.4%; Pred. No. 82; Matches 5; Conservative 2; Mismatches 0; Indels
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3 IDNYNKF 9 :||||:| 76 LDNYNRF 82

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Search completed: June 29, 2005, 01:44:33 Job time : 17.9126 secs

us-08-170-344-8.rpr

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June 28, 2005, 18:23:48; Search time 11.2 Seconds (without alignments) 77.317 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                  Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

283416

PIR_79:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aypothetical prote hypothetical prote hypothetical prote ATP adenylyltransf hypothetical prote hypothetical prote E protein - human Be protein - human hydrolase, haloaci molybdopterin bios hypothetical prote tumor suppressor p small heat shock p E6 protein - human antigen, P35 homol E6-III protein - h E6-I protein - hum E6 protein - human protein E6 - human protein F15D4.7 [i hypothetical prote hypothetical prote regu hypothetićal prote hypothetical prote protein-tyrosine protein R09H3.1 unknown protein transcription E6-II protein Description SUMMARIES W6WLHS F88349 T20984 T19833 S62419 A13163 T03814 H83709 W6WLPR H70214 XXBYP1 S36515 W6WL35 B32352 T45586 D82485 S24550 T04742 S23825 A61237 T19942 T32255 A87284 F89467 S19909 T16594 Query Match Length DB Score Result Š.

E6 protein - human	E6 protein - human	E6 protein - rhesu	RNA polymerase sig	probable dehydroge	hypothetical prote	probable phospholi	hypothetical prote	hypothetical prote	hypothetical prote	protein-tyrosine-p	hypothetical prote	F1003.12 protein -	early protein E7 -	RP3 candidate gene	E6 protein - human
S36573	W6WL33	W6WLR1	AI2215	D83371	T45587	T00421	F84643	T27859	T39287	TDFFLK	T01083	D86161	A61399	138410	W6WL58
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148	149	191	218	291	296	326	742	1276	1297	2029	3449	3600	86	116	149
68.8	68.8	68.8	68.89	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	66.7	66.7	66.7
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F88349
R;anonymous, The C. elegans Sequencing Consortium.
R;anonymous, The C. elegans Sequencing Consortium.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elay.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: F88349
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protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Nirology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A2355; MUID:85246220; PMID:2990099
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C;Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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IHDIILECV 38
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C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C; Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C; Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C; Date: 17-1996 C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
Submitted to the EMBL Data Library, October 1995
A; Reference number: Z21776
A; Actorsaion: T38187
A; Actorsaion: T38187
A; As a sidues: 1-1428 LY2>
A; Residues: 1-1428 LY2>
A; Residues: 1-1428 LY2>
A; Residues: 1-1428 LY2>
A; Cross-references: UNIPROT: Q09773; EMBL: Z54285; NID: g1008429; PIDN: CAA91069.1; PID: g10
A; Experimental source: strain 972h-; cosmid c22F3
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C; Species: Agrobacterium tumefaciens
C; Species: 1-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C; Accession: A13163
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Atuthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:OBUKR5; GB:AE008687; PIDN:AAL45727.1; PID:gl7743458; GSPDB:
A;Experimental source: strain C58 (Dupont)
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A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                   hypothetical protein SPAC22F3.04 - fission yeast (Schizosaccharomyces pombe)
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24772
R;Sims, M.
R;Sims, Data Library, May 1996
A;Reference number: Z19934
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77.1%; Score 37; DB 2; Length 1428;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 0; Indels
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A;Map position: 1L
A;Introns: 1042/1; 1114/1; 1187/3; 1308/2; 1381/2
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Best Local Similarity 71.4
Matches 5; Conservative
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1344 HEIILDCV 1351
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A;Molecule type: DNA
A;Residues: 1-75 <KUR>
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A; Reference number: 219354
A; Accession: T20984
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1140 < WILL>
A; Experimental source: clone F15D4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19833
R;Ainscough, R.
B;Ainscough, R.
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               A;Molecule from the control of the c
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20984
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Pred. No. 30;
3; Mismatches 1; Indels
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Pred. No. 30;
3; Mismatches
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
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551 IHDMVAECI 559
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A;Status: preliminary
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A; Introns: 786/3
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A; Introns: 747/3
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Me protein - human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
C;Species: human papillomavirus type ME180
C;Species: human papillomavirus type ME180
C;Accession: C40509
R;Reuter: A: Dellus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
R;Reuter: A: 5.564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: C40509
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 cREU>
A;Residues: 1-158 cREU>
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dividen, P35 homolog - Lyme disease spirochete plasmid A/lp54
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Reb-1998 #sequence_revision 13-Reb-1998 #text_change 09-Jul-2004
C;Accession: H70214
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt is Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, R.; Roberts, K.; Hatch, B. Naturer 390, S80-S86, 1997
A;Authors: Smith, H.O.; Ventex, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: H70214
A;Accession: H70214
A;Accession: creation not shown
A;Molecule type: DNA
A;Residues: 1-307 <kli>MID:ACCESSION AND A;ACCESSION 
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A;Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP adenylyltransferase (EC 2.7.7.53) I - yeast (Saccharomyces cerevisiae)
N;Alternate names: diadenosinetetraphosphate alpha-beta-phosphorylase I; protein YCL050
       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 35; DB 1; Length 158; 44.4%; Pred. No. 16; ive 4; Mismatches 1; Indels
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   Indels
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   2; Mismatches
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nes 4; Conservative
   5; Conservative
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288 IHDIILDLV 296
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25 LHDVTIDCV 33
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48 HEVILEC 54
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                                                                        2 HDIILEC
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Matches
   Matches
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C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03814
R, van Slegtenhorst, M.; de Hoogt, R.; Hermans, C.; Nellist, M.; Janssen, B.; Verhoef, S.
Science 277, 805-808, 1997
A;Ruthors: Richardson, P.; Wilmer, F.; Munro, C.; Hawkins, T.L.; Sepp, T.; Ali, J.B.M.;
atkowski, D.J.
A;Title: Identification of the tuberous sclerosis gene TSC1 on chromosome 9q34.
A;Reference number: Z15098; MUID:97390505; PMID:9242607
A;Accession: T03814
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                  A; Residues: 1-519 <WIL>
A; Residues: 1-519 <WIL>
A; Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:T1
A; Experimental source: clone T10810
C; Genetics: CESP:T10810.7
A; Gene: CESP:T10810.7
A; Map position: X
A; Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3
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A;Molecule type: DNA
A;Residues: 1-145 <STO>
A;Cross-references: UNIPROT:Q9KFJ9; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB041
A;Experimental source: strain C-125
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:Cross-references: UNIPROT:Q92574; EMBL:AF013168; NID:g2331280; PIDN:AAC51674.1; PID:g2
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Mucleic Acids Res. 28, 4317-431, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
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C,Specias: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83709
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C;Superfamily: alpha-crystallin-related small heat shock protein
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                          Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Score 36; DB 2; 75.0%; Pred. No. 33; tive 2; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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335 IYDLILEC 342
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253 HDVVIEC 259
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A; Accession: T24772
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A; Status: prelimina
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A;Cross-references: UNIPROT:O17043; EMBL:AF022985; FIDN:AAB69973.1; GSPDB:GN00023; CESP A;Experimental source: strain Bristol N2; clone T15B7 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-148 <DEL>
A,Residues: 1-148 <DEL>
A,Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g396
C,Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                       Cispecies: Caenorhabditis elegans
Cibate: 29-0c1-1999 #sequence_revision 29-0c1-1999 #text_change 09-Jul-2004
Cibacesion: T3255
R;Pauley, A.; Gattung, S.
submitted to the RMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid T15B7.
A;Reference number: Z21139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S36515
B6 protein - human papillomavirus type 34
C5 protein - human papillomavirus type 34
C5 protein: human papillomavirus type 34
C5 pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C5 pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C5 pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C5 pate: 20-Feb-1995 #sequence 1993
B7 pescription: Miman papillomavirus types.
A5 pescription: Primer-directed sequencing of human papillomavirus types.
A5 pescription: 836515
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                                   Indels
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                                   1;
                                                                                                                                                                                                                                                                                                                hypothetical protein T15B7.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: T32255
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-146 <PAU>
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Pred. No. 23;
1; Mismatches
   Pred. No. 71;
4; Mismatches
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A;Introns: 13/2; 87/3
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A; Residues: 1-31 < FULD.

A; Residues: 1-31 < FULD.

A; Crossidues: 1-31 < FULD.

A; Crossidues: 1-31 < FULD.

A; Crossidues: 1-31 < FULD.

B; Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.

B; Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.

A; Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.

A; Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.

A; Fitle: Isolation, characterization, and inactivation of the APA1 gene encoding yeast d

A; Reference number: S07847; MUID:90078083; PMID:2556364
                                C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence revision 30-Jun-1993 #text change 09-Jul-2004
C;Accession: S12946; S17970; S19380; S07847; A37535; J00793
R;Kauchal, V.; Avila, D.M.; Hardies, S.C.; Barnes, L.D.
Gene 95, 79-84, 1990
A;Titles: Sequencing and enhanced expression of the gene encoding diadenosine S',5'''-P(1 A;Reference number: J00793; MUID:91071609; PMID:2174812
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A;Molecule type: DNA
A;Residues: 1-704 <MILD.
A;Residues: 1-704 <MILD.
A;Cross-references: UNIPROT: Q93376; EMBL: Z79598; PIDN: CAB01868.1; GSFDB: GN00028; CESP: C4
A;Experimental source: clone C44H4
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A;Introns: 15/2; 50/3; 82/3; 107/2; 146/3; 183/3; 229/1; 335/1; 401/1; 514/3; 540/3; 629
C;Superfamily: Caenorhabditis elegans hypothetical protein C44H4.4
                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: P16550; GB:M35204; NID:g171425; PIDN: AAA34581.1; PID:g171426
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C;Keywords: acetylated amino end; blocked amino end; nucleotidyltransferase
F;2-321/Product: ATP adenylyltransferase I #status predicted <MAT>
F;2-Modified site: acetylated amino end (Ser) (in mature form) #status predicted
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Residues: 1-99,'E', 101-321 <PLA>
A;Cross-references: GB:M31791; NID:g171063; PIDN:AAA34427.1; PID:g171064
A;Accession: A37535
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A;Residues: 49-78,'W', 80-84;281-321 <KAU2>
K;Fuller, L.J.; Kelly, A.; Lewis, C.; McKee, R.A.; Pearson, B.M.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19380
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      N;Contains: sulfate adenylyltransferase (ADP) (EC 2.7.7.5)
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A,Residues: 15-33;39-99,'B',101-260;263-321 <PLA2>
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A;Cross-references: SGD:S0000555; MIPS:YCL050c
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MEDLINE=21046-229; PubMed=11857370;

MEDLINE=21046-229; PubMed=11857370;

WALTS K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874 (2002).

EMBL; AF404701; AAL01359-1; -.
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98grd6
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Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, 1059001, ABB03505.1; -.
GO; GO:0004205; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE-21046229; PubMed=11857370;
MEDLINE-21046229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Matts K.J., Thompson C.H., Cossart state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
GO; GO:0044055; AAL01347.1;
GO; GO:0044025; Chost cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; B6; 1.
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MEDLINE=21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart V.E., Rose B.R.;
Matts K.J., Thompson C.H., Cossart Late of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874[2002).
EMBL; AR404694; AAL01345.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
NON TER
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SEQÜENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
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                                                     100.0%; Score 48; DB 2; Length 130; 100.0%; Pred. No. 0.14;
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Human papillomavirus type 16.

Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

NCBI_TaxID=10581;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 NON TER 1 1 1 SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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0-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=10581;
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF046699; AAL01355.1; -.
EMBL; AF046699; AL01355.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:004507; F:DNA binding; IEA.
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100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.14;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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E6 protein (Fragment type 16.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
PFam; PF00518; E6; 1.
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SEQÜENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
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WEDLINE-97437474; PubMed-9292007;
WEDLINE-97437474; PubMed-9292007;
WADLINE-97437474; PubMed-9292007;
WADLINE-97437474; PubMed-9292007;
WADLINE-97437474; PubMed-9292007;
WADLINE-97437474; PubMed-9292007;
WADLINE-Giraldo E., Giraldo G.,
Wadline cariations and viral genomic state of human papillomavirus
TYPE 16 in penila carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
WADLINE-PRO0316; AAB70733.1;
WADLINE-PRO0316; AB70733.1;
WADLINE-PRO0316; PRO01334; E.

MADLINE-PRO0318; E6; 1.

SEQUENCE 151 AA; 18206 MW; 51C12ABB149C6DBA CRC64;
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MEDLINE=97437474; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo Giral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
EMBL, AF003015; ABA70732.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.

Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

NCBI_TaxID=10581;
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01-OCT-2003 (TrEMBLE). 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; debux viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI TAXID=10581;
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SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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MEDLINE=21846229; PubMed=11857370;
MALTS K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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MEDLINE=21846229; PubMed=11857370;

WATER K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, FAP04698; ALL01533.1; -..

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBL_TaxID=10581;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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MEDLINE-20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.G., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
EMBL; AJ388056; CAB45114.1;
EMBL; AJ388066; CAB45114.1;
GO, GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                     "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments."; J. virol. 69:7743-7753 (1995).
                                                                                                                                                                                                        MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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EMBL; U34114; AAA91661.1; -.

EMBL; U34131; AAA91677.1; -.

EMBL; U34131; AAA91677.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.

InterPro; IFRO01334; E6.

Ffam; PF00518; E6; 11.

SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                              Early transforming protein E6.
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 0.16;
ive 0; Mismatches
                                                                            151 AA
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                                                                                                                                                                Papillomavirus.
NCBI_TaxID=10566;
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E6 protein.
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Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
"Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang.";
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MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
van Duin M., Snijders P.J., Wossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
EMBL; AA388063; CA845118.1; -.
EMBL; AA388063; CA845118.1; -.
EMBL; AA388063; CA845118.1; -.
EMBL; CA90035077; F:DNA binding; IEA.
InterPro; IPRO01334; E6.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Barly transforming protein E6 variant (Transforming protein E6).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
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SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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Last annotation update)
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Q77E16;
Q77E16;
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05-JUL-2004 (TERMELRel. 27, Le
E6 oncoprotein (B6 protein).
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RY MEDINES-9143744, bubMed=9292007;

RX MEDINES-9147474, bubMed=9292007;

RA Torneeello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Torneeello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Torneeello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Torneeello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Gorialdo E., Giraldo G.;

RT Sequence variations and viral genomic state of human papillomavirus

RT Sequence variations and viral genomic state of human papillomavirus

RT Sequence variations and viral genomic state of human papillomavirus

RT Sequence variations and viral genomic state of human papillomavirus

RT Sequence variations and viral genomic state of human papillomavirus

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MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
DeFilippis V.R., Ayala F.J., Villarreal L.P.;
"Evidence of diversifying selection in human papillomavirus type 16 E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S., Martins C.R.F.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                             SEQUENCE FROM N.A.
MEDLINE-20112892; PubMed=10644829;
MEDLINE-20112892; PubMed=10.04929;
Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to pp53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
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Subditted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A7237851; A245540.1; -.
REMBL; A7388057; CAB45100.1; -.
REMBL; A73880657; CAB45130.1; -.
REMBL; A70899551; AAM11875.1; -.
REMBL; A70899551; AAM11875.1; -.
REMBL; A70899551; AAM11875.1; -.
REMBL; A70899551; AAM11875.1; -.
REMBL; A715663; AAM51854.1; -.
REMBL; A71089555; Chost cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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J. Mol. Evol. 55:491-499(2002).
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NCBI_TaxID=10581;
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Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: June 28, 2005, 19:19:22
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Sequence 33593, A Sequence 205547, Sequence 58813, A Sequence 65774, A Sequence 145297,

Sequence 187372, Sequence 52907,

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Sequence 72, Application US/10128711
Publication No. US20030099634A1
GENERAL INFORMATION:
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES::153
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                       US-10-000-903-4
US-10-000-903-4
US-10-000-903-10
US-10-000-903-10
US-10-000-903-14
US-10-000-903-14
US-10-899-771-14
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US-10-368-046-10
US-10-367-955-10
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US-10-476-570-24
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US-10-484-063-27
US-10-858-384-2
US-10-367-057-16
US-10-472-724-2
US-09-367-309A-1
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APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: California
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   RESULT 1
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-133-210-280
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US-10-476-570-13
US-10-476-570-13
US-10-476-570-14
US-10-476-570-9
US-10-476-570-9
US-10-476-570-19
US-10-476-570-19
US-10-476-570-19
US-10-484-063-20
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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seq length: 200000000
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Perfect score:
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OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: MAILLERER, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOUNGAULT-VILLADA, Sandra
APPLICANT: BOUNGAULT-VILLADA, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived freeof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/76,570
CURRENT FILING DATE: 2003-11-04
PRIOR PLING DATE: 2003-05-03
PRIOR PLING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 23
LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH: LENGTH:
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
                           APPLICANT: MAILERE, BELLEAR
APPLICANT: MAILERE, BELLEAR
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-NORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: DEPTIDES 2010-103
FILE REPERENCE: 45636-507-108
CURRENT PAPLICATION NUMBER: PCT/FR02/01533
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN Ver. 2.1
SERO ID NO 22
LENGTH: 15
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100.0%; Score 48; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
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Matches 9; Conservative
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APPLICANT: Berzofeky, Jay
APPLICANT: Berzofeky, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Gulukota, Kamalakar
APPLICANT: Wong, Zhiping
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
FILE REFERENCE: BU-035AR
CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT PILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PATENTIN VET. 2.0
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                                                                                                                                                                                                                            FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-Jan-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Publication Wo. USZO040170644A1
Publication No. USZO040170644A1
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
             APPLICATION NUMBER: US 07/874,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 280, Application US/10133210 Publication No. US20030103964A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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2 IHDIILECV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-133-210-280
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LENGTH: 10
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16 IHDIILECV 24
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                                                                         GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE BETNATÉ
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: MAXTURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXTURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXTURE OF 1004476,570
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: DCT/FR02/01533
PRIOR FILING DATE: 2003-11-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOUTWARE PETENTION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COWNISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: MALLE SANTE SANTE
TITLE OF INVENTION: MALLE SANTE SANTE
FILE REFERENCE: 45636-5071-03
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
FRIOR FILING DATE: 2003-10-05-04
NUMBER OF SEQ ID NOS: 63
SONTWARE: Patentin Ver. 2.1
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                         Sequence 10, Application US/10476570
Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: artificial sequence
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LENGTH: 30
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; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment; OTHER INFORMATION: for E6 of HPV US-10-858-384-4
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US-10-476-570-9
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: BOURGAUIT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from BC
TITLE OF INVENTION: Mixture of peptides derived from BC
TITLE OF INVENTION: Mixture of peptides derived from BC
TITLE OF INVENTION: Mixture of peptides derived from BC
TITLE OF INVENTION: Mixture of peptides derived from BC
TITLE OF INVENTION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID NO 9
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial sequence
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Gaps ö

1 IHDIILECV 9

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Sequence 27, Application US/10484063
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: USC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR PRILOR DATE: 2004-01-19
; PRIOR APPLICATION NUMBER: 60/36,809
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 27.
                                                                                                                                                                                         APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERWO
APPLICANT: TORTOLERO-LUNA, GUILLERWO
APPLICANT: TORTOLERO-LUNA, GUILLERWO
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT PILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOOTHWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 48; DB 17; Length 151; 100.0%; Pred. No. 0.52; tive 0; Mismatches 0; Indels (
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ORGANISM: Human papillomavirus type 16
                                                                                                                            Sequence 20, Application US/10484063; Publication No. US20050048467A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Human papillomavirus
US-10-484-063-20
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Best Local Similarity 100.
Langery 9, Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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23 IHDIILECV 31
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SOFTWARE: Pater
SEQ ID NO 20
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Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynuclectides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 151
                                                                                                                                                                                                                                US-10-46-570-19
Sequence 19, Application US/10476570
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: MAILLERE, BERTANAL
APPLICANT: MAILLERE, BERTANAL
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
TITLE OF INVENTION: MAXILUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXILUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXILUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXILUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXILUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXILER: US/10/476,570
CURRENT APPLICATION NUMBER: PR 01 05980
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 19
LENGTH: 33
LENGTH: 33
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100.0%; Score 48; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
                           0; Indels
100.0%; Pred. No. 0.1; rative 0; Mismatches
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US-10-177-390-6
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-177-390-6
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RESULT 13 US-10-858-384-2

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DB 16; Length 171; 0.59; es 0; Indels

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Query Match
100.0%; Score 48; DB 16
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches
                         CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
FRIOR APPLICATION NUMBER: PCT/EP02/03271
FRIOR PILING DATE: 2002-03-22
FRIOR APPLICATION NUMBER: BP 01107271.77
FRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 171
                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Synthetic Construct US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: June 29, 2005, 03:24:07
Job time : 57.55 secs
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ORGANISM: Artificial Sequence
       FILE REFERENCE: 4121-154
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Publication No. US20040171806A1
GANEAL INFORMATION:
APPLICANT: Cid-Arregul, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
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                                                                                            APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OF B7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: F9 9907012
PRIOR APPLICATION NUMBER: F9 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VET: 3.2
SEQ ID NO 2
LENGTH: 158
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100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0: Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jackson, Amanda;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
; TITLE OF INVEXTION: Complexes and Methods of Using Same;
FILE REFERENCE: 21402-559
CURRENT PELLORION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR PELLOR DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList Version 0.1
; SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.54;
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US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
Sequence 2, Application US/10858384 Publication No. US20050033025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human Papillomavirus
                                                                          APPLICANT: CHOPPIN, JEANNINE APPLICANT: BOURGAULT VILLADA APPLICANT: GUILLET, JEAN-GER
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ORGANISM: Homo sapiens
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Best Local Similarity
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loigzuj Andia agogą 24

Sequence 5595, Ap Sequence 43808, A Sequence 4381, A Sequence 1331, A Sequence 6713, Ap Sequence 24727, A Sequence 24727, A Sequence 5486, Ap Sequence 568, Ap Sequence 60201, A Sequence 22181, A Sequence 22181, A Sequence 22434, A Sequence 22434, A Sequence 12, Appl

Sequence 12,

Run on:

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Sequency 73, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Settle, Alessandro
APPLICANT: Settle, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: His Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                        US-09-270-767-33608

US-09-489-039A-13381

US-09-489-039A-13381

US-09-638-937-4

US-09-638-937-6713

US-09-252-991A-17124

US-09-252-991A-27124

US-09-252-991A-27124

US-09-513-999C-558

US-09-513-999C-558

US-09-513-999C-558

US-09-270-767-60201

US-09-270-767-6201

US-09-28-991A-29181

US-09-270-767-4745

US-09-278-758-8022

US-08-28-808-808-802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: Diskette COMPUTER: DISKETE COPERATING SYSTEM: DOS
SOFTWARE: PAREISEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/05/339A
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGESTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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US-08-159-339A-73
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   STATE:
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Sequence 989, App
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15013, A
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                                                                                                                                                                                  June 28, 2005, 18:27:48; Search time 17.15 Seconds (without alignments) 39.174 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4,
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-197-484-72
US-09-601-72-73
US-09-90-612-72-73
US-09-90-523A-4
US-09-90-523A-4
US-09-90-523A-2
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-09-359-382-14
US-09-359-382-10
US-09-359-382-10
US-09-485-885-4
US-09-485-885-4
US-09-485-885-6
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US-09-950-046A-2
US-09-976-594-989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                  US-08-170-344-8
48
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Perfect score:
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Result No.

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JERNEAL INCOMATION:

APPLICANT: THIAM, KADER

APPLICANT: AURIAULT, CLAUDE

APPLICANT: GRAS-MASES, HELENE

APPLICANT: GRAS-MASES, HELENE

APPLICANT: COING, ESTELLE

APPLICANT: VERWAERDE, CLAUDIE

APPLICANT: VERWAERDE, CLAUDIE

APPLICANT: OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS

TITLE APPLICATION NUMBER: PCT/FR99/00259

PRIOR PLING DATE: 1999-02-06

PRIOR PLING DATE: 1999-02-06

PRIOR PLING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 281

SEQ ID NO 273

MANDER DE CLENTER DATE: 100

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US-09-601-729-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELITIVE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1995
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
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                                                                                                                                                                                                                                  ; Sequence 273, Application US/09601729; Patent No. 6683052; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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1 IHDIILECV 9
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US-08-197-484-72
is Sequence 72, Application US/08197484
is Patent No. 641931
is GENERAL INFORMATION:
is APPLICANT: VITIBLIO, Maria A.
is APPLICANT: SETTE, Alessandro D.
is APPLICANT: ELIS, Esteban
is APPLICANT: GRAY, Howard
it TILE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
it TILE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES:
is ADDRESSE:
is ADDRESSE:
is Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
is CONTACTORY.
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                                                                                  100.0%; Score 48; DB 3; Length 10; 100.0%; Pred. No. 0.0096; rive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSITECATION 1424
PRIOR APPLICATION NUMBER: US 07/935,811
PRIOR APPLICATION NUMBER: US 07/935,811
PRIOR APPLICATION NUMBER: US 07/874,491
PRIOR APPLICATION NUMBER: US 07/874,491
PRIOR APPLICATION NUMBER: US 07/827,682
PRIOR APPLICATION NUMBER: US 07/827,682
PRIOR APPLICATION NUMBER: US 07/749,568
PRIOR APPLICATION NUMBER: 1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,990
REPERRENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                            1 IHDIILECV 9
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        US-08-159-339A-73
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GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BUURCAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: PROTEFINE OF HPPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REPREBACHE: WOB1 AO INS
CURRENT FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-04-29
FRIOR PELICATION NUMBER: PCT/FRO0/01513
FRIOR APPLICATION NUMBER: PCT/FRO0/01513
FRIOR APPLICATION NUMBER: PCT/FRO0/01513
FRIOR PELING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 48; DB 3; Length 59; Best Local Similarity 100.0%; Pred. No. 0.058; Matches 9; Conservative 0; Mismatches 0; Indels
             APPLICANT: KLEIN, Michel H.
APPLICANT: TARTAGLIA, James
APPLICANT: TARTAGLIA, James
APPLICANT: MOINGEON, Phillipe
APPLICANT: MOINGEON, Phillipe
TITLE OF INVENTION: TREATMENT OF CERVICAL CANCER
FILE REFERENCE: 1038-982 MIS:jb
CURRENT APPLICATION NUMBER: US/09/390,027
CURRENT FILLING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: 60/099,291
EARLIER FILLING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 6
LENGTH: 59
LENGTH: 59
TYPE: PRI:
ORGANISM: Artificial Sequence
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GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09980523A ; Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human Papillomavirus
US-09-980-523A-2
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US-08-316-239B-3
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA,
APPLICANT: CONNAN, FRANCINE
APPLICANT: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: POT-FR00/01513
FRIOR PILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 30
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; Pred. No. 0.0096;
0; Mismatches 0; Indels
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100.0%; Pred. No. 0.029;
/ative 0; Mismatches 0; Indels
                     APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATORNEY/AGENT: 18-AUG-1991
NAME: PARTEINE 18-1910
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 543-5043
INFORMATION FOR SEQ ID NO: 72: SEQUENCE CHARACTERISTICS:
LEARCH: 10 amino acide
TYPE: amino acide
TYPE: amino acide
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09980523A Patent No. 6783763
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sequence 6, Application US/09390027;
Patent No. 623523;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human Papillomavirus
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                   SS: unknown
unknown
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MOLECULE TYPE: peptide
PCT-US95-02121-72
PRIOR APPLICATION DATA:
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US-08-860-165-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEB, Elizabeth Ann
APPLICANT: WEB, Elizabeth Ann
APPLICANT: WEB, Elizabeth Ann
APPLICANT: WEB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT FILING DATE: 1997-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14

LENGTH: 172
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                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION UNDRER: 35,205
REFERENCE/DOCKET UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPHONE: (703) 817-9453
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
APPLICATION NUMBER: US/08/316,239B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
18-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09359382; Patent No. 6306397; GENERAL INFORMATION: APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper, APPLICANT: WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                    FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-09-359-382-14
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APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF INVENTION: Cervical Cancer
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                     STAIL: 'AA
COMPUTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PARCHINE Release #1.0, Version #1.30
SOFTWARE: PARCHINE NESION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION A13:
CURSIFICATION 435
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REFERENCE/DOCKET: 35,205
REFERENCE/DOCKET: 35,205
REFERENCE/DOCKET: 1703) 817-9453
TELEPHONE: (703) 817-9453
TELEPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FERTILE FAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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ZIP: 20120-3400
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                       ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Jagtiani & Associates
6126 Rocky Way Court
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                       CITY: Cent
STATE: VA
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/note= "Xaa refers to stop codon in
the open reading frame."
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ORGANISM: Artificial Sequence
                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-117-083-10
                                                                                                                                                                                                                                                                                                                                                      31 IHDIILECV 39
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Patent No. 5719054
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
                   TITLE OF INTENTION VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER PLING DATE: 1997-09-22
EARLIER PLING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: WCT/AU95/00868
EARLIER PLING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157/94
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 48; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.17; Matches 9; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPOTER: IBM PC compatible

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,083

FLING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REGISTRATION NUMBER: 24,190

REGISTRATION INFORMATION:

TELEPHONINICATION INFORMATION:

TELEPHONINICATION INFORMATION:

TELEPHONINICATION INFORMATION:

TELEPHONINICATION 110PRAMINION:

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STREET: 4 Embarcadero Center, Suite 3400
GITY: San Francisco
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELER: 910 277299
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 182 amino acids TYPE: amino acids
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LOCATION: 1..182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-359-382-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 14
LENGTH: 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10. Application US/09359382

Sequence 10. Application US/09359382

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: NUMBER: US/09/359,382
CURRENT APPLICATION NUMBER: US/09/359,382
BEALLIER FILING DATE: 1997-09-22
BEALLIER PILING DATE: 1997-09-22
BEALLIER FILING DATE: 1995-07-23
BEALLIER FILING DATE: 1995-12-20
BEALLIER FILING DATE: 1995-12-20
NUMBER OF SEQ 1D NOS: 277
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
FILE OF INVENITY ON: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFRENCE: 1722/130
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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                      DB 1; Length 182;
100.0%; Score 48; DB 1; Lengture... 100.0%; Pred. No. 0.18; wiematches 0; Indels
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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Sequence 1, Application US/09367309A
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
; CURRENT PAPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; RIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SQOTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 48; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 0.26; Matches 9; Conservative 0; Mismatches 0; Indels
                                                               Query Match
100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
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Job time : 17.15 secs
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June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
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283416 Total number of hits satisfying chosen parameters: 283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-170-344-79 48 1 AVDLYHFLK 9 Title: Perfect score: Sequence: Scoring table: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	_	protein	nef protein - huma	nef protein - huma	nef protein - huma	HIV accessory prot	nef protein - huma	nef protein - huma		nef protein (clone		nef protein (clone		nef protein - huma		nef protein - huma	hypothetical prote	protein H06H21.1 [nef protein - huma	nef protein - huma	SNF2 protein - yea		served hyp	NEF protein - simi	protein -	protein -	NEF protein - simi	nef protein - simi
	ID	C75038	S03247	S03246	S24985	ASLJH3	S43467	JC7975	ASLJ12	ASLJFV	ASLJVL	S03245	833986	S03244	JC5400	QULJOO	QQLJZR	ASLJBR	T34461	F88678	S54385	144001	S15047	T16784	E70434	S61204	ASLJM4	S61205	S61206	S54852
	DB	2	7	~	~	-	7	~	Н	-	н	~	N	~	7	7	ч	-	7	N	7	-	~	~	ч	~	-	~	7	7
	Query Match Length	110	182	204	204	205	205	205	206	206	206	206	206	206	206	207	212	218	279	401	97	214	1703	107	132	209	229	238	239	239
۰ (Match	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	81.2	79.2	77.1	75.0	75.0	75.0	72.9	72.9	72.9	72.9	72.9	72.9	72.9
	Score	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	38	37	36	36	36	32	35	32	35	35	35	35
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Gaps

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Query Match

81.2%; Score 39; DB 2; Length 182;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels

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S24572	S54853	S61207	ASLJGN	853099	ASLJCZ	A70949	C59098	A34164	AC0609	A24075	E88197	T28055	T30811	T34274
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240	246	250	255	255	260	429	477	526	552	641	688	848	1425	2018
72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9
35	35	32	32	35	35	32	35	32	32	35	32	35	35	35
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 C75038 hypothetical protein PABO853 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 C;Accession: C75038 R;anonymous, Genoscope Submitted to the EMBL Data Library, July 1999 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str A;Reference number: A75001 A;Accession: C75038 A;Actus: preliminary A;Molecule type: DNA A;Residues: 1-110 <kaw> A;Cross-references: UNIPROT:09UZ59; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB502 A;Genetics: A;Genetics: A;Genetics:</kaw>
Query Match 81.2%; Score 39; DB 2; Length 110; Best Local Similarity 77.8%; Pred. No. 1.8; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Cy 1 AVDLYHFLK 9
 RESULT 2 \$03247 nef protein (clone C15) - human immunodeficiency virus type 1 (fragment) N;Alternate names: 3'-orf protein C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Jun-2000
C;Accession: S0344/ R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettew R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettew Nucleic Acids Res. 13, 8219-8229, 1985 A;Title: Polymorphism of the 3' open reading frame of the virus associated with the act A;Reference number: S03244; MUID:86067228; PMID:2999715
A, Accession: \$03247 A, Molecule type: mRNA A, Residues: 1-182 <rat> A, Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562 C, Genetics: A, Genetics: A, Corf; orf-F C; Superfamily: AIDS nef protein</rat>

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nef protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 843467
R;Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
R;Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
A;Title: Stability and proteolytic domains of Nef protein from human immunodeficiency v
A;Reference number: 843467; MUID:94229079; PMID:8174561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cidate: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
Cidate: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
Cidate: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
Cidector Profession: UCT975
Biochem. Biophys. Res. Commun. 305, 1061-1066, 2003
A;Title: Selection of peptides with affinity for the N-terminal domain of GATA-1: Ident A;Title: Selection of Jord Profession: UCT975
A;Residues: UCT975
A;Residues: 1-205 <SEC>
Cicomment: This protein, an accessory viral protein, acts as a nuclear regulatory facto binds p53 via its amino-terminal domain and protects cell against p53-mediated apoptos C;Keywords: GATA-1; Nef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: UNIPROT: Q9YYU9; UNIPROT: Q9WM30; UNIPROT: Q9PXW9; UNIPROT: O40177; UNI
                                                                                                                                                                                                                                                                                                                                                      Gaps
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nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)
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Pred. No. 3.6;
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Pred. No. 3.6;
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Pred. No. 3.6;
0; Mismatches
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   A; Molecule type: DNA
A; Mesidues: 1-205 < RAT>
A; Cross-references: UNIPROT: P03404
C; Genetics:
                                                                                                                                     A,Gene: nef; 3'-orf; orf-F
C,Superfamily: AIDS nef protein
C,Keywords: AIDS; immunodeficiency
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88.9%;
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AVDLSHFLK 91
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A;Molecule type: protein
A;Residues: 1-205 <FRE>
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C;Species: human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 824985
R;Harris, M.; Hislop, S.; Patsilinacos, P.; Neil, J.C.
Bubmitted to the EMBL Data Library, November 1991
A;Reference number: 824985
A;Reference number: 824985
A;Accession: S24985

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A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu A;Reference number: S03244; MUID:86067228; PMID:2999715
A;Accession: S03246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F. ature 313, 277-284, 1985.
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A;Reference number: A93353; MUID:85111123; PMID:2578615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1-204 <HAR>
A,Cross-references: UNIPROT:Q76352; EMBL:X63044; NID:g60123; PIDN:CAA44770.1; PID:g60124
C,Superfamily: AIDS nef protein
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                                                                                                                                                                                                          ef protein (clone HAT3) - human immunodeficiency virus type 1
Ablernate names: 3'-orf protein
Species: human immunodeficiency virus type 1, HIV-1
Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, BH10) N;Alternate names: 3'-orf protein; orf-F protein C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) (man) (c;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004 C;Accession: A04005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 3.6;
0; Mismatches
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0; Mismatches
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88.9%;
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A,Gene: nef; 3'-orf; orf-F
C,Superfamily: AIDS nef protein
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Best Local Similarity 88.9
Matches 8; Conservative
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AVDLSHFLK 68
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Matches 8; Conserv
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R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. Nature 313, 450-458, 1985
A;Title: NuClaic acid structure and expression of the human AIDS/lymphadenopathy retrov A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A04007
                                                                                                                                                              A; Cross-references: UNIPROT: P03405; GB: K02083; NID: g555008; PIDN: AAB59874.1; PID: g32856
C; Genetics:
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Accession: S03245
R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettew
Nucleic Acida Res 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acq
A;Reference number: S03244; MUID:86067228; PMID:2999715
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*Kesidues: 1-20G <CARA.
A;Cross-references: UNIPROT:Q78244; EMBL:211530; NID:g60192; PIDN:CAA77629.1; PID:g6020
C;Superfamily: AIDS nef protein
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C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Adression: S33986
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Reference number: S33986
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 3.6;
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Pred. No. 3.6;
0; Mismatches
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Pred. No. 3.6;
0; Mismatches
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                                                                                                                                                                                                                                             A,Gene: nef, 3'-orf, orf-F
C,Superfamily: AIDS nef protein
C,Keywords: AIDS, immunodeficiency
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88.9%;
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88.9%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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A,Gene: nef; 3'-orf; orf-F
C,Superfamily: AIDS nef protein
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8, Conservative
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84 AVDLSHFLK 92
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Best Local Similarity '
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                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-206 <MUE>
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A; Residues: 1-206 <RAT>
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Best Local S
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                                                                               Cidate: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A04006
A;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2208-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of A;Reference number: A94093; MUD:86177573; PMID:3008154
A;Accession: A04006
A;Molecule type: DNA
A;Residues: 1-206 <ARY>
A;Cross-references: UNIPROT:P04324; EMBL:M11840; NID:9328453; PIDN:AAA45001.1; PID:93284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA
A,Residues: 1-206 <WALD:
A,Cross-references: UNIPROT:P03406; GB:K02013; NID:G326417; PIDN:AAB59752.1; PID:G326425
A,Experimental source: isolate LAV-la
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C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Dacte: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Date: 17-May-1985 #sequence 0; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Hitle: Nucleotide sequence of the AIDS virus, LAV.
A;Fitle: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
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N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A04007
     N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 206;
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88.9%; Pred. No. 3.6;
ative 0; Mismatches
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C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ciccarelli, R.B.
submitted to the EMBL Data Library, March 1991
A;Reference number: S14607
A;Accession: S14609
                                                                                                                                                                                                                                                                                                                                                                        AjGene: nef; 3'-orf; orf-F
C; Superfamily: AIDS nef protein
C; Keywords: AIDS; immunodeficiency
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-206 <CIC>
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Nucleic Acids Res. 13, 8219-8229, 1985

A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acquay Reference number: S03244; MUID:86067228; PMID:2999715

A;Accession: S03244
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NyAlternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JQ0068
R;Spire, B; Sire, J; Zachar, V; Rey, F; Barre-Sinoussi, F; Galibert, F; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immunon A;Reference number: JQ0065; MUID:90034200; PMID:2806917
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9WM30; UNIPROT:Q9PXW9; UNIPROT:O40177; UNIPROT:O90179; UNIP
L:X03187
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A,Residues: 1-206 <MAC>
A;Cross-references: UNIPROT:Q9YVU9; UNIPROT:Q9WM10; UNIPROT:Q9PXW9; UNIPROT:O40177; UNIP
C;Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activitie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JCS400
R;Macreadie, I.G.; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.
Biochem, Biophys. Res. Commun. 212, 707-711, 1997
A;Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to yeast A;Reference number: JCS400; MUID:97271389; PMID:9126340
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nef protein (clone HXB2) - human immunodeficiency virus type 1
NiAlternate names: 3'-orf protein
C.Species: human immunodeficiency virus type 1, HIV-1
C.Spacie: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
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C;Species: Human immunodeficiency virus type 1, HIV-1
C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
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Pred. No. 3.6;
0; Mismatches 1; Indels
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Pred. No. 3.6;
0; Mismatches 1; Indels
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C;Superfamily: AIDS nef protein
C;Superfamily: AIDS nef protein #status predicted <MAT>
F;2-206/Product: nef protein #status
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88.9%;
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Best Local Similarity 88.9%;
Matches 8; Conservative
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A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
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Best Local Similarity 88.9
Matches 8; Conservative
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84 AVDLSHFLK 92
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A; Residues: 1-206 <RAT>
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Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,

Brownlie J.C., McGraw B.A., Martin W., Esser C., Ahmadinejad N.,

Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,

Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,

Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,

Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;

"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:

a streamlined genome overrun by mobile genetic elements.";

EMBL; AB017258; AAS14318.1; -.
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Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae,
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBI_TaxID=66077;
            Q8adho
Q8u156
Q8au26
Q8au26
Q78916
P88431
Q89wx3
Q74918
Q74918
Q9drp1
Q86820
28aij8
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                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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llarity 87.5%; Pred. No. 18;
Conservative 1; Mismatches
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OrderedLocusNames=WD0617;
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                        Q80156
Q8AU26
Q8AU28
Q74916
Q89WX3
Q8AU33
Q8AU33
Q8AU31
Q8Q8CD
Q9DRN9
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Pfam; PF01212; Beta_elim_lyase; 1.
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01-WAY-2000 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
Hypothetical protein.
ORFNames-PABO853;
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157 VELYHFLK 164
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Best Local Similarity
Matches 7; Conserv
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NCBI_TaxID=29292;
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                                                                                         June 28, 2005, 23:28:22; Search time 54.2473 Seconds (without alignments) 84.958 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q40241
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Gapop 10.0 , Gapext 0.5
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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
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            Rbodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J., Deacon N.;
Deacon N.;
Deacon N.;
Deacon N.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY00662; AAG15584.1; --
HSSP; P043-24; 1QA-
GO; GO:0005525; F:GTP binding; IEA.
Probon; PB00469; F-protein; 1.
Probon; PB00031; HIV Nef; 1.
AIDS; Lipoprotein; Myrisate.
SEQUENCE 110 AA; 12192 MW; 767997C8F181D3C4 CRC64;
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STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;

Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;

Weiss Complete sequence of the Pyrococcus furiosus genome.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AE010175; AAL80651.1; --

GO; GO:000577; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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MEDILINES 96190564; PubMed=8627686;
GAO F., MOLTISON S.G., Robertson D.L., Thornton C.L., Craig S.,
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
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88.9%; Pred. No. 8.5;
ive 0; Mismatches 1; Indels
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SEQUENCE 113 AA; 13433 MW; F91E60CEFF81C47D CRC64;
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1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein PP0527.
OrderedLocusNames=PF0527;
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Last sequence update)
Last annotation update)
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Best Local Similarity 77.8
Best Local Similarity 77.8
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01-OCT-2003 (
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Rhodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J.,
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88.9%; Pred. No. 8.5;
ive 0; Mismatches 1; Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY0060653; AAG15585.1;
GO; GO:0005525; F:GTP binding; IEA.
Ffam; PP00469; F:protein; 1.
Probom; PD000031; HIV Nef; 1.
AIDS; Lipoprotein; MyTistate.
SEQUENCE 110 AA; 12193 MW; 767337C8FB21D3C4 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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Viruses, Retroid viruses, Retroviridae, Lentivirus
VCBI_TaxID=11676;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
Truncated nef protein.
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les 8; Conservative
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69 AVDLYYYLK 77
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Q903T9
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Human immunodeficiency virus 1.
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ProDom, PD000031; HIV Nef; 1.
AIDS; Lipoprotein; Myristate.
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01-OCT-2003 (TrEMBLrel
Nef protein (Fragment)
Name=nef;
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   NCBI_TaxID=11676;
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                                    Hahn B.H.; "Molecular cloning and analysis of functional envelope genes from human immunodeficiency virus type 1 sequence subtypes A through G. The WHO and NIAID Networks for HIV Isolation and Characterization."; J. Virol. 70:1651-1667(1996).
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   von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
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Pred. No. 8.9;
0; Mismatches 1; Indels
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Allen B.E.;
Allen B.E.;
Submitted (NAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U27408; AAB06247.1; -.
GO; GO:0005525; F:GTP binding; IEA.
InterPro; IPR001558; HIV Nef.
Pfam; PF00469; F-protein; 1.
Propon; PD000031; HIV Nef; 1.
AIDS; Lipoprotein; Myristate.
NON TER
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
Last annotation update)
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NCBL_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Human immunodeficiency virus 1.
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88.9%;
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Matches 8; Conservative
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Name=nef;
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84 AVDLSHFLK 92
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Best Local Similarity
Matches 8; Conserv
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MEDLINE=96190564; PubMed=8627686;
Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig &
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
Hahn B.H.;
SEQUENCE FROM N.A.
MEDLINE=96190564; PubMed=8627686;
Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig :
Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
Von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.2%; Score 39; DB 2; Length 116; 88.9%; Pred. No. 8.9; ive 0; Mismatches 1; Indels
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Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                                                            Allen E.E.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U21401; AAB06243.1; -.
HSSP; P04324; 1ZEC.
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Allen E.E.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 116 AA; 13023 MW; 678FD1EF6C1AAB62 CRC64;
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Last annotation update)
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NCBL_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005525; F:GTP binding; IEA.
InterPro; IPR001558; HIV Nef.
Pfam; PF00469; F-protein; 1.
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GO; GO:0005525; F:GTP binding; IEA.
InterPro; IPR001558; HIV_Nef.
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SEQUENCE FROM N.A.
MEDLINE-92385194; PubMed=1515209;
MEDLINE-92385194; PubMed=1515209;
MEDLINE-92385194; PubMed=1515209;
MEDLINE-92385194; PubMed=1515209;
MEDLINE-92385194; New A.A.
M
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13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-2004 (Rel. 45, Last annotation update)
Se-OCT-2004 (Regative factor) (F-protein) (3'ORF) [Contains: C-terminal core protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.2%; Score 39; DB 2; Length 121;
88.9%; Pred. No. 9.4;
ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Length 121;
Pred. No. 9.4;
0; Mismatches 1; Indels
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Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; X63045; CAA44771.1; -
GO; GO:005525; F:GTP binding; IEA.
InterPro; IRR001558; HIV Nef.
Pfam; PF00469; P-protein; 1.
ProDom; PD000031; HIV Nef; 1.
AIDS; Lipoprotein; Myristate.
SRQUENCE 121 AA; 13506 MW; 0B9226A9052A2CC7 CRC64;
                                                  Harris M.P.G.;
Submitted (NOV-1991) to the EMBL/GenBank/DDBJ databases.
EMBL; X63040; CAA44766.1; -.
                                                                                                                                                                                                                                                                                             BB2417415263B423 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus 1.
Viruees; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIDS Res. Hum. Retroviruses 8:537-543(1992).
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                                                                                                                                                 GO; GO: 0005525; F: GTP binding; IEA. InterPro; IPR001558; HIV_Nef. Pfam; PF00469; F-protein; 1. Probom; PD000031; HIV_Nef; 1. AIDS; Lipoprotein; Myristate. SEQUENCE 121 AA; 13458 MW; BB24
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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[2]
SEQUENCE FROM N.A.
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ID NEF_HV1B1
AC P03404;
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Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
Fenamore E., Cao Y., Gao P., Kalama S., Kunstanan K.J., McDonald D.,
McWilliams N., Trkola A., Moore J.P., Wollinsky S.M.;
"Immunological and virological analyses of persons infected by human immunodeficiency virus type I while participating in trials of Trecombinant gpl20 subunit vaccines.";
J. Virol. 72:1552-1576(1998).
  Gaps
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A Wolinsky S., Hahn B.;

K Robert Condon Service Strain Stra
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  Indels
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(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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Mismatches
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01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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  Conservative
                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                       84 AVDLSHFLK 92
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                                                     1 AVDLYHFLK 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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01-JAN-1998 (
01-OCT-2003 (
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041540;
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  Matches
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Gaps

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PTM: Myristoylation is essential for inner plasma membrane targeting of Nef and virion incorporation and thereby for infectivity. Also required to reduce CD4 expression at the cell surface (By similarity). similarity) + + + <u>:</u> + <u>:</u> +

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Nature 313:277-284 (1985).

-!- FUNCTION: Early protein that seems to play a role in optimizing the host cell environment for viral replication without causing cell death by apoptosis. Enhances virus infectivity and
                                  MEDLINE=85111123; PubMed=2578615;
Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R., Josephs S.P., Doran B.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
                                                                                           "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
Retroid viruses; Retroviridae; Lentivirus.
                           SEQUENCE FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; MIS654; NEFSBH102.
InterPro; IPR001558; HIV Nef.
Pfam; PF00469; F-protein; 1.
Prodom; PD000011; HIV Nef; 1.
AIDS; Apoptosis; Early Nefein; Lipoprotein; Membrane; Myristate;
Phosphorylation; Repeat; SH3-binding; Viral immunoevasion; Virulence.
CHAIN
                                                                          stop codon and the protein is much shorter than in other isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal core protein (By similarity).
Anchor (By similarity).
Acidic cluster.
4 X 3 AA tandem repeats of P-X-X.
                          similarity).
MISCELLANEOUS: In this isolate a mutation in position 124 adds a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface
Phosphorylated on serine residues, probably by host PKC (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interaction, Nef-induced CD4 and MHC-I down-modulation and enhancement of infectivity (By similarity).

Involved in reducing surface MHC-I molecules by both impeding cell surface retrieval of MHC-I molecules and diverting them instead to the TGN (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEF HV1H2 STANDARD; PRT; 123 AA.
P04601; 009780; Q85587;
13.4MC-1987 (Rel. 05, Created)
15.4ML-1999 (Rel. 38, Last sequence update)
25.0CT-2004 (Rel. 45, Last annotation update)
Nef protein (Negative factor) (F-protein) (3'ORF) [Contains: C-
                                                                                                                             SIMILARITY: Belongs to the lentiviruses Nef protein family.
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N-myristoyl glycine (by host
0811735345F0EBBB CRC64;
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88.9%;
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Best Local Similarity 88.>°,
Best Local Similarity
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Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).

Name=nef;

Viruses; Retroid viruses; Retroviridae; Lentivirus

MEDLINE=86067228; PubMed=2999715;

SEQUENCE FROM N.A. NCBI_TaxID=11706;

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Mangasarian A., Piguet V., Wang J.-K., Chen Y.-L., Trono D.; "NeF-induced CD4 and major histocompatibility complex class I (MHC-I) down-regulation are governed by distinct determinants: N-terminal alpha helix and proline repeat of Nef selectively regulate MHC-I
Ratner L., Starcich B.R., Josephs S.F., Hahn B.H., Reddy E.P., L'Jvak K.J., Petteway S.R., Jr., Pearson M.L., Haseltine W.A., Arya S.K., Wong-staal F.
                                                                                                                                                                                                                                                                                                            Aiken C., Konner J., Landau N.R., Lenburg M.E., Trono D.; "Nef induces CD4 endocytosis: requirement for a critical dileucine motif in the membrane-proximal CD4 cytoplasmic domain."; Cell 76:853-864(1994).
                                                   with the acquired immune deficiency syndrome, human T-lymphotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Isolate HXB2/Clone R7;
PubMed=10707087; DOI=10.1038/35004038;
Piguet V., Wan L., Borel C., Mangasarian A., Demaurex N., Thomas
                                                                                                      SEQUENCE FROM N.A. MEDLINE=81299196; PubMed=3040055; Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.; Complete nucleotide sequences of functional clones of the AIDS
                                                                                                                                                                                                                         Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou
                                                                                                                                                                                                                                      Gallo R.C., Wong-Staal F.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   AIDS Res. Hum. Retroviruses 3:57-69(1987).
                                                                             Nucleic Acids Res. 13:8219-8229(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                         STRAIN=Isolate HXB2/Clone R7; PubMed=8124721;
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                                                                 virus type III.
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Nef downregulates MHC-I by a PACS-1- and PI3K-regulated ARF6 STRAIN-Isolate HXB2D; PubMed=12526811; Blagoveshchenskaya A.D., Thomas L., Feliciangeli S.F., Hung C.-H., FUNCTION, AND MUTAGENESIS OF MET-20; 62-GLU--GLU-65; PRO-72 AND "HIV-1 Nef protein binds to the cellular protein PACS-1 to downregulate class I major histocompatibility complexes."; Nat. Cell Biol. 2:163-167(2000).

molecules.Internalized molecules are sequestred to the trans-Golgi network (TGN). Also decreases cell surface CD4 antigen by interacting with the Src family kinase LCK thereby inducing LCK-CD4 dissociation and by increasing clathrin-dependent endocytosis of this antigen to target it to lysosomal degradation. Peroxisomal acyl-coenzyme A thioseter hydrolase I (PTEI) seems to be involved in this process (By similarity). May serve as a direct bridge between CD4 and the cellular endocytic machinery by interacting with beta-COP and adaptins. In consequence, surface MHC-I and CD4 endocytic pathway.";

Cell 11:853-866[2002).

-- FUNCTION: Early protein that seems to play a role in optimizing the host cell environment for viral replication without causing cell death by apoptosis (By similarity). Enhances virus infectivity and pathogenicity.

-- FUNCTION: Down-modulates surface MHC-I molecules through the PI3-Kinase-mediated ARF6 endosomal pathway. Combines with PACSI and accelerates the ARF6-dependent internalization of MHC-I

immune recognition decreased and infected cells are masked for

- - similarity).
 - PTM: Myristoylation is essential for inner plasma membrane targeting of Nef and virion incorporation and thereby for infectivity. Also required to reduce CD4 expression at the cell surface (By similarity).
- PTM: Phosphorylated on serine residues, probably by host PKC (By similarity)
- MISCELLANEOUS: In this isolate a mutation in position 124 adds a stop codon and the protein is much shorter than in other isolates (210 AA).
- SIMILARITY: Belongs to the lentiviruses Nef protein family. CAUTION: In clone pNL4-3 (AC P03406), it has been show that down-modulation of surface MHC class I molecules is independent of ARF6 endosomal pathway.

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InterPro; IPR001558; HIV Nef. Pfam; PF000469; F-protein; 1. ProDom; PD000031; HIV Nef; 1. AF033819; AAC82597.1; P04324; 1ZEC. HIV; K03455; NEF\$HXB2.

us-08-170-344-79.rup

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                                                                                                                                                                                                                                                                                                                                                                                                               Mediates dimerization, Nef-PTB1 interaction, Nef-induced CD4 and MHC-I down-modulation and enhancement of infectivity (By similarity).

Involved in reducing surface MHC-I molecules by both impeding cell surface retrieval of MHC-I molecules and diverting them instead to the TGN.

Cleavage (by viral proteinase PR) (By similarity).
AIDS; Apoptosis; Early protein; Lipoprotein; Membrane; Myristate; Phosphorylation; Repeat; SH3-binding; Viral immunoevasion; Virulence. CHAIN 1 123 Nef protein (By similarity).

CHAIN 58 123 C-terminal core protein (By similarity).

CHAIN 62 65 Acidic cluster.

DOMAIN 62 80 4 X 3 AA tandem repeats of P-X-X.

REPEAT 72 74 2.

REPEAT 72 74 2.

REPEAT 75 77 3.

Mediates dimerization, Nef-PTB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3-binding (By similarity).
N-myristoyl glycine (by host).
M->A: Complete loss of Nef-induced MHC-I down-modulation, MHC-I is internalized but not sequestred in TGN.
EEEE->AAAAA: Complete loss of Nef-induced MHC-I down-modulation, MHC-I is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 P-A: Complete loss of Nef-induced MHC-I down-modulation, MHC-I is not internalized; when associated with A-75.
75 P-A: Complete loss of Nef-induced MHC-I down-modulation, MHC-I is not internalized; when associated with A-72.
29 R-> G (in Ref. 1).
13692 MM; BS007753CCD244CF CRC64;
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EMBL, AX371158; AAR22204.1; -
GO; GO: 0005525; F: GTP binding; IEA.

InterPro.; IPRO01558; HIV Nef.
ProDom; PRO0469; F-protein; 1.
ProDom; PD000031; HIV Nef; 1.
ProDom; PD000031; HIV Nef; 1.
BLDS; Lipoprotein; Myristate.
NON TER.
SEQÜENCE 131 AA; 14700 MW; B5429C85C5E218F0 CRC64;
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Pred. No. 9.5;
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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      Query Match
      81.2%; Score 39; DB 2; Length 131;

      Best Local Similarity 88.9%; Pred. No. 10;

      Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

      Qy 1 AVDLYHPLK 9

      Db 84 AVDLSHPLK 92

      Search completed: June 29, 2005, 01:34:59

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US-10-833-745-58
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   Sequence 4197, Ap Sequence 2184, Ap Sequence 2184, Ap Sequence 2490, App Sequence 26, App 1 Sequence 2, App 1 Sequence 18, App 1 Sequence 62, App 1 Sequence 62, App 1 Sequence 62, App 1 Sequence 61, App 1
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12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S US-10-149-138-4197

S US-10-149-135-2184

6 US-10-149-135-2184

6 US-10-149-13-2-490

7 US-10-54-84-26

US-08-34-824-26

US-08-34-824-26

US-08-34-824-26

US-08-34-824-26

US-10-128-711-2

US-10-128-711-2

US-10-136-8338-18

US-10-136-838-65

US-10-442-909-11
                                                                                                                                                                                                                  Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                1717557 seqs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                      - protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
                                                                                                                     US-08-170-344-79
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Match Length
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Query Match
100.0%; Score 48; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;

Score

Result No.

2 6 4 5 9 7 6 6 11

Length 9; Indels

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SEQ ID NO 2490
LENGTH: 9
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFUGRATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sathay, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Clais, Esteban
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Reogh, Elissa
ITILE OF INVENTION: Inducing Cellular Immune Responses to
ITILE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
ITILE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
ITILE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
ITILE REPERENCE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR PELING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR APPLICATION NUMBER: US 08/105,146
PRIOR APPLICATION NUMBER: US 08/103,205
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR APPLICATION NUMBER: US 08/073,705
PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2184
                                                                                                                                                                                                              Sequence 2184, Application US/10149135 Publication No. US20040053822A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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                                AVDLYHFLK 9
AVDLYHFLK 9
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APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2000.0060007
CURRENT APPLICATION NUMBER: US/10/654,601
CURRENT FILING DATE: 2003-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2003-09-04

PRIOR APPLICATION NUMBER: US/09/239,043

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1999-01-27

PRIOR PILING DATE: 1998-11-10

PRIOR PILING DATE: 1999-11-10

PRIOR PILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 60/013,363

PRIOR APPLICATION NUMBER: US 60/013,363

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1995-06-03-13

PRIOR PILING DATE: 1995-06-03

PRIOR PILING DATE: 1995-11-20

PRIOR PILING DATE: 1994-12-01

PRIOR APPLICATION NUMBER: US 68/344,824

PRIOR PILING DATE: 1994-11-23

PRIOR PILING DATE: 1994-03-04

PRIOR PILING DATE
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US-10-654-601-2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 48; DB 16;
100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: PCT/USO0/33591
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SEQ ID NO 4197
LENGTH: 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2490, Application US/10654601
Publication No. US20050063983A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Livingston, Brian D.
Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sidney, John
Southwood, Scott
Vitiello, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kubo, Ralph T.
Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Gaps

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COUNTY: US

ZIP: 94105-1493

ZIP: 94105-1493

COMPUTER READALE FORM:
MEDIUU TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE: CDOS/MS-DOS
SOFTWARE: PACENTIN RElease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION NUMBER: US/08/197,484
APPLICATION NUMBER: US/08/197,484
APPLICATION NUMBER: US/07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US/07/874,491
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US/07/874,491
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US/07/874,682
FILING DATE: 20-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: PARMELE SE-SEEVEN W.
NAME: PARMELE SE-SEEVEN W.
NAME: PARMELE SE-SEEVEN W.
NAME: PARMELE SE-SEEVEN W.
NAME: PARMELE NUMBER: 11,990
REGISTRATION UNMBER: 11,990
REGISTRATION UNMBER: 11,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                              Score 39; DB 8; Length 9;
Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
ATTORNEY AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION UNDERS: 34,774
REFERENCE DOCKET NUMBER: 14137-80-1
TELECHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-6043
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 623-6793
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
FOOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-344-824-26
                                                                                                                                                                                                                                                                                                                                81.2%;
88.9%;
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9
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WS-10-751-845-120

Sequence 120, Application US/10751845

Publication No. US20050100928A1

GENERAL INPORMATON:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Urban, Robert G.

APPLICANT: Urban, Robert G.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES

PRICA PELICATION NUMBER: US/09/664,225

PRIOR PILING DATE: 2004-01-05

PRIOR PLING DATE: 1999-12-09

PRIOR PLING DATE: 1999-12-09

PRIOR PLING DATE: 1999-12-09

PRIOR PLING DATE: 1999-09-16

PRIOR PLING DATE: 1999-09-16

SOFTWARE: PASCE FOR Windows Version 4.0

SEQ ID NO 120

LENGTH: -
                                              Gaps
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Publication No. US20030152580A1

GENERAL INFORMATION:
APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
ITILE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
CITY: San Francisco
STATE: California
COUNTRY: USA
      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIONS
SOFTWARE: PATORIL Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILLING DATE: 23-NOV-1994
CLASSIPICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 48; DB 17; 100.0%; Pred. No. 1.6e+06; wiematches 0;
  Query Match 100.0%; Score 48; DB 17; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-751-845-120
                                                                                                                      1 AVDLYHFLK 9
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US-10-360-836-62
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                     SEQ ID NO 58
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                                                                                                        FEATURE:
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APPLICANT: University of Nairobi
TITLE OF INVENTION: Improvements in or Relating to Immune Responses to HIV
TITLE OF INVENTION: MAL/C12481/M
CURRENT APPLICATION NUMBER: US/10/168,843A
CURRENT APPLICATION NUMBER: US/10/168,843A
SOFTWAREN FILING DATE: 2002-09-24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                          81.2%; Score 39; DB 14; Length 9; 88.9%; Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-079-167-58

US-10-079-167-58

US-10-079-167-58

Sequence S9, Application US/10079167

Publication No. US20030138454A1

GENERAL INFORMATION:

APPLICANT: Hill, Adrian V.S.

APPLICANT: Gilbert, Sarah C.

APPLICANT: Schneider, Joerg

ITILE OF INVENTION: Vaccination Method

FILE REFERENCE: 2907-1000-001

CURRENT APPLICATION NUMBER: US/10/079,167

CURRENT FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-10-09

PRIOR FILING DATE: 1999-6-06-09

PRIOR FILING DATE: 1999-06-09

PRIOR FILING DATE: 1999-06-09

PRIOR FILING DATE: 1999-06-09

PRIOR FILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13

PRIOR FILING DATE: 2001-09-13

PRIOR PILING DATE: 2001-09-13
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                               TOPOLGGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-128-711-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/10168843A Publication No. US20030108562A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Medical Research Council
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                               TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                          Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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RESULT 10

US-10-360-836-62

Sequence 62, Application US/10360836

Sequence 62, Application No. US2030185854A1

GENERAL INFORMATION:

APPLICANT: Zavala, Fidel

APPLICANT: Zavala, Fidel

APPLICANT: Zavala, Fidel

TITLE OF INVENTION: DARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS

TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS

TITLE OF INVENTION: AND MALICHANICLES

CURRENT APPLICATION NUMBER: US/10/360,836

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: 60/354,963

PRIOR APPLICATION NUMBER: 60/354,963

NUMBER OF SEQ ID NOS: 86

NUMBER OF SEQ ID NOS: 86
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Sequence 11, Application US/10442909

Publication No. US20040001845A1

GENERAL INFORMATION:

APPLICANT: Alteld, Marcus

APPLICANT: Walker, Bruce

CURRENT PROBOTON: 2402-010

CURRENT PILING DATE: 2003-05-20

FILE REPERBUCE: 2002-05-20

FRIOR APPLICATION NUMBER: 60/382,120

FRIOR APPLICATION NUMBER: 60/382,120

FRIOR APPLICATION NUMBER: 60/382,120

FRIOR PILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 77

SEQ ID NO 11

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.2%; Score 39; DB 14; Length 9; 88.9%; Pred. No. 1.6e+06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                          81.2%; Score 39; DB 14; Length 9; 88.9%; Pred. No. 1.6e+06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: human immunodeficiency virus (HIV-1)
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; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-11
                                                                                                                                          ) OTHER INFORMATION: CTL EDITOPE OF HIV-1 nef
US-10-079-167-58
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.5
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                             TYPE: PRT
ORGANISM: Unknown
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             Gaps
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APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Blanchart, Magdalena
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Methods and Reagents for Vaccination
TITLE OF INVENTION: Methods and Reagents for Seponse
FILE REPERENCE: 2907.100-00
CURRENT APPLICATION NUMBER: US/10/686,943
FRIOR APPLICATION NUMBER: US/09/454,204
FRIOR APPLICATION NUMBER: US/09/454,204
FRIOR APPLICATION NUMBER: US/09/454,204
FRIOR APPLICATION NUMBER: US/09/454,204
FRIOR APPLICATION NUMBER: US/09/680,913
FRIOR APPLICATION NUMBER: US/09/680,913
FRIOR APPLICATION NUMBER: US/09/6120
FRIOR FILING DATE: 1999-06-09
FRIOR FILING DATE: 1999-06-09
FRIOR FILING DATE: 1997-06-09
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APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Glibert, Sarah C.
APPLICANT: Schneider, Jordan
APPLICANT: Plebanski, Magdalena
APPLICANT: Blanchard, Tomas
APPLICANT: Blanchard, Tom
TITLE OF INVENTION: Mchods and Reagents for Vaccination
TITLE OF INVENTION: Mhich Generate A CD8 T Cell Immune Response
FILE REFERRICE: 2007.100-000
CURRENT FILING DATE: 2004-04-28
PRIOR APPLICATION NUMBER: US/10/686,943
PRIOR PILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: US/09/454,204
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             Indels
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             Mismatches
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                                                                                                                                                                                                                                                                                         ; Sequence 58, Application US/10833439; Publication No. US20040175365A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/10833745 Publication No. US20040191272A1 GENERAL INFORMATION:
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             8; Conservative
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Matches 8; Conservative
                                                                            1 AVDLYHFLK 9
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ORGANISM: Unknown
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US-10-833-745-58
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TITLE OF INVENTION: Recombinant Poxvirus for Chimeric Proteins of the Human Immunodef
FILE REPERENCE: 976-14 PCT/US
CURRENT APPLICATION NUMBER: US/10/469,256
CURRENT FILING DATE: 2003-08-27
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.1
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Fublication No. US20040131594A1
GENERAL INFORMATION:
APPLICANT: Hill, Adrian V.S.
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Gilbert, Sarah C.
APPLICANT: Schneider, Jorg
APPLICANT: Schneider, Jorg
APPLICANT: Smith, Geoffrey L.
APPLICANT: Blanchard, Tomas
APPLICANT: Manchard, Tomas
APPLICANT: Manchard, Tomas
APPLICANT: Manchard, Tomas
APPLICANT: Manchard, Tomas
APPLICANT: WorkINON: Which Generate A CD8 T Cell Immune Response
FILE REFERENCE: 2907.1000.000
CURRENT APPLICATION NUMBER: US/10/653,624
CURRENT APPLICATION NUMBER: US/09/454,204A
FRIOR PILING DATE: 1999-12-09
FRIOR APPLICATION NUMBER: GB 97 11957.2
FRIOR APPLICATION NUMBER: GB 97 11957.2
FRIOR PILING DATE: 1999-06-09
FRIOR FILING DATE: 1999-06-09
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81.2%; Score 39; DB 15; Length 9; 88.9%; Pred. No. 1.68+06; ive 0; Mismatches 1; Indels
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; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-10-653-624-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 78
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                          US-10-469-256-44
; Sequence 44, Application US/10469256
; Publication No. US20040073008A1
; GENERAL INFORMATION:
                                                                     8; Conservative
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Matches 8; Conservative
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Best Local Similarity
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Matches 8; Conserv
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ORGANISM: Unknown
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      Query Match
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PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR FILING DATE: 1998-06-09
NUMBER OF SEQ 1D NOS: 78
NUMBER OF SEQ 1D NOS: 78
SOFTWARE: PASLESC for Windows Version 4.0
SEQ 1D NO 58
LENGTH: 9
TYPE: PRT
ORGANISM: Unknown
FEATURE: ACT OF SEQ 1D NOS: 78
ORGANISM: Unknown
FEATURE: OF SEQ 1D NOS: 78
ORGANISM: Unknown
SEATURE: OF SEQ 1D NOS: 78
ORGANISM: Unknown
FEATURE: 100 OF SEQ 1D NOS: 78
ORGANISM: Unknown
FEATURE: 745-58
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1 AVDLSHFLK 9
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Run on:

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Sequence 53, Appl
Sequence 372, Ap
Sequence 5172, Ap
Sequence 4133, Ap
Sequence 26, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 2433, A
Sequence 466, Ap
Sequence 4966, Ap
Sequence 1956, Ap
Sequence 165, App
                                                                                                                                                                                                                                                                                                              Sequence 1
Sequence 1
Sequence 5
                           Sequence
Sequence
Sequence
          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 125, Application US/08159339A

Sequence 125, Application US/08159339A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban

TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
US-08-679-493A-76
US-08-815-809-5
US-08-815-809-5
US-09-1079-587-43
US-09-079-587-43
US-09-824-574-3
US-09-134-000C-4133
US-09-134-000C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-134-00C-4133
US-09-248-082-4
US-09-248-796A-24433
US-09-107-532A-4966
US-09-248-796A-24433
US-09-107-532A-4966
US-09-248-796A-24433
US-09-107-532A-4966
US-09-248-796A-17687
US-09-248-796A-17687
US-09-248-796A-17687
US-09-489-039A-12056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY-AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAILDIE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
      233
266
280
280
224
1703
174
634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                              811.2
811.2
775.0
772.9
772.9
770.8
770.8
770.8
68.8
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USA
33.
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US-08-159-339A-125
      Sequence 125, App
Sequence 46, Appl
Sequence 1153, Ap
Sequence 1153, Ap
Sequence 2, Appli
Sequence 186, Appl
Sequence 186, Appl
Sequence 186, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                       June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-159-339A-125
US-09-543-608A-46
US-09-239-0431-2490
US-08-197-484-2
US-08-197-484-2
US-09-601-729-186
PCT-US95-02121-2
US-09-601-729-186
PCT-US95-02121-2
US-08-370-476-43
US-08-370-476-43
US-08-370-476-43
US-08-371-45-408-16
US-08-145-708A-16
US-08-145-708A-16
US-08-145-708A-16
US-08-145-708A-16
US-08-145-708A-16
US-08-145-708A-16
US-08-145-108-96
US-08-148-5518-644
US-08-188-5518-644
US-08-188-5518-644
US-08-188-5518-644
US-08-188-5518-644
US-09-18-09-24
US-09-952-060-10
US-09-952-060-11
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
                                                                                                                                                                                                                 US-08-170-344-79
48
                                                                                                                                                                                                                                                              1 AVDLYHFLK 9
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                   OM protein
                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
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Result No.

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; Sequence 1153, Application US/08159339A; Patent No. 6037135; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AVDLYHFLK 9
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UKS-09-2490

Sequence 2490, Application US/09239043D

SEREAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Utiello, Maria A.

APPLICANT: Livingston, Brian D.

APPLICANT: Calis, Esteban

APPLICANT: Kubo, Ralph T.

APPLICANT: Calis, Esteban

APPLICANT: Calis, Esteban

APPLICANT: Calis, Esteban

APPLICANT: Calis, Howard M.

APPLICANT: Chesnut, Robert

APPLICANT: Using Peptide and Nucleic Acid Compositions

FILE REFERENCE: 2060.006007

CURRENT APPLICATION NUMBER: US 09/189,702

PRIOR APPLICATION NUMBER: US 08/978,291

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                                                                                                                                                                                                                                                                                 Sequence 46, Application US/09543608A

Sequence 46, Application US/09543608A

Patent No. 6602510

GENERAL INFORMATION:

APPLICANT: Fikes, John D.

APPLICANT: Sette, John D.

APPLICANT: Southwood, Scott

APPLICANT: Southwood, Scott

APPLICANT: Cells, Esteban

APPLICANT: Keogh, Elissa A.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen

TITLE OF INVENTION: Peptides and Vaccine Compositions

FILE REFERENCE: 018623-012710US

CURRENT APPLICATION NUMBER: US/09/543,608A

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 52

SOFTWARE: FSELED for Windows Version 3.0

SEG ID NO 46
                                      100.0%; Score 48; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 48; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Standard Peptide 940.06
US-09-543-608A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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1 AVDLYHFLK 9
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US-08-159-339A-125
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PRIOR FILING DATE: 1997-03-12
PRIOR PLILING DATE: 1996-03-13
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1995-06-05
PRIOR PLILOR DATE: 1995-06-05
PRIOR PLILOR DATE: 1995-06-05
PRIOR PLILOR DATE: 1994-12-01
PRIOR PLILOR DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-07-01
PRIOR PLILING DATE: 1994-07-01
PRIOR PLILING DATE: 1994-07-01
PRIOR PLILING DATE: 1994-03-04
PRIOR PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR PLILING DATE: 1994-03-06
PRIOR PLILING DATE: 1994-03-09
PRIOR PLILING DATE: 1994-03-09
PRIOR PLILING DATE: 1994-03-09
PRIOR PLILING DATE: 1994-03-03-04

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US-09-239-043D-2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 48; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Grey, Howard M.
APPLICANT: Settle, Alessandro
APPLICANT: Settle, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: CA COUNTRY: USA

ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: WEADER: Blen Lauver:
NAME: WEADER: Blen Lauver
```

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APPLICANT: THIAM. KADER
APPLICANT: THIAM. KADER
APPLICANT: THIAM. KADER
APPLICANT: THIAM. KADER
APPLICANT: THE GRAS-MASSE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: USRWARRDE, CLAUDIE
APPLICANT: USRWARRDE, CLAUDIE
APPLICANT: TURE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARWACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: US/09/601,729
CURRENT FILING DATE: 2000-11-20
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US-09-454-204A-58

i Sequence 58, Application US/09454204A

j Retent No. 6663871

i GENERAL INFORMATION:
    APPLICANT: Hill, Adrian V.S.
    APPLICANT: Gilbert, Sarah C.
    APPLICANT: Schneider, Jorg
    APPLICANT: Schneider, Jorg
    APPLICANT: Blanchard, Toma
    APPLICANT: Smith, Geoffrey L.
    APPLICANT: Blanchard, Tom
    APPLICANT: Blanchard, Tom
    APPLICANT: Blanchard, Tom
    APPLICANT: Math, Geoffrey L.
    APPLICANT: Math, Geoffrey L.
    APPLICANT: Smith, Geoffrey L.
    APPLICANT: Blanchard, Tom
    APPLICANT: NUMENTION: Which Generate A CD8 T Cell Immune Response
    CURRENT APPLICATION: Which Generate A CD8 T Cell Immune Response
    CURRENT PILING DATE: 1999-12-09
    PRIOR APPLICATION NUMBER: US/09/454,204A
    PRIOR APPLICATION NUMBER: GB 97 11957.2
    PRIOR PILING DATE: 1999-06-09
    NUMBER OF SEQ ID NOS: 78
    SEQ ID NOS: 78
    SEQ ID NOS: 78
    SEQ ID NOS: 78
    INENGTH: 0
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88.9%; Pred. No. 4.1e+05;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-09-454-204A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 186, Application US/09601729
Patent No. 6683052
GENERAL INFORMATION:
                                             unknown
                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
          LENGTH: 9 amino acids
                                 TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                             1 AVDLYHFLK 9
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-601-729-186
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US-08-197-484-2
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US-08-197-484-2
; Sequence 2, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
    APPLICANT: VITIELLO, Maria A.
    APPLICANT: CHESTNUT, Robert W.
    APPLICANT: SETTE, Alessandro D.
    APPLICANT: GRAY, Howard
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
    TITLE OF INVENTION: CTL IMMUNITY
    NUMBER OF SEQUENCES: 15.3
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend Khourie and Crew
    STREET: Steat Street Tower, One Market Plaza
    CITY: San Francisco
    STATE: California
    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                    Length 9;
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MEDIUM TYRE: B193

COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.25
SOFTWARE: PEPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAMME: PARMELE-
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION NUMBER: 14137-26-4
                                                                                                                                                                                                                                                                                                                                                                        4.1e+05;
                                                                                                                                                                                                                                                                                                                                            81.2%; Score 39; DB 3;
88.9%; Pred. No. 4.1e+05
trive 0; Mismatches
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                               INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS.
LENGTH: 9 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide US-08-159-339A-1153
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVDLYHFLK 9
                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                   TYPE: amino a STRANDEDNESS:
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1; Indels

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Sequence 43, Application US/08484905
; Sequence 43, Application US/08484905
; Patent No. 597651
; GENERAL INFORMATION:
    APPLICANT: Mottez, Estelle
    APPLICANT: Mottez, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; TITLE OF INVENTION: Determinan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 39; DB 2; Length 16; 88.9%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy Disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: 33,332
REGISTRATION NUMBER: 33,332
REFERENCE/COKET NUMBER: 33,332
Pred. No. 4.1e+05;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
   88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
       Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 88.9
Matches 8; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AVDLSHFLK 14
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                                                                                                                        1 AVDLYHFLK 9
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3Y: linear
                                                                                                                                                                       1 AVDLSHFLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING TITLE OF INVENTION: CTL INMUNITY

NUMBER OF SEQUENCES: 153

COMPUTER EADABLE FORM:

MUDIOUM TYPE: PLOPPY disk

COMPUTER IBM FOR COMPATIBLE OF COMPATIBLE OF SEQUENCES: 153

COMPUTER IBM FOR COMPATIBLE OF SEQUENCES: 153

COMPUTER IBM FOR COMPATIBLE OF SEQUENCES: 153

COMPUTER IBM FOR COMPATIBLE OF SEQUENCES: 150

SOFTWARE: BATCHING DATA:

APPLICATION NUMBER: PCT/US95/02121

FILING DATE: 16-FEB-1995

FILING DATE: 16-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/197,484

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,811

FILING DATE: 27-APR-1992

PRIOR APPLICATION NUMBER: US 07/827,682

FILING DATE: 27-APR-1992

PRIOR APPLICATION NUMBER: US 07/827,682

FILING DATE: 28-AUG-1991

APPLICATION NUMBER: US 07/749,568

FILING DATE: 28-ANG-1991

APPLICATION NUMBER: US 07/749,568

FILING DATE: 28-AUG-1991

APPLICATION NUMBER: US 07/749,568

FILING DATE: 28-AUG-1991

APPLICATION NUMBER: 114137-26-4PC

TELEFONMENT/AGENT INFORMATION:

NAME: PARMENCE/DOCKET NUMBER: 114137-26-4PC

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION INFORMATION:

TELEFONMUNICATION NUMBER: 129-360

TELEFONMUNICATION NUMBER: 129-360

TELEFONMUNICATION NUMBER: 129-360

TELEFONMUNICATION NUMBER: 27-9600

TELEFONMUNICATION NUMBER: 129-360
                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: peptide US-09-601-729-186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.2%; Score 39; DB 4; Length 9; Best Local Similarity 88.9%; Pred. No. 4.1e+05; Matches 8; Conservative 0; Mismatches 1; Indels
   PRIOR APPLICATION NUMBER: PCT/FR99/00259
PRIOR FLING DATE: 1999-02-05
PRIOR PPLICATION NUMBER: 98 01439
PRIOR FLING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 186
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVDLYHFLK 9
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STRANDEDNESS: unk
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                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
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Gaps
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1; Indels
                                                                                                             US-08-481-985B-43; Sequence 43, Application US/08481985B; Patent No. 6011146; GENERAL INFORMATION:
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DB 5;

81.2%; Score 39;

Query Match

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### 18-20-1-1-1-23

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 16;
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Pred. No. 0.41;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Floppy disk
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
PILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
DATO: COMPUTER: US 07/166
DATO: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
DATO: COMPUTER: COMPUTER: US 07/792,473
PRIOR APPLICATION NUMBER: US 07/792,473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REPERBNCE, DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 3;
Pred. No. 0.41;
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88.9%;
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: peptide US-08-370-476-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 AVDLSHFLK 14
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Best Local Similarity
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APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kouzilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Abstated, Jean-Pierre
APPLICANT: Abstated, Jean-Pierre
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                              CITI: WABLILLY CONTY.

STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/1818
FILING DATE: 07-DOS-1991
CLASSIFICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION NUMBER: 25,146
REFERENCYS/DOCKET NUMBER: 25,146
REFERENCYS/DOCKET NUMBER: 03-406-4000
TELEPHONE: 202-408-4000
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 3,
Pred. No. 0.41;
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Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.9%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AVDLYHFLK 9
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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US-08-370-476-43
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US-08-417-210A-96

| Sequence 96, Application US/08417210A
| Patent No. 5863542
| CENERAL INFORMATION:
| APPLICANT: PACLETI, DAMES
| APPLICANT: COX, WILLIAM I.
| APPLICANT: COX, WILLIAM I.
| TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
| TOWNER OF SEQUENCES: 148
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
| STREET: SJ0 PIFTH AVENUE
| COTTY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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COUNTRY: USA
ZIP: 10036
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: OS-APR-1995
CLASSIFICATION: 435
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.2%; Score 39; DB 2
88.9%; Pred. No. 0.99;
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NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333
                                                                                                                                                                    FILING DATE:
CLASSIFICATION NUMBER: US/US/331,133
FRIOR PAPPLICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/145,708
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
ATTORNEY/GENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRANICH/OCKET NUMBER: UF135
TELECOMMINICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sin
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COUNTRY: U
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Patent No. 596614

GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Yeares, Barbara A.
APPLICANT: Yearencto, Janet K.
ITLE OF INVENTION: Retroviral Superantigens, Superantigen
ITILE OF INVENTION: Peptides, and Methods of Use
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.2%; Score 39; DB 1; Length 38; 88.9%; Pred. No. 0.99; tive 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 29-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/ACENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPRAX: 904-372-8600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-145-708A-16
                                   6 AVDLSHFLK 14
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AVDLYHFLK 9
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USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 32606
                                                                                                                US-08-145-708A-16
                                                                                                                                                                                                                                                                                                                                                                                                  STATE: FI
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Gaps

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DNA-directed DNA p
DNA polymerase del
DNA-directed DNA p
dnaK-type molecula
dnaK-type molecula
dnaK-type molecula
hypothetical prote
dnaK-type molecula
bypothetical prote
sulfate permease f
probable Athila re
dnaK-type molecula
dnaK-type molecula
DNA-directed RNA p
pagypol polyprotei
pagypol polyprotei
probable iron-sulf
dnaK-type molecula
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                                                                                                                                                                     June 28, 2005, 23:32:21; Search time 12.5275 Seconds (without alignments) 76.805 Million cell updates/sec
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   5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283416 seqs, 96216763 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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T18222
S38890
S38890
S38890
T18222
T43715
T143715
T10500
T10500
T10408
T10408
T10408
T10408
T10408
T10408
T10508
T
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Maximum DB seq length: 200000000
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52
1 KVFPYALINK 10
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Query
Match Length DB
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pir2:*
pir3:*
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Perfect score:
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No.
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C84512 probable retroelem T20698 hypothetical prote F89792 hypothetical prote b90372 mcD protein - McD b00372 mcD protein - McD b00372 protein alcohol dehydrogen 160973 alcohol dehydrogen c837050 protein hypothetical protein - McD b00372 pr	ALIGNMENTS	1.7.7) III - yeast (Candida albicans) III sion 10-Sep-1999 #text_change 27-Oct-2003 naracterisation of the POL3 gene from Candida 7149294; PMID:8996102	zinc fi hotif hotif hotif ore 38; ed. No. Mismat	(Candida albicans) sion 15-Oct-1999 #text_change 09-Jul-2004 , November 1998 from GB/EMBL/DDBJ ; EMBL:AL033396, PIDN:CAA21949.1
501 2 2 2 3 3 4 5 1 1 1 2 2 3 3 4 5 1 1 2 2 3 3 4 5 1 1 2 3 3 4 5 1 1 2 3 3 4 5 1 1 2 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		(EC 2.7 merase] ce_revis cular ch MUID:97	rase ansferase; nger CCCC m inger CCCC 73.1%; Sc 87.5%; Pr	east (revisi i.A. rary, ted fr
######################################		scted DNA polymerase (E aste names: DNA polymerase (10-Sep-1999 #sequence—iion: JC5777; S6677 7. 159-165, 1996 Isolation and moleculation: JC5757; Mulion: JC5757; Mulion: JC5757; Mulion: JC5757; Mulion: JC5757; Mulion: JC5757; Mulion: JC5757 Ile type: DNA references: EMBL:X8880 submitted to the EMBL	(; DNA polymer ucleotidyltra jon: zinc fin sgion: zinc fin simularity 7; Conservat	PPYLLINK 741 a delta chain - 3 dida albicans 11822 3. Rajandream, 12, Rajandream, 11822 Ilminary, transl. Ilminary, transl. 1038 <brs 1038="" 1<="" <brs="" td=""></brs>
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ESULT 1	Abdire Abdire Specie Specie Specie Nolan, Nolan, Molecus Residu Cross-	Gigenetics: A;Genetics: A;Genetics: C;Superfamily: DNA polymerase C;Keywords: nucleotidyltransferase; F;942-961/Region: zinc finger CCCC nr;992-1010/Region: zinc finger CCCC ncccy Match Best Local Similarity 87:3%; Pr Matches 7; Conservative 0; Matches 3; POYALINK 10 QY 3 FPYALINK 10	RESULT 2 T1822 DNA DOLYMERASE delta chain - y C1822 C2 Date: 15-Oct 1999 #sequence C3 Accession: T1822 R Barrell, B.G.; Rajandram, M Submitted to the EMBL Data Lib A; Reference number: Z18831 A; Accession: T1822 A; Status: preliminary; transla A; Rotus: preliminary; transla A; Rotus: preliminary; transla A; Rotus: preliminary; transla A; Rotus: preliminary; Cross-references: UNIPROT:P4 C; Genetics: A; Note: Cal5A5.06c C; Superfamily: DNA polymerase

S21880 S71171 T46574 T15791

albicar

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A; Molecule type: DNA
A; Residues: 1-658 < LEH3-
A; Cross-references: UNIPROT: Q12752; EMBL: X75673; NID: 9429117; PIDN: CAA53369.1; PID: 9429
R; Lehnen, L.P.; Duniec, J.; Hardham, A.R.
submitted to the EMBL Data Library, November 1993
A; Reference number: 838889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: involved in protein folding and assembling/disassembling of protein comp C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004 C;Accession: S38890; S38889 R;Lehnen, L.P.; Wilkinson, J.M.; Hardham, A.R. Astenier, L.P.; Wilkinson, J.M.; Hardham, A.R. A;Bescription: A Phyrophthora cinnamomi gene encodes a protein similar to rat glucose A;Reference number: S38890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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A;Residues: 158-658 <LE2>
A;Cross-references: EMBL:X75672; NID:g429115; PIDN:CAA53368.1; PID:g429116
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                                                                                                                               dnaK-type molecular chaperone GRP78/BiP - Phytophthora cinnamomi
N'Alternate names: heat shock protein BiP
C'Species: Phytophthora cinnamomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 2; Length 658;
Pred. No. 25;
2; Mismatches 2; Indels
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A, Experimental source: ATCC 22342
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2; Mismatches
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.2%;
60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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KHFPYKVVNK 142
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113 KLLPYLLVNK 122
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806 FPYLLINK 813
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nes 6; Conserv
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Nucleic Acids Res. 20, 375, 1992
A;Title: Nuclectide sequence of the POL3 gene encoding DNA polymerase III (delta) of Sac A;Reference number: S19638; MUID:92158636; PMID:1741270
A;Accession: S19638
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-1097 <BAL>
A;Cross-references: UNIPROT:P15436; EMBL:Z74150; NID:g1431141; PIDN:CAA98669.1; PID:g143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-188,'R', 190-203,'D', 205-346,'YL',349,'LRNHS',355,'VMCYSD',364-646,'HY',656
A; Residues: 1-188,'R',190-203,'D', NID:93479; PIDN:CAA33504.1; PID:93480
R; Boskovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine submitted to the EMBL Data Library, February 1996
A; Reference number: 867406
A; Accession: 867417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-1097 (8DS)
A; Residues: 1-1097 (8DS)
A; Residues: 1-1097 (8DS)
A; Residues: 1-1097 (8DS)
B; Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.
Yeast 12, 1077-1084, 1996
A; Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerev A; Reference number: $72094; MUID:97051597; PMID:8896274
A; Accession: $72105
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                                                                                                                                                                                                                                                                             DNA-directed DNA polymerase (EC 2.7.7.7) III large chain - yeast (Saccharomyces cerevisi
N/Alternate names: DNA-directed DNA polymerase delta large chain; protein D2366; protein
                                                                                                                                                                                                                                                                                                                                                                                                                      J.M.; Bo
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A; Cross-references: EMBL:X61920; NID:g4190; PIDN:CAA43922.1; PID:g4191
A; Cross-references: EMBL:X61920; NID:g4190; PIDN:CAA43922.1; PID:g4191
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
B; Boulet, A.; Simon, M.; Faye, G.; Bauer, G.A.; Burgers, P.M.J.
EMBO J. 8, 1849-1854, 1989
A; Title: Structure and function of the Saccharomyces cerevisiae CDC2 gene encoding the A; Reference number: S05743; MUID:89356661; PMID:2670563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues: 1-1097 <SAI>
Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64911.1; PID:g1199547
Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                               C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence revision 23-Aug-1996 #text change 09-Jul-2004
C;Accession: S67644; S19638; S05743; S67417; S72105; S19058
R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, submitted to the Protein Sequence Database, July 1996
A;Reference number: S67629
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27;
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ed. No. 26;
Mismatches
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A;Cross-references: MIPS:YDL102w; SGD:S0002260
Pred. No.
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87.5%;
                               Conservative
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C,Superfamily: DNA polymerase
                                                                                                                                     734 FPÝLLÍNK 741
                                                                              3 FPYALINK 10
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Best Local Similarity
Matches 7; Conserv
Best Local Similarity
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                       Matches
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dnaK-type molecular chaperone bipA [imported] - Aspergillus awamori C;Species: Aspergillus awamori

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hypothetical protein F16J13.30 - Arabidopsis thaliana ($\text{Species}$) Arabidopsis thaliana ($\text{mouse-ear}$ cress)
C;\text{Species}$ Arabidopsis thaliana ($\text{mouse-ear}$ cress)
C;\text{Species}$ Ara-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;\text{Accession: T06603}
M;\text{Milbert, H.} Braun, M.;\text{Holzer, E.};\text{Brandt, A.};\text{Duesterhoeft, A.};\text{Bancroft}
submitted to the Protein Sequence Database, April 1999
A;\text{Reference number: Z15789}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sulfate permease family protein VC2031 [imported] - Vibrio cholerae (strain N16961 serc
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*Residues: 1-521 <HEI. *
A,Cross-references: UNIPROT:Q9KQG7; GB:AE004277; GB:AE003852; NID:g9656571; PIDN:AAF951
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiSpecies: Vibrio cholerae
CiSpecies: Wibrio cholerae
CiDate: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
CiAccession: B82127
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J
Abardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9SZ61; EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.30 A;Experimental source: cultivar Columbia; BAC clone F16J13
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Pred. No. 50;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.3%; Score 35; DB 2; Length 338;
60.0%; Pred. No. 31;
tive 1; Mismatches 3; Indels
      DB 2; Length 85;
                                                                  2; Indels
                                                               3; Mismatches
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C;Superfamily: integral membrane protein HP0228
   67.3%; Score 35;
50.0%; Pred. No.
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85.7%;
   Query Match 67.3
Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                 21 KLLPYKIVNK 30
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nes 6; Conserva
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A; Molecule type: DNA
A; Residues: 1-338 <BEV>
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Best Local S:
Matches 6
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02909
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuel submitted to the Protein Sequence Database, February 1999
A;Reference number: Z14766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dnak-type molecular chaperone - Douglas fir (fragment)
Nylternate names: luminal binding protein
C;Species - Beeudotsuga menziesii (Douglas fir)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09500
C;Accession: T09500
S;Tranbarger, T.1; Missra, S:
Submitted to the EMBL Data Library, May 1995
A;Description: The molecular characterization of a set of cDNAs differentially expressed
                                                     Ryon Gemeren, 1.A.; Punt, P.J.; Drint-Kuyvenhoven, A.; Broekhuijsen, M.P.; van't Hoog, Gene 198, 43-52, 1997
A.Title: The ER chaperone encoding bipA gene of black Aspergilli is induced by heat shock A; Accession: T43723
A; Accession: T43723
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-672 < vAN>
A; Residues: 1-672 < vAN>
A; Cross-references: UNIPROT: P59769; EMBL: Y08867; PIDN: CAA70090.1
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C;Superfamily: heat shock protein 70
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A;Molecule type: mRNA
A;Residues: 1-85 <TRA>
A;Cross-references: UNIPROT:Q40924; EMBL:249764; NID:g1006701; PID:g1006702
C;Function:
21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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A;Residues: 1-1791 <BEV>
A;Cross-references: UNIROT:09SUD1; EMBL;AL035524
A;Experimental source: cultivar Columbia; BAC clone T13J8
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C;Superfamily: heat shock protein 70
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133 KHFPYKVVNK 142
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|S1 FPYSLVNR 158
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A; Description: involved in protein folding and assembling/disassembling of protein comp C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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C;Species: Campylobacter jejuni
C;Accession: 841868
R;Bustamante, V.; Sanchez-Lopez, F.; Bobadilla, M.; Puente, J.L.; Calva, E.
A;Reference number: 841868
A;Reference number: 841868
A;Accession: 841868
A;Molecule type: DNA
A;Residues: 1-694 < RUS>
A;Accession: Campylobacter control of the control of t
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A;Gene: rpoB
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywordes: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 2
Pred. No. 82;
2; Mismatches
                                                                                                                                                                                                                                    Score 35; DB Pred. No. 64; 2; Mismatches
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A;Genetic code: SGC3
C;Superfamily: ATP-dependent Lon protease
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ilarity 60.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
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117 KLVPYKIINK 126
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189 IFPKALLNK 197
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Best Local Similarity
Matches 6; Conserva
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A;Accession: H84474
A;Stcus: preliminary
A;Molecule type: DNA
A;Residues: 1-616 <STO>
A;Residues: 1-616 <STO>
A;Cross-references: UNIPROT:Q9ZQ03; GB:AE002093; NID:g4388724; PIDN:AAD19762.1; GSPDB:GN
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-663 <MRO>
A;Cross-references: UNIPROT:024581; EMBL:U58209; NID:g1575129; PIDN:AAC49900.1; PID:g157
C;Function:
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A; Actual translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mesidues: 1-663 - 4MD.
C; Function: 1.663 - 4MD.
C; Function: 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1.001 - 1
                                                                        C;Accession: H84474

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Axture 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Accession: 1090 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04080
R;Wrobel, R.L.; OBrian, G.R.; Boston, R.S.
Gene 204, 105-113, 1997
A;Title: Comparative analysis of BiP gene expression in maize endosperm.
A;Reference number: Z15191; MUID:98094260; PMID:9434171
A;Reference number: Z15191; MUID:98094260; PMID:9434171
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NiAlternate names: lumenal binding protein cBiPe2
CiSpecies: Zea mays (maize)
CiSpecies: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CiAccession: T04078
CiAccession: T04078
Gene 204, 105-113, 1997
                      C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 59;
4; Mismatches
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117 KLVPYKIINK 126
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172 KLFPYSLVGE 181
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A,Map position: 2
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Goffard N., Prangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaten C.,
Boistame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zanlou-Meyer M., Zuvanovic I., Bolotin-Pukuhara M., Thierry A.,
Mincker P., Souciet J.L.,
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Saccharomycetales, Saccharomycetaceae, Kluyveromyces.
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Q8Klx9
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Q9rdg3
Q9kg37
Q9kg97
Q9kg97
Q9kg97
Q9kg97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.8%; Score 42; DB 2; Length 519; 70.0%; Pred. No. 14; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382126; CAG98304.1; -.
SEQUENCE 519 AA; 58955 MW; 1A196B9E6F89E3AF CRC64;
                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                  ALIGNMENTS
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QGTBIS
QGTBLQ
QBGTBLQ
QBGYC7
QBGYC7
Q7V1I6
Q9X561
Q7RTX2
Q9XQG7
Q9XQG7
Q9XQG7
Q9ENG3
Q9ENG3
BNAK BUCAP
Q9ENG3
BNAK BUCAP
                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity.
ORFNames=KLLAOF11341g;
Kluyveromyces lactis NRRL Y-1140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 70.0%;
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
231
331
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616
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663
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KVFPYSTLNK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KVFPYALINK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=284590;
Genolevures;
 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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OGCKE3

OGCKE3

OGCKE3

DT 25-0

DT 25
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ID 07
AC 07
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candida alb
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yarrowia li
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saccharomyc
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aspergillus
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aspergillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                  June 28, 2005, 23:28:22; Search time 60.2747 Seconds (without alignments) 84.958 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ashbya
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09jad2
09jad3
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                                                                                                                                                                                                                                                                                                             1612378
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            1612378 seqs, 512079187 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         077164
Q6NXA8
DPOD CANAL
Q6BH09
Q6CH16
DPOD ARATH
Q755K6
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GR78_ASPKA
GR78_ASPNG
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Q6CPW9
                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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Q6AFH3
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Q7DM14
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Q7YYD2
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Q9JAD3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
                                                                                                                                                                US-08-170-344-78
52
1 KVFPYALINK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length DB
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4445
608
658
346
4496
672
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672
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672
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Perfect score:
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                                                                        OM protein
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Maximum DB
                                                                                                                                                                                                  Sequence:
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                                                                                                         Run on:
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EMBL; X88804; CAA61282.1; -.
EMBL; AL033396; CAA21949.1; -.
                                                    and mouse cDNA sequences.";
                                                                                                                                                                                          Query Match
Best Local Similarity 75.v.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                  185 FPYSIINK 192
                                                                                                                                                                                                                                                         3 FPYALINK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                        SEQUENCE FROM N.A.
                                                                                                   TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DNA) (N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CA124;
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TISSUERCE TROM N.A.

TISSUERCIDENCE TROM N.A.

TISSUERCIDENCE TROM N.A.

TISSUERCIDENCE T., Felingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

A trausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A thopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wullahy S.J.,

Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe, J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                      Samuelson J., Feld J.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1998) to the heat shock protein 70 family.
EMBL; AF082519; AAC64065.1; -..
HSSP; P04475; 105L.
R GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006457; P:protein folding; IEA.
GO; GO:0006986; P:response to unfolded protein; IEA.
R InterPro; IPR000886; ER target_S.
R InterPro; IPR0001023; HSP70.
R InterPro; IPR001023; HSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 661;
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                                                                                                                                                                                                                                                                                                                                                                                        73546 MW; 8FC1384158DFD922 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:77058.
          (TrEMBLrel. 08, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                            PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
ATP-binding; Heat shock.
                                                                                                                                                                                                                                                                                                                                                                                                               80.8%; Score 42; DB 2; 70.0%; Pred. No. 18; ive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA.
 Created)
                                     70 kDa heat shock protein Hsp70-Bip
                                                        Entamoeba histolytica.
Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||| :|||
113 KLFPYKIINK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KVFPYALINK 10
                                                                                                                                                                                                                                                                                                                                                                                        661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                             STRAIN=HM-1:IMSS;
            01-NOV-1998
                         01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                    Name=BiP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6NXA8;
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Matches
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M. Redriguez A.C., Grimmond, D. Schmarto, N., Werger R.M., Butterfield Y.S., REZPATIEN M.I., Skalaka U., Smallus D.E., Schmarto, A., Schmarto, A., Schmarto, M., Stara M.A., ```

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RGO; GO:0008408; F:3'-5' exonuclease activity; IEA.

GO; GO:000387; F:DNA binding; IEA.

GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.

GO; GO:0006260; F:DNA-ceplication; IEA.

RICEPTO; IPR006132; DNA_pol_B.

RICEPTO; IPR006133; DNA_pol_B.

RICEPTO; IPR006133; DNA_pol_B.

RICEPTO; IPR006134; DNA_pol_B.

RICEPTO; IPR005829; Sug_transporter.

R Pfam; PF00136; DNA_pol_B.

R Pfam; PF00136; DNA_pol_B.

R PFRNTS; SN00486; POLBC; 1.

R RPNTS; SN00486; POLBC; 1.

R PROSITE; PS00116; DNA_POLZ; 1.

R PROSITE; PS00116; PNA_POLZ; 1.
 73.1%; Score 38; DB 2; Length 1054; 87.5%; Pred. No. 1.7e+02; ive 0; Mismatches 1; Indels
 1054 AA; 120974 MW; 12A1BB47D60B6E84 CRC64;
 Wincker P., Souciet J.L.;
 Local Similarity 87.5
hes 7; Conservative
 PRELIMINARY;
 Nature 430:35-44(2004)
 752 FPYLLINK 759
 3 FPYALINK 10
 NCBI_TaxID=284591;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 STRAIN=CLIB99;
 STRAIN=CLIB99;
 Senoscope;
 SEQUENCE
 Query Match
 06CHI6;
 Q6CHI6
 Best Loca
Matches
 RESULT 6
Q6CHI6
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AR PIR; T18222; T18222.

AR HSSP; Q56366; 10HT.

BR InterPro; IPR006132; DNA_DOl_B.

InterPro; IPR006133; DNA_DOl_B exo.

BR InterPro; IPR006134; DNA_DOl_B region.

BR InterPro; IPR006134; DNA_DOl_B region.

BR InterPro; IPR006134; DNA_DOl_B region.

BR PRO136; DNA_DOl_B rol_B.

BR MRT; SM0486; POLBC; 1.

BR SMART; SM0486; POLBC; 1.

BR PROSTTE; PS00116; DNA POLYMERASE B; 1.

BR ROSTTE; PS00116; DNA POLYMERASE B; 1.

BR NOSTTE; PS00116; DNA POLYMERASE B; DNA POLYMERASE; PS00116; DNA POLY
 ö
 Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Prangeul L., Asigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Rabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A. Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellorz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P., Souciet J.L.;
"Genome evolution in yeasts.";
 Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-1- CATALYȚIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P46588 Candida albicans DNA polymerase delta catalytic
 + {DNA}(N).
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
EMBL; CR382139; CAG91022.1; -.
GO; GO:0005634; C:nucleus; IEA.
 PRT; 1054 AA.
 PRELIMINARY;
 734 FPYLLINK 741
 3 FPYALINK 10
 SEQUENCE FROM N.A. STRAIN=CBS767;
 SEQUENCE FROM N.A.
 STRAIN=CBS767;
 Genolevures
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Gaps

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Genolevures;
A pulon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,
Senon-Meyer M., Zivanovic I., Bolotchin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P46588 Candida albicans DNA polymerase delta catalytic
 ORFNames=YAL10A08426g;
Yarrowia lipolytica CL1B99.
Bukaryota; Fungi; Saccomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
 -i- SIMILAKITY: Belongs to the DNA polymerase type-B family EMBL; CR382127; CAG83802.1; -.
PRT; 1072 AA.
 "Genome evolution in yeasts.";
1D DTT TD ```

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.1%; Score 38; DB 1; I
87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1092 AA.
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Pfam; PF03104; DNA pol B, 2.
PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBS; 1.
TIGRFAMS; TIGR00592; pol2; 1.
PROSITE; PS00116; DNA POLYMERASE_B; 1.
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Interpro; IPR006133; DNA_pol_B exo.
Interpro; IPR006134; DNA_pol_B_region.
Interpro; IPR004578; Pol2.
                                                                                                  EMBL; AB019227; BAA96899.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=33169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=AFL189W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFL189Wp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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DNA Res. 7:31-63(2000).
-!- FUNCTION: This polymerase possesses two enzymatic activities: DNA synthesis (polymerase) and an exonucleolytic activity that degrades single stranded DNA in the 3' to 5' direction.
-!- CATALYHIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Heterodimer with subunits of 125 kDa and 50 kDa. The 125 kDa subunit contains the polymerase active site and most likely the active site for the 3'-5' exonuclease activity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
SUBCELULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
MISCELLANBOUS: In eukaryotes there are five DNA polymerases:
alpha, beta, gamma, delta, and epsilon which are responsible for
different reactions of DNA synthesis.
SIMILARITY: Belongs to the DNA polymerase type-B family.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 44, Last annotation update)
17-OCT-2001 (Rel. 44, Last annotation update)
18-OCT-2001 (Rel. 44, Last annotation u
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MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0003401; F:3'-5' exonuclease activity; IEA.

R GO; GO:000367; F:DNA binding; IEA.

GO; GO:000387; F:DNA-directed DNA polymerase activity; IEA.

R GO; GO:000166; F:nucleotide binding; IEA.

R INCEPTO: IPRO06132; DNA_DOl_B.

R INTERPO: IPRO06133; DNA_DOl_B.

R INTERPO: IPRO06134; DNA_DOl_B.

R INTERPO: IPRO06134; DNA_DOl_B.

R INTERPO: IPRO06134; DNA_DOl_B.

R INTERPO: IPRO06134; DNA_DOl_B.

R Pfam; PF00136; DNA_DOl_B.

R Pfam; PF00136; DNA_DOl_B.

R PRINTS; RNO046; DNAPOLB.

R SWART; SNO0486; POLBC; 1.

R PROSITE; PS00116; DNA_DOLS; 1.

R PROSITE; PS00116; DNA_DOLS; 1.

R PROSITE; PS00116; DNA_DOLWERASE B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Pred. No. 1.8e+02;
0; Mismatches 1; Indels
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Best Local Similarity 87.5%;
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Q9LVN7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabata S.;
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            DAY X MANAGEMENT OF A MANAGEME
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PubMed=15001125; DOI=10.1126/science.1095781;
Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S., Mohr C., Pohlmann R., Lucdi P., Choi S., Wing R.A., Flavier A., Gaffney T.D., Philippsen P.;
"The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome.";
science 304:304-307(2004).
-!- CAMALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
HSSP; Q56366; 1QHT.

REPPROSED TO THE CONTROL OF TH
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
EMBL; AEO1699; AAS53185.1; -.
AGD; AFL189W; -.
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GO:0008408; F:3'-5' exonuclease activity; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0003877; F:DNA-directed DNA polymerase activity; IEA.
GO:0001667; F:nucleotide binding; IEA.
GO:0016740; F:transferase activity; IEA.
GO:0006260; P:DNA replication; IEA.
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DPOD YEAST
P15436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lafontaine I., de Montigny J., Marck C., Neuvegilse C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnein S., Beckerich J.M., Beyne E., Bleykaeten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., Ge Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L.,
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                    ORFNames=CAGLOGO73489;
Candida glabrata CBS138.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Candida glabrata strain CBS138 chromosome L complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            + {DNA}(N).

-1- SIMILARITY: Belongs to the DNA polymerase type-B family.
EMBL; CR380958; CRG62067.1;
GO; GO:0005634; Cinucleus; IEA.
GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
GO; GO:0003877; F:DNA binding; IEA.
GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
GO; GO:000166; P:DNA replication; IEA.
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                                                                         Length 1092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.
DNA replication; DNA-binding; DNA-directed DNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00592; pol2; 1.
PROSITE; PS00116; DNA POLYMERASE B; 1.
DNA replication; DNA-binding; DNA-directed DNA polymerase;
                                                      Score 38; DB 2; Length 105. Pred. No. 1.8e+02;
                                  1092 AA; 123389 MW; 2C97077B54B7D6DD CRC64;
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                                                                                                            0; Mismatches
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InterPro; IPR006133; DNA_pol_B exo.
InterPro; IPR006134; DNA_pol_B_region.
InterPro; IPR004578; Pol2_
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Pfam; PF03104; DNA pol B exo; 1.
PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome evolution in yeasts.";
Nature 430:35-44(2004).
                                                                     73.1%;
87.5%;
                                                                                        Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SM00486; POLBC;
                                                                                                                                                                               801 FPYLLINK 808
                                                                                                                                              3 FPYALINK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CBS138;
                 Transferase.
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05-JUL-2004
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                                    SEQUENCE
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                                                                       Query Match
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Gaps

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MEDLINE=97313263; PubMed=9169867;

MEDLINE=974; PubMed=97, Bureckner M., Blugeon C., Hankeln T., Hankeln T., Moster H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S., Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricko N., Moeller-Aloer S., Nussbaumer B., Paricko N., Moeller-Aloer S., Nussbaumer B., Pohl T.M., Parist M., Salom D., Saluz H.P., Satz J.E., Saren A.-M., Schwaffer M., Schwidt B.R., Schweider C., Scholler P., Schwarz S., Votet M., Volckaert G., Wagner G., Wambutt R., Wedler E., Wedler H., Woelfi S., Harris D.E., Mannin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D., Odell C., Oliver K., Rajandream M.A., Richards C., Shore L., Analos E., Berno A., Carpenter J., Chen E., Cherry J.M., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Mosedale D., Nakahara K., Manath A., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Manath A., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Manath A., Schram S., Schramm S., Schroeder M., Shogren T., Shroff N., Winnath A., Yelton M.A., Botstein D., Ding H., Davis R.W., Johnston M., Andrews S., Brinkman R., Ding H., Davis R.W., Johnston M., Andrews S., Brinkman R., Ding H., Ding H., Davis R.W., Johnston M., Andrews S., Brinkman R., Ding H., Ding H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
STRAIN=S288C / FY1679;
STRAIN=S288C / FY1679;
MEDLINE=97051597; PubMed=8896274;
DOI=10.1002/(SICI)1097-0061(199609)12:10B<1077::AID-YEA8>3.3.CO;2-Q;
Saiz J.E., Buitrago M.J., Garcia R., Revuelta J.L., del Rey F.;
"The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevisiae chromosome IV contains the KIN28, MSS2, PHO2, POL3 and DNA genes, and six new open reading frames.";
                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-0C7-1996 (Rel. 34, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
DNA polymerase delta catalytic subunit (EC 2.7.7.7) (DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boulet A., Simon M., Faye G., Bauer G.A., Burgers M.J.;
Structure and function of the Saccharomyces cerevisiae CDC2 gene
encoding the large subunit of DNA polymerase III.";
EMBO J. 8:1849-1854(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morrison A., Sugino A.;
MucLeotide sequence of the POL3 gene encoding DNA polymerase III
(delta) of Saccharomyces cerevisiae.";
Nucleic Acids Res. 20:375-375(1992).
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                           Name=POL3; Synonyms=CDC2, TEX1; OrderedLocusNames=YDL102W;
                                                                                                                                                             1097 AA
                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
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                                                                                                                                                             STANDARD;
                                           805 FPYLLINK 812
3 FPYALINK 10
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                                                                                                                                                                                                                                                                                                                                              ORFNames=D2366;
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E of strain NRRL Y-

1101 AA.

Created)

(TrEMBLrel. 28, (TrEMBLrel. 28, PRELIMINARY;

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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Kluyveromyces lactis strain NRRL Y-1140 chromosome 1
1140 of Kluyveromyces lactis.
                                                                                                                                 25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                Q6CPW9
                                                   O6CPW9
                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-1293091; PubMed=1648480;
Simon M., Giot L., Faye G.;
"The 3' to 5' exonuclease activity located in the DNA polymerase delta
subunit of Saccharomyces cerevisiae is required for accurate
Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K., Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L., Kirsten T., Kucaba T., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaddin M., Wilson R., Waterston R., Albermann K., Hani J., Heumann K., Kleine K., Mewes H.-W., Zollner A., Zaccaria P.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome IV.", Nature 387:75-78(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LISUBUNIT: Heterodimer with subunits of 125 kDa and 55 kDa. The 125 kDa subunit contains the polymerase active site and most likely the active for the 3'-5' exonuclease activity.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: In eukaryotes there are five DNA polymerases: alpha, beta, gamma, delta, and epsilon which are responsible for different reactions of DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERM: PR00136; DNA POL B; 1.
Pfam; PR00104; DNA POL B = x0; 1.
Pfam; PR00104; DNA DOL B = x0; 1.
SMART; SM00486; POLBS.
TIGREAMS; TIGR00592; pol2; 1.
TIGREAMS; TIGR00592; pol2; 1.
TIGREAMS; TIGR00592; pol2; 1.

BROSITE; PS00116; DNA POLYMERASE B; 1.
DNA replication; DNA-Dinding; DNA-directed DNA polymerase;
Exonuclease; Hydrolase; Nuclear protein; Transferase;
ZN FING 1009 1027 C4-type (Potential).
ZN FING 1056 1074 C4-type (Potential).
CONFLICT 78 79 DV -> EL (in Ref. 1 and 2).
SEQUENCE 1097 AA; 124590 MW; 16542589BB4168DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 1097;
Pred. No. 1.8e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Germonline; 140344; -.
SGD; 8000002260; CDC2.
InterPro; IPR006417; DNA_POL_B.
InterPro; IPR006417; DNA_POL_B.
InterPro; IPR006434; DNA_POL_B.
InterPro; IPR006434; DNA_POL_B.
InterPro; IPR006434; DNA_POL_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X15477, CAA33504.1, ALT_SEQ.

EMBL, X61920; CAA43922.1; -.

EMBL, X95644, CAA64911.1; -.

EMBL, Z74150; CAA98669.1; -.

PIR, S67644; RNBYL3.

HSSP, Q56366; IQHT.
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87.5%;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {DNA} (N).
          SO THE FEW WAS A COUNTY OF THE
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Goffard N., Frangeul L., Beckerich J.M., Beyne E., Bleykasten C.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Oztar-Kalogeropoulos O.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.,
"Strong M., Mincker P., Souciet J.L.,
"Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
ORFNames=KLÍAAOEO1606g;
Kluyveronnyces lactis NRRL Y-1140.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + (Junilariur)

C -1 - SIMILARIURY

R GO; GO:0005634; C:nucleus; IEA.

R GO; GO:0005634; C:nucleus; IEA.

GO; GO:000567; F:DNA binding; IEA.

GO; GO:000387; F:DNA binding; IEA.

GO; GO:000186; F:Nuclected DNA polymerase activity; IEA.

R GO; GO:000186; F:Nuclected DNA polymerase activity; IEA.

GO; GO:0000186; F:Nuclectide binding; IEA.

GO; GO:0000186; F:Nuclectide binding; IEA.

R GO; GO:0000187; F:DNA pol B.

R InterPro; IPR006132; DNA pol B.

InterPro; IPR006133; DNA pol B.

InterPro; IPR006134; DNA pol B.

R InterPro; IPR006134; DNA pol B.

R Pfam; PF00104; DNA pol B.

R PRINTS; RR00106; DNAPOLB.

R SWART; SM0486; POLBC; 1.

R SWART; SM0486; POLBC; 1.

R PROSITE; PS00116; DNA POLYMERASE B; 1.

R PROSITE; PS00116; DNA POLYMERASE B; 1.
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Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101 AA; 124365 MW; B45D1DD9837C8203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 430:35-44(2004)
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                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=NRRL Y-1140;
                                                                                                                                                  NCBI_TaxID=284590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [DNA] (N).
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Gaps

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7; Conservative

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TISSUE=Embryo;

X PubMed=12477932; DDI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rapleton M., Soares M.B., Donaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R Jones S.J., Marra M.A.;

R Jones S.J., Marra M.A.;

R "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Leptomonas
NCBI_TaxID=5686,
           "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yurchenko V.;
L. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
R. Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351198; AAK30251.1; -.
R. HSSP; Q56366; 1QHT.
R. GO; GO:000367; F:DNA binding; IEA.
GO; GO:0003867; F:DNA binding; IEA.
GO; GO:000166; F:nucleotide binding; IEA.
R. GO; GO:00166; F:nucleotide binding; IEA.
R. GO; GO:00166; F:nucleotide binding; IEA.
R. GO; GO:001679; P:DNA replication, IEA.
R. InterPro; IPR006172; DNA_POl B.
R. InterPro; IPR006134; DNA_POl B.
R. PFan; PF00136; DNA_POL B.
R. PRINTS; PR00106; DNAPOLB.
R. PRINTS; PR00106; DNAPOLB.
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-VINR-2004 (TrEMBLrel. 26, Last annotation update)
DNA polymerase delta catalytic chain (EC 2.7.7.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.1%; Score 38; DB 2; Length 1109; 87.5%; Pred. No. 1.8e+02; ive 0; Mismatches 1; Indels
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                                                                               Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
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1es 7; Conservative
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                                                     initiative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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               RETAR SERVICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Embryo;
PEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITURE TO STATE THE PROPERTY OF THE PROPERTY O
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                                                                                                                                                                                                                                                                                                                    Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1104;
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87.5%; Pred. No. 1.8e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1104 AA; 125507 MW; 3B5A1A0BFD26042F CRC64;
                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Probable DNA-directed DNA polymerase III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                               PRT; 1104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1109 AA
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                     Name=B10H4.020;
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                                                                                                                                                                                                                                                                                                 Query Match 71.2%; Score 37; DB 2; Length 314; Best Local Similarity 75.0%; Pred. No. 82; Matches 6; Conservative 2; Mismatches 0; Indels
Nucleotidyltransferase, Transferase.

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SEQÜENCE 314 AA; 35243 MW; 749789DBF04F668F CRC64;
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136 FPYSLMNK 143
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Run on:

Sequence:

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US-08-344-824-12
| Sequence 12, Application US/08344824
| Publication No. US20030152580A1
| GENERAL INFORMATION:
| APPLICANT: SETTE, Alessandro
| APPLICANT: SIDNEY, John
| TILLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
| NUMBER OF SEQUENCES: 399
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FLING DATE: 23-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/278,634
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REPERENCE/POCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
              US-10-149-135-2295
US-10-149-135-2296
US-10-149-135-2296
US-10-149-135-2299
US-10-149-138-2299
US-10-149-138-4196
US-10-149-138-4359
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US-10-149-138-4359
US-10-149-138-4359
US-10-149-138-4359
US-10-16-118-44
US-10-16-118-44
US-10-16-118-44
US-10-170-186-9
US-10-270-186-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-810-486-45
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: USA
94105
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 Sequence 29, Appl
Sequence 4196, Ap
Sequence 4108, Ap
Sequence 4356, Ap
Sequence 4356, Ap
Sequence 4358, Ap
Sequence 2183, Ap
Sequence 2183, Ap
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Sequence 4200, A
Sequence 4356, A
Sequence 4356, A
Sequence 4359, A
Sequence 2183, A
Sequence 2183, A
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                                                                                                               June 29, 2005, 05:18:25 ; Search time 59.8352 Seconds (without alignments) 64.268 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-116-118-29

US-10-149-138-4196

US-10-149-138-4200

US-10-149-138-4355

US-10-149-138-4355

US-10-149-138-4356

US-10-149-138-4359

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US-10-149-138-2183
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                                                                                                                                                                                                                                                                                                      1717557 segs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
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Match Length
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Perfect score:
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Minimum DB E Maximum DB E

Database

2 3 4 4 7 7 10 10

Result No.

Searched:

Sequence Seq

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 3

Gaps

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Query Match
Best Local Similarity 100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0: Indale
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR PPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4196
; LENGTH: 10
                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4196
                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
FILLE REPERENCE: 2060.0140001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT PILING DATE: 2002-06-10
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Sublication No. US20030143672A1

GENERAL INFORMATION:

APPLICANT: Tangiri, Shabnam

APPLICANT: Sette, Alessandro

APPLICANT: Ishioka, Glenn

APPLICANT: Fike, John D.

TITLE OF INVENTON: Heteroclitic Analogs and Related Methods

FILE REFERENCE: 2060.0090003

CURRENT PAPLICATION NUMBER: US/10/116,118

CURRENT FLING DATE: 1999-11-18

PRIOR PELICATION NUMBER: US 60/166,529

PRIOR FILING DATE: 1999-11-18

PRIOR PELICATION NUMBER: US 60/239,008

PRIOR FILING DATE: 2000-10-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PARENTIN VERSION 3.1

SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 52; DB 14; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0019; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          100.0%; Score 52; DB 8; Length 10; 100.0%; Pred. No. 0.0019; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), OTHER INFORMATION: No. US20030143672Ale US-10-116-118-29
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Publication No. US20040018971A1
GENERAL INFORMATION:
            (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial sequence
                              TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                       LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
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            TELEPHONE:
                                                                                                                                                                                                                             US-08-344-824-12
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Sequence 4198, Application US/10149138
; Sequence 4198, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sette, Alessandro
; APPLICANT: State, John
; APPLICANT: State, John
; APPLICANT: State, Mobert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HERZ/neu USing Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-66-10
; FRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR PILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SEQ ID NO 4198
: LENGTH: 10
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; Sequence 4200, Application US/10149138
; Publication No. US20040018971A1
; FUNDICALION No. US20040018971A1
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4198
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Best Local Similarity 100.
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GENERAL INFUGANT:
GENERAL INFUGANT:
GENERAL INFUGANT:
GENERAL INFUGANT:
GENERAL INFUGANT:
GENERAL GAMES GENERAL
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Chesnut, Robert
APPLICANT:
Celis, Esteban
APPLICANT:
Celis, Esteban
APPLICANT:
Celis, Esteban
APPLICANT:
APPLICANT:
COLIS, Esteban
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COLIS, Esteban
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COLIS, Esteban
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FILE REFERENCE:
CURRENT APPLICATION NUMBER:
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APPLICANTION NUMBER:
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Sequence 4358, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Celis, Esteban

APPLICANT: Cesteban

APPLICANT: Consult, Robert

APPLICANT: Loop, Rissa

TILLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

TILLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 19458, 299

PRIOR APPLICATION NUMBER: US 09/458, 299

PRIOR PILING DATE: 1099-12-11

NUMBER OF SEQ ID NOS: 4641

SEQ ID NO 4358

LENGTHARE: PatentIn version 3.1

LENGTH: 10
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                        US20040018971A1
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Best Local Similarity
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## APPLICANT: Celis, Esteban
### APPLICANT: Keogh, Elissa
### TITLE OF INVENTION: Inducing Cellular Immune Responses to
### TITLE OP INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
### TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
### TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
### TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
### TITLE OF INVENTION UNMER: US/10/149,138
### CURRENT FILING DATE: 2000-12-11
### PRIOR FILING DATE: 1999-12-11
### PRIOR FILING DATE: 1999-12-11
### NUMBER OF SEQ ID NOS: 4641
### SEQ ID NO 4200
### SEQ ID NO 4200
### SEQ ID NO 4200
### TITLE OF INVENTION UNMER: PARCHIN VETSION 3.1
### SED ID NO 4200
### TITLE OF INVENTION UNMER: PARCHIN VETSION 3.1
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, John
APPLICANT: Sette, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Chesnut, Robert
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT APPLICATION NUMBER: US/200/33591
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 1999-12-11
PRIOR FILING DATE: 1999-12-11
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn Version 3.1
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US-10-149-138-4355
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Publication No. US20040018971A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 10, Conservative
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US-10-149-138-4356
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LENGTH: 10
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GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, John
APPLICANT: Sette, John
APPLICANT: Sette, John
APPLICANT: Chis, Bateban
APPLICANT: Celis, Bateban
APPLICANT: Celis, Bateban
APPLICANT: Celis, Bateban
APPLICANT: Keogh, Elisea
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.013001
CURRENT APPLICATION NUMBER: US 09/189,135
CURRENT APPLICATION NUMBER: US 09/189,702
PRIOR PILING DATE: 1994-12-10
PRIOR PLING DATE: 1994-03-04
PRIOR PLING DATE: 1993-03-05
PRIOR DATE: 1993-03-05
PRIOR DATE: 1993-03-05
PRIOR DATE: 1000-03-04
PRIOR DATE: 1000-03-04
PRIOR DATE: 1000-04
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PRIOR DATE
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100.0%; Score 52; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: Patentin version 3.1
SEQ ID NO 2183
LENGTH: 10
                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Artificial Peptide US-10-149-135-2183
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Sequence 2185, Application US/10149135

; Publication No. US20040053822A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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1 KVFPYALINK 10
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US-10-149-135-2187
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, John
APPLICANT: Sette, John
APPLICANT: Stancy, John
APPLICANT: Stancy, John
APPLICANT: Stancy, John
APPLICANT: Stancy, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HERZ/heu Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.014001
CURRENT APPLICATION NUMBER: US/10/149,138
FILE REPLICATION NUMBER: US/200/13591
PRIOR APPLICATION NUMBER: US/201/201
PRIOR FILING DATE: 1099-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: Patentin Version 3.1
ERNGTH: 10

LENGTH: 10

LENGTH: 10
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APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Scheban
APPLICANT: Celis, Esteban
APPLICANT: Colis, Esteban
APPLICANT: Colis, Esteban
APPLICANT: NAGEZ/3 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: MAGEZ/3 Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: UNMBER: US/10/149,135
CURRENT APPLICATION NUMBER: US/00/33545
PRIOR APPLICATION NUMBER: US 09/458,298
PRIOR PILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-11-10
PRIOR PELING DATE: 1999-11-10
PRIOR PELING DATE: 1999-11-10
PRIOR PELING DATE: 1993-11-20
PRIOR PELING DATE: 1993-11-29
PRIOR FILING DATE: 1993-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2183, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
                                                                                                                                                                                                                  Sequence 4359, Application US/10149138 Publication No. US20040018971A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KVFPYALINK 10
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US-10-19-13-12-2296, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Schev, John
APPLICANT: Chesnut, Robert
APPLICANT: Reegh, Elissa
TITLE OF INVENTION: MAGREZ 3010101
TITLE OF INVENTION: WAGREZ 105/10/149,135
CURRENT APPLICATION NUMBER: US 09/458,298
FRIOR PILING DATE: 1999-11-10
FRIOR PILING DATE: 1999-11-10
FRIOR PILING DATE: 1999-11-29
FRIOR PILING DATE: 1999-11-20
FRIOR APPLICATION NUMBER: US 08/205,713
FRIOR PILING DATE: 1993-11-29
FRIOR PILING DATE: 1993-11-29
FRIOR APPLICATION NUMBER: US 08/027,146
FRIOR FILING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SEQUENCE: DATE OF THE OF T
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100.0%; Score 52; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0;
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100.0%; Score 52; DB 15;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: U. V., PRIOR FILING DATE: 1993-11-29
PRIOR PLLING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR FILING DATE: 1993-05-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: Patentin version 3.1
SEQ ID NO 2295
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Artificial Peptide US-10-149-135-2295
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                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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1 KVFPYALINK 10
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1 KVFPYALINK 10
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                                                                                                                                                                                                                                                                                     | SERVEAL INFORMATION:
| SAPPLICANT: Fikes, John
| APPLICANT: Sette, Alessandro
| APPLICANT: Sette, Alessandro
| APPLICANT: Sidney, John
| APPLICANT: Southwood, Scott
| APPLICANT: Chennt, Robert
| APPLICANT: Chennt, Robert
| APPLICANT: Celis, Esteban
| APPLICANT: Celis, Esteban
| APPLICANT: Ready, Elissa
| TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
| TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
| TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
| TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
| FILE REFREENCE: 2060-12-11
| PRIOR PILING DATE: 2000-12-11
| PRIOR PILING DATE: 1999-12-10
| PRIOR PILING DATE: 1999-12-10
| PRIOR PILING DATE: 1998-11-10
| PRIOR FILING DATE: 1998-11-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Artificial Peptide
Sequence 2187, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2295, Application US/10149135
Publication No. US20040053822A1
GENERAL INFORMATION:
                                                                                         APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Staney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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US-10-149-135-2295
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Search completed: June 29, 2005, 05:48:17 Job time: 59.8352 secs

1 KVFPYALINK 10

6, Appli 7, Appli 7, Appli 7, Appli 42096, A 2, Appli 3474, Ap 47783, A

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Seq

Sequence

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Sequence 124, Application US/08159339A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Celis, Alessandro
APPLICANT: Betteban
ITITLE OF INVENTION: HLA Binding peptides and Their
ITITLE OF INVENTION: Uses
WUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                US-09-585-858-10

US-10-270-878-10

US-09-585-858-6

US-09-585-858-7

US-10-270-878-6

US-10-270-878-6

US-09-270-77-2

US-09-270-77-2

US-09-134-000C-3474

US-09-134-000C-3474

US-09-270-76-744783

US-09-328-352-7325

US-09-110-279-628

US-09-110-279-628

US-09-110-279-628

US-09-54-6818
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ZIF: 94111-384

COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DOS
SOFFWARE: FASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 05-MAR-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Ellen Lauver
REGESTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 31,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELLEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                     633.5
633.5
633.5
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US-08-159-339A-124
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  CITY: 8
  Sequence 124, App
Sequence 45, Appl
Sequence 2489, Ap
Sequence 2576, Ap
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 16, Appli
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43904, A
2, Appli
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7650, Ap
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14, Appl
44723, A
7342, Ap
1121, Ap
15066, A
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39.842 Million cell updates/sec
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                                                                                                                                     June 28, 2005, 23:37:59 ; Search time 18.7363 Seconds
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-543-608A-45
US-09-239-043D-2489
US-09-239-043D-2576
US-09-585-888-9
US-10-270-878-9
US-10-270-878-9
US-09-328-328-32-8079
US-09-328-328-32-8079
US-09-328-328-32
US-09-489-039A-12279
US-09-489-039A-12279
US-09-816-503B-2
US-09-816-503B-2
US-09-816-503B-4
US-08-816-503B-4
US-08-816-503B-4
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US-08-816-503B-4
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US-09-248-796A-15066
US-09-270-767-39283
US-09-270-767-54500
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                                                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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52
1 KVPPYALINK 10
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Match Length
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Perfect score:
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US-09-239-043D-2576
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CURRENT APPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, John D.
APPLICANT: Staney, John
APPLICANT: Southwood, Scott
APPLICANT: Calis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: His ACLass I A2 Tumor Associated Antigen
TITLE OF INVENTION: However to the first of 
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                                                               100.0%; Score 52; DB 3; Length 10; 100.0%; Pred. No. 0.00041; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Standard Peptide 941.12
US-09-543-608A-45
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PRIOR FILING DATE: 1998-11-10
PRIOR PELICATION NUMBER: US 08/978,291
PRIOR PLILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-543-608A-45
; Sequence 45, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
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Celis, Esteban
Kubo, Ralph T.
Grey, Howard M.
Chesnut, Robert
Epimmune Inc.
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ORGANISM: Artificial Sequence
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                               Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                        1 KVFPYALINK 10
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1 KVFPYALINK 10
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US-08-159-339A-124
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APPLICANT: Calis, Esteban
APPLICANT: Calis, Esteban
APPLICANT: Calis, Esteban
APPLICANT: Cary, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Callular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Unducing Callular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Unducing Callular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Unducing Callular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Unducing Callular Invention Number: US 09/189,702
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1994-11-20
PRIOR APPLICATION NUMBER: US 08/441,610
PRIOR FILING DATE: 1994-11-23
PRIOR FILING DATE: 1994-11-23
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1997-03-12
PRIOR PLING DATE: 1996-03-13
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1995-06-05
PRIOR PLICATION NUMBER: US 08/461,603
PRIOR PLICATION NUMBER: US 08/44,610
PRIOR PLICATION NUMBER: US 08/347,610
PRIOR PLING DATE: 1994-12-01
PRIOR PLING DATE: 1994-12-01
PRIOR PLING DATE: 1994-12-01
PRIOR PLING DATE: 1994-07-21
PRIOR PLING DATE: 1994-07-21
PRIOR PLING DATE: 1994-07-21
PRIOR PLING DATE: 1994-03-04
PRIOR DATE: 1994-03-04
PRI
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; Patent No. 6689363
; GENERAL INFORMATION:
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Cells, Esteban
Kubo, Ralph T.
Grey, Howard M.
Chesnut, Robert
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ORGANISM: Artificial Sequence
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A
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Best Local Similarity 100.
Matches 10; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/10270878;
Sequence 8, Application US/10270878;
Patent No. 6818425;
GENERAL INFORMATION:
APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Arnthor Beceriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
CURRENT APPLICANTON WHOBER: US/10/270,878
FILE REFERENCE: 2739.1001-011
CURRENT FILING DATE: 2000-10-11
PRIOR PRILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 734
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Patent No. 6818425

GENERAL INPORMATION:
APPLICANT: Signidur Hjorleifsdotter
APPLICANT: Gudmudur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Olafur H. Fridjonsson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
TITLE OF INVENTION: Bocteriophage RM378 of a Thermophilic
CURRENT APPLICATION UNMBER: US/10/270,878
CURRENT APPLICATION NUMBER: US/10/270,878

CURRENT FILING DATE: 2000-10-11

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 4; Length 734;
Pred. No. 25;
0; Mismatches 1; Indels
                                                                                                                                                            Score 38; DB 4; Length 734;
Pred. No. 25;
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                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Candida albicans (Yeast)
                                                             TYPE: PRT ; ORGANISM: Saccharomyces cerevisiae US-09-585-858-9
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; ORGANISM: Saccharomyces cerevisiae
US-10-270-878-9
                                                                                                                                                       73.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.1%;
87.5%;
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Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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SEQ ID NO 9
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LENGTH: 734
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                                                                                                                                                            Query Match
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  PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2576
LENGTH: 10
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APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Gudmundur O. Hreggvidsson
APPLICANT: Olafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
APPLICANT: Jakob K. Kristjansson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILLE REPERSONG: 2739.1001-001
CURRENT PILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/09/585,858
CURRENT PILLOATION NUMBER: 60/137,120
PRIOR PILLING DATE: 1999-06-02
NUMBER: OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sigridur Hjorleifsdotter
APPLICANT: Glamundur O. Hreggvidsson
APPLICANT: Glamundur O. Hreggvidsson
APPLICANT: Glafur H. Fridjonsson
APPLICANT: Arnthor Aevarsson
TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
TITLE OF INVENTION: Host Organism
FILE REFERENCE: 2739,1001-001
CURRENT APPLICATION NUMBER: 60/137,120
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/137,120
PRIOR FILING DATE: 399-06-02
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                           100.0%; Score 52; DB 4; Length 10; 100.0%; Pred. No. 0.00041; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.1%; Score 38; DB 4; Length 734; Best Local Similarity 87.5%; Pred. No. 25; Matches 7; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/09585858
Patent No. 6492161
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; Sequence 9, Application US/09585858
; Patent No. 6492161
                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                TYPE: PRT; ORGANISM: A3CON1 peptide US-09-239-043D-2576
                                                                                                                                                                                                                                                                                                                                                                                                     1 KVFPYALINK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
US-09-585-858-8
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Sequence 2, Application US/09836503B
Patent No. 6696415
Fatent No. 6696415
GENERAL INFORMATION:
APPLICANT: Children's Hospital Research Foundation
APPLICANT: Gendron, Robert L.
APPLICANT: Paradis, Helene
TITLE OF INVENTION: Treatment of Ocular Neovascularization and Related Diseases;
FILE REFERENCE: 10872/518
CURRENT PFLICATION NUMBER: US/09/816,503B
CURRENT PFLING DATE: 2001-04-17
FRIOR APPLICATION NUMBER: US 60/197,977
FRIOR APPLICATION NUMBER: US 60/197,977
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TOS 09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43304
LENGTH: 458
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                                                                                                                                                                                                                                                      Length 749;
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                               3; Mismatches
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US-09-270-767-43904
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ 1D NOS: 14342
SEQ ID NO 12279
LENGTH: 749
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US-09-270-767-43904
Sequence 43904, Application US/09270767
Perent No. 6703491
GENERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
                                                                                                                                                                       TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                        67.3%;
62.5%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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ORGANISM: Homo sapiens
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132 FPYWLLNK 139
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447 FPYAVLNR 454
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LENGTH: 593
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Patent No. 6440674

GENERAL INFORMATION:

APPLICANT: Mistar, Santosh et al.

TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH

TITLE OF INVENTION: 1TS USE

TITLE OF INVENTION: 08-04

CURRENT APPLICATION NUMBER: US/09/632,538C

CURRENT APPLICATION NUMBER: US/09/632,538C

CURRENT PILING DATE: 2000-08-04

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 36

LENGTH. 655
                                                                                                                                                                                                                                         Sequence 8079, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER: OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 39;
1; Mismatches 2; Indels
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Pred. No. 88;
                            Length 734;
                                                                     1; Indels
                          Score 38; DB 4;
Pred. No. 25;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Acinetobacter baumannii
US-09-328-352-8079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pseudotsuga menziesii
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                          Query Match 73.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 66...
6; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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110 KLLPYKIVNK 119
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US-09-489-039A-12279
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US-09-632-538C-36
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LENGTH: 306
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US-09-836-503B-5

Sequence 5, Application US/09836503B

Patent No. 6696415

GENERAL INFORMATION:

APPLICANT: Children's Hospital Research Foundation

APPLICANT: Gendron, Robert L.

APPLICANT: Paradis, Helene

TITLE OF INVENTION: Treatment of Ocular Neovascularization and Related Diseases

FILE REFERENCE: 1082/2518

CURRENT FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: US 60/197,977

PRIOR PLING DATE: 2000-04-17

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 700
                                                                                                                                                                                                                 Sequence 1, Application US/09836410A
Patent No. 6812340
GENERAL INFORMATION:
APPLICANT: Children's Hospital Research Foundation
APPLICANT: Children's Hospital Research Foundation
APPLICANT: Gendron, Robert L.
APPLICANT: Gendron, Robert L.
APPLICANT: Paradis, Helene
TITLE OF INVENTION: Inhibition of Bone Tumor Formation Using Antisense cDNA Therapy
FILE REFERENCE: 10872/518
CURRENT APPLICATION NUMBER: US/09/836,410A
CURRENT FILING DATE: 2001-08-15
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
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Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels
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Job time : 18.7863 secs
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Best Local Similarity 85.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
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664 KLFPYAL 670
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US-09-836-503B-5
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557 KLFPYAL 563
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557 KLPPYAL 563
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US-09-836-410A-1
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LENGTH: 593
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                                              June 28, 2005, 23:32:21 ; Search time 12.5275 Seconds
5.1.6
Compugen Ltd.
                                                                                                                                                Fotal number of hits satisfying chosen parameters:
                                                                                                                                  283416 segs, 96216763 residues
GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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S53181
S53260
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S43490
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No.
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A,Molecule type: DNA A,Residues: 1-181 < LAA> A,Cross-references: UNIPROT:Q67995; EMBL:X85278; NID:g736069; PIDN:CAA59580.1; PID:g736 A,Experimental source: isolate patient Addis'89 A,Note: due to a stop codon between the alternative initiatiors the e antigen precursor P.; Leadbetter, G.; ö precurso Core antigen - hepatitis B virus (isolate patient Addis'89)
NyAlternate names: HBC antigen
NyContains: core antigen
CySpecies: hepatitis B virus, HBV
CySpecies: hepatitis B virus, HBV
CyAccession: S53178
CyAccession: S53178
RyLai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
AyReference number: S53112
AyReference number: S53112 core antigen - hepatitis B virus (subtype adyw)
C;Species: hepatitis B virus, HBV
A;Variety: subtype adyw
C;Date: 30-Jun-1992 #text_change 09-Jul-2004
C;Dates: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B93217; A03711
R;Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; MacKay, P.; Lead Nature 282, 575-579, 1979
A;Title: Hepatitis B virus genes and their expression in B. coli.
A;Reference number: A93217; MUID:81012115; PMID:399329
A;Accession: B93217. Gaps e antigen antigen antigen e antigen ô Score 51; DB 2; Length 181; Pred. No. 0.062; 1; Mismatches 0; Indels ALIGNMENTS C;Superfamily: hepatitis B virus core antigen C;Keywords: core protein SS3240 SS3272 SS3272 SS3223 SS32516 SS3257 SS325746 SS3255 SS3255 SS3256 SS32264 SS32264 SS32264 SS32264 92.7%; Local Similarity 90.(1 FLPSDYFPSV 10 ||||||:|||| FLPSDFFPSV 27 A; Accession: S53178 18 Query Match Best Local S C;Genetics: Matches RESULT 1 0126459666444444 NKVLA2 셤 8

A;Molecule type: DNA A;Residues: 1-183 <PAS-\$\text{Lores-references: UNIPROT:P03147; GB:J02202; NID:g329637; PIDN:AAA45486.1; PID:g32963 A;Experimental source: subtype adyw A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics: A;Gene: C C;Superfamily: hepatitis B virus core antigen ~

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A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68060; EMBL:X85311; NID:g736187; PIDN:CAA59655.1; PID:g736
A;Experimental source: isolate patient Mannoni-3'94
A;Experimental source: isolate patient mannoni-3'94
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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A,Residues: 1-183 <LAI.>
A,Cross-treferences: UNIPROT:Q68023; EMBL:X85292; NID:g736120; PIDN:CAA59614.1; PID:g736
A,Experimental source: isolate patient Castag-2.86
A,Experimental source: isolate patient Castag-2.86
A,Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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                                                                                                                                                                                                                                                             core antigen - hepatitis B virus (isolate patient Mannoni-3'94)
N;Alternate names: HBc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Mannoni-3'94
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NiAlternate names: HBC antigen
NiContains: core antigen
NiContains: core antigen
Cispecies: hepatitis B virus, HBV
A;Variety: isolate patient Castag-2'86
Cispate: 08-401-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Cispate: 08-401-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
Ciscossion: S53214
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
BiReference number: S53112
A;Reference number: S53112
                           Gaps
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Pred. No. 0.063;
1; Mismatches 0; Indels
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                           Indels
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R;Lal, M.B.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53260
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Pred. No. 0.063;
1; Mismatches
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C,Superfamily: hepatitis B virus core antigen
C,Keywords: core protein
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Matches 9; Conservative
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  Best Local Similarity
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A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67997; EMBL:X85279; NID:g736073; PIDN:CAA59583.1; PID:g7360
A;Experimental source: isolate patient Bitti'89
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A28885
R;Vaudin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated A;Reference number: A92796; WUID:88258473; PMID:2838576
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A;Cross-references: EMBL:X85233; NID:3736232; PIDN:CAA59538-1; PID:9736235
A;Experimental source: isolate patient Amoroso6'89
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-183 <VAU>
A;Cross-references: UNIPROT:P12901; EMBL:D00220; NID:g221505; PIDN:BAA00157.1; PID:g221:A;Experimental source: strain LSH, chimpanzee
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
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N'Alternate names: HBC antigen
C;Species: hepatitis B virus, HBV
A;Variety: strain LSH, chimpanzee
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                         Gaps
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                                                                               Length 183;
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                                                                                                                                 0; Indels
C;Keywords: core protein F;1-183/Product: core antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 1;
Pred. No. 0.063;
                                                                             Score 51; DB 1;
Pred. No. 0.063;
1; Mismatches
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C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0%;
                                                                             Query Match 92.7%;
Best Local Similarity 90.0%;
Matches 9; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                core antigen - hepatitis B virus
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                                                                                                                                                                                        1 FLPSDYFPSV 10
                                                                                                                                                                                                                    18 FLPSDFFPSV 27
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A; Molecule type: DN
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Matches

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27

|||||:|||| 18 FLPSDFFPSV

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RESULT 7

DB 2;

92.7%; Score 51;

Query Match

A;Gene: C C;Superfamily: hepatitis B virus core antigen C;Keywords: core protein

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submitted to the EMBL Data Library, March 1995
A;Reference number: $53112
A;Accession: $53125
A;Accession: $53155
A;Accession: $53155
A;Accession: $63155
A;Accession: $63156
A;Crose-references: UNIPROT:067976; EMBL:X85270; NID:g736037; PIDN:CAA59559.1; PID:g736
A;Experimental source: isolate patient Usai'89
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-183 < LAI>
A, Residues: 1-183 < LAI>
A, Cross-references: University EMBL: X85269; NID: 9736033; PIDN: CAA59556.1; PID: 9736
A, Experimental source: isolate patient Tutariello'89
A, Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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N;Alternate names: HBc antigen
N;Contains: core antigen
N;Contains: core antigen
A;Variety: isolate patient Giulioc'92
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Giulioc'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53211
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
A;Reference number: S53112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   core antigen - hepatitis B virus (isolate patient Tufariello'89)
N;Alternate names: HBc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Tufariello'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S53152
R;Lai, M.B.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 2;
Pred. No. 0.063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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C.Superfamily: hepatitis B virus core antigen
C.Keywords: core protein
                                                                                                                                                                                                                                                               C;Superfamily: hepatitis B virus core antigen C;Keywords: core protein
                                                                                                                                                                                                                                                                                                                                                 92.7%;
90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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FLPSDFFPSV 27
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A;Molecule type: DNA
A;Residues: 1-183 <LAI>
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Matches
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A;Experimental source: isolate patient Boi'90
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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A;Cross-references: UNIPROT:Q68064; EMBL:X85260; NID:g736197; PIDN:CAA59530.1; PID:g7362
A;Experimental source: isolate patient Lucianoc'92
A;Experimental source: between the alternative initiatiors the e antigen precursor
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                           core antigen - hepatitis B virus (isolate patient Boi'90)
NyAlternate names: HBC antigen
NyContains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Boi'90
C;bate: 08-ul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Lucianoc'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Usai'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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N;Alternate names: HBc antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: 553267
R; Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A. submitted to the EMBL Data Library, March 1995
A; Reference number: 553112
A; Accession: 553267
A; Mesidues: 1-183 < LAI>
                                                                                                                                                                                C'Accession: S53175
R'Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53175
A;Molecule type: DMA
A;Residues: 1-183 <LAI>
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90.0%; Pred. No. 0.063;
tive 1; Mismatches
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Pred. No. 0.063;
1; Mismatches
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C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 FLPSDYFPSV 10
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18 FLPSDFFPSV 27
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A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67946; EMBL:X85254; NID:g736003; PIDN:CAA59512.1; PID:g736.
C;Genetics:
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A; Residues: 1-183 <LAI>
A; Cross-references: UNIPROT: Q68079; EMBL: X85261; NID: 9736224; PIDN: CAA59533.1; PID: 9736
A; Cross-references: isolate patient Salvatorec' 92
A; Note: due to a stop codon between the alternative initiatiors the e antigen precursor
                                                                                                                                                                   S33129

Core antigen - hepatitis B virus

NyAlternate names: HBC antigen

NyAlternate names: HBC antigen

NyContains: core antigen

CySpecies: hepatitis B virus, HBV

CyBate: 08-401-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

CyAccession: S53129

RyLai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

Submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core antigen - hepatitis B virus (isolate patient Salvatorec'92)
NyAlternate names: HBC antigen
NyContains: core antigen
NyContains: core antigen
A;Variety: isolate patient Salvatorec'92
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Salvatorec'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S52386
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
A;Reference number: S53112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 183;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 2;
Pred. No. 0.063;
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C;Superfamily: hepatitis B virus core antigen
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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18 FLPSDFFPSV 27
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18 FLPSDFFPSV 27
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18 FLPSDFFPSV 27
                     FLPSDYFPSV 10
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A, Molecule type: DNA
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A;Experimental source: isolate patient Dettori-2'87
A;Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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A, Residues: 1-183 <LON>
A, Crose-references: UNTROT: 067951, EMBL: X52939, NID: 9457780, PIDN: CAA37112.1, PID: 94577
A, Experimental source: subtype adr
A, Experimental source: subtype adr
A, Note: due to a stop codon between the alternative initiatiors the e antigen precursor
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Nucleic Acids Res. 18, 4940, 1990
Aritile: Sequence of a replication competent hepatitis B virus genome with a preX open A; Reference number: S12598; MUID:90370503; PMID:2395664
A; Accession: S43490
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N;Alternate names: HBc antigen
N;Contains: ore antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Dettori-2'87
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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N;Alternate names: HBc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S43490
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R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
                                                                                         92.7%; Score 51; DB 2;
90.0%; Pred. No. 0.063;
tive 1; Mismatches (
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Best Local Similarity 90.0%; Pred. No. 0.063;
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Best Local Similarity 90.0%; Pred. No. 0.063;
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C,Superfamily: hepatitis B virus core antigen
C,Keywords: core protein
                  C;Superfamily: hepatitis B virus core antigen C;Keywords: core protein
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18 FLPSDFFPSV 27
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Fran H.T., Ushilima H., Quang V.X., Win K.M., Luengrojanakul P., Kikuchi K., Sata T., Abe K.;

"Genotype C of hepatitis B virus can be classified into at least two subgroups.";

J. Gen. Virol. 85:283-292(2004).

EMBL, AB112408; BAD05052.1;

InterPro; IPR002006; Hepatitis_core.
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Name-prec/C;
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus
NCBI_TaxID=10407,
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Tagger A., Binelli G., Donato F., Ribero M.L.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF289942; AAG25224.1; ...
InterPro; IPR002006; Hepatitis core.
Pfam; PF00906; Hepatitis core; J.
SEQUENCE 42 AA; 4753 MW; 93672F3BACDE3194 CRC64;
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SEQUENCE 212 AA; 24445 MW; B34413EB32E80F75 CRC64;
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1; Mismatches
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MEDLINE=20037812; PubMed=10573161;
Preikschat P., Meisel H., Will H., Gunther S.;
"Hepatitis B virus genomes from long-term immunosuppressed virus carriers are modified by specific mutations in several regions.";
J. Gen. Virol. 80:2685-2691(1999).
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NCBI_TaxID=10407;
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Hippatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
VCBI_TaxID=10407;
92.7%; Score 51; DB 2; Length 42; 90.0%; Pred. No. 0.061; ive 1; Mismatches 0; Indels
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90.0%; Pred. No. 0.097;
ive 1; Mismatches 0; Indels
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TISSUB-Serum;
Saxena A., Acharya S.K., Nayak B., Panda S.K.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF115421; AAD49186.1; -.
InterPro; IPR002006; Hepatitis core.
Pfam; PF00906; Hepatitis core; 1.
SEQUENCE 64 AA; 7196 MW; 12AB9C46EE302D80 CRC64;
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InterPro, IPR002006, Hepatitis core.
Pfam; PF00906; Hepatitis core; 1.
SEQUENCE 56 AA; 6313 WW; 2F5B075F0F39CC7B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Core mutant protein.
Hepatitis B virus.
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Last sequence update)
Last annotation update)
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Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                            56 AA
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Best Local Similarity 90.0-
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18 FLPSDFFPSV 27
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18 FLPSDFFPSV
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Best Local Similarity
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MEDLINE-2018739; PubMed=10720502;
Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
"Selective transmission of hepatitis B virus after percutaneous
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                              COS-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Core protein (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Pred. No. 0.098;
1; Mismatches 0; Indels
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                                                                                                                                                                                                              Hallett R.L., Teo C.G.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY374227; AAQ83759.1; -.
InterPro; IPR002006; Hepatitis_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 AA; 7129 MW; 63034F0ADA7831CE CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
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J. Infect. Dis. 181:838-843(2000).
EMBL, AF204958; AAF67531.1; -.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
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PRT;
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NON TER 65 65
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Best Local Similarity 90.vv,
Best Local Similarity
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PubMed=11472654; DOI=10.1186/1471-2180-1-10;
Castro L.D., Niel C., Gomes S.A.;
"Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=11472634; DOI=10.1186/1471-2180-1-10; Castro L.D., Miel C., Gomes S.A.; "Low frequency Of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers.";
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 Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
"Selective transmission of hepatitis B virus after percutaneous
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Q91A48;
Q91A48;
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 20, Last annotation update)
Precore/core protein (Fragment).
Prepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NGEL TAXID=10407;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precore/core protein (Fragment).
Hepatitis B vinus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
                                                                                                                                                                                                Score 51; DB 2; Length 65;
Pred. No. 0.098;
1; Mismatches 0; Indels
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De Castro L., Niel C., Gomes S.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF390015; AAL16423.1; -.
Pfam; PF00906; Hepatitis_core; 1.
                                                                                                                                                            65 AA; 7129 MW; 62B34FE4C0C831CA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                  66 AA.
                             exposure.";
J. Infect. Dis. 181:838-843(2000).
EMBL; AF204955; AAF67528.1; -.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00906; Hepatitis_core; 1.
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                                                                                                                                                                                                92.78;
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Best Local Similarity 90.0°
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Best Local Similarity 90.0
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Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
"Selective transmission of hepatitis B virus after percutaneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDILINE=210187639; PubMed=10720502;
Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
"Selective transmission of hepatitis B virus after percutaneous
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Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-OCT-2000 (TERMLrel. 15, Created)
01-OCT-2000 (TERMLrel. 15, Last sequence update)
01-UN-2001 (TERMLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                      Score 51; DB 2;
Pred. No. 0.098;
1; Mismatches
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                                                                                                                       exposure.";
J. Infect. Dis. 181:838-843(2000).
EMBL; AF204957; AAF67530.1;
InterPro; IPR002006; Hepatitis_core.
Pfan; PF00906; Hepatitis_core; 1.
NON TER
65 65
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J. Infact. Dis. 181:838-843(2000).
BEMBL, AF204956; AAF67529.1; -.
InterPro; IPR002006; Hepatitis_core.
Pfam; PF00306; Hepatitis_core.
NON TER 65 65
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FLPSDFFPSV 18
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Best Local Similarity
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              NCBI_TaxID=10407;
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Pubbled=11472654; DOI=10.1186/1471-2180-1-10;
Castro L.D., Niel C., Gomes S.A.;
"Low frequency of mutations in the core promoter and precore regions
of hepatitis B virus in anti-HBe positive Brazilian carriers.";
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

PubMed=11472634; DOI=10.1186/1471-2180-1-10;

Castro L.D., Niel C., Gomes S.A.;

"Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers.";

BMC Microbiol. 1:10-10(2001).
                                                                                                                                                                                                                                                                                                              091A51;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precore/core protein (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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Hepatitis B virus.
Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus.
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                                                                                                                                  Score 51; DB 2; Length 66;
Pred. No. 0.1;
1; Mismatches 0; Indels
[2]
SEQUENCE FROM N.A.
DE Castro L., Niel C., Gomes S.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390011; AAL16419.1; -.
Pfam; PF00906; Hepatitis_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

De Castro L., Niel C., Gomes S.A.;

Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF390010; AAL16418.1; -.

Pfam; PF00906; Hepatitis_core; 1.
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66 AA; 7492 MW; 95BA4FF652C1C4D3 CRC64;
                                                                                                     66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
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0-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                    92.7%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Matches 9; Conservative
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Castro L.D., Niel C., Gomes S.A.;
"Low frequency of mutations in the core promoter and precore regions of hepatitis B virus in anti-HBe positive Brazilian carriers.";
BMC Microbiol. 1:10-10(2001).
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Castro L.D., Niel C., Gomes S.A.;
"Low frequency of mutations in the core promoter and precore regions
of hepatitis B virus in anti-HBe positive Brazilian carriers.";
BMC Microbiol. 1:10-10(2001).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precore/core protein (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Precore/core protein (Fragment).
Hepatitis B virus.
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
NCBI_TaxID=10407;
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                                                                                                                                                     Length 66
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                           SECUENCE FROM N.A.

De Castro L., Niel C., Gomes S.A.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390111, 1.
Pfam; PF00906; Hepatitis_core; 1.
NON_TER 66
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De CASTRO L., Niell C., Gomes S.A.;
Submitted (UNN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390012; AAL16420.1;
Pfam; PF00906; Hepatitis_core; 1.
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                                                                                                                    66 AA; 7370 MW; 8EA6375595C43E96 CRC64;
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Pred. No. 0.1;
1; Mismatches
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   BMC Microbiol. 1:10-10(2001).
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les 9; Conservative
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47 FLPSDFFPSV 56
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47 FLPSDFFPSV 56
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RA De Caretro L., Niel C., Gomes S.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

BR BEA; AF390009; AAL16417.1; -.

DR Pfam; PF00906; Hepatitis_core; 1.

FT NOW TER 66 AA; 7370 MW; 8EA6175595C43E96 CRC64;

Query Match

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Query Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 1 FLPSDYFPSV 10

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Search completed: June 29, 2005, 01:34:54

Job time: 60.2747 secs
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Sequence 108, App
Sequence 25, Appl
Sequence 226, Appl
Sequence 86, Appl
Sequence 226, Appl
Sequence 226, Appl
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Sequence 24, Appl
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-359-431-25

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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ALIGNMENTS

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APPLICANT: SETTE, Alessandro
APPLICANT: SINEY, John
TITLE OF INVENTION: HIA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                 STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FLING DATE: 23-NOV-1994
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION:
           Sequence 11, Application US/08344824 Publication No. US20030152580A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
COUNTRY: USA
US-08-344-824-11
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Sequence

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Sequence 108, Application US/10094699

Publication No. US20030046714A1

GENERAL INFORMATION:

APPLICANT: SIMARD, John, J.L.

APPLICANT: DIAMOND, David, C.

TITLE OF INVENTION: CANCER;

TITLE OF INVENTION: CANCER;

FILE REPERENCE: CTLIMM.015A

CURRENT APPLICATION NUMBER: US/10/094,699

CURRENT PILING DATE: 2002-66-21

PRIOR FILING DATE: 2001-03-07

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 108
                                                                                                                                                                                                                                                   APPLICANT: Epiment, Inc.
APPLICANT: Epiment, John
APPLICANT: Sidney, John
APPLICANT: State, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Scuthwood, Scott
TITLE OF INVENTION: SUBUNIT VACCINES WITH A2 SUPERMOTIFS
FILE REFERENCE: 39963-20029.20
CURRENT APPLICATION NUMBER: US/09/935,476
CURRENT FILING DATE: 1999-06-20
PRIOR APPLICATION NUMBER: US 60/264,969
PRIOR PILLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 10
  Indels
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ORGANISM: Artificial Sequence
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Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
    10; Conservative
                                                                           1 FLPSDYFPSV 10
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-094-699-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-094-699-108
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    Matches
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                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MELANOMA ANTIGENS AND THERAPEUTIC THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 10; Length 10;
Pred. No. 0.021;
                                                                                                                                                                                                                                 100.0%; Score 55; DB 8; Length 10; ilarity 100.0%; Pred. No. 0.021; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: ITES: FORTAL STATES: COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/898,860
FILING DATE: 03-Jul-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE: CURKNOWN>
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/21,565
FILING DATE: US-APR-1995
APPLICATION NUMBER: US/08/21,565
FILING DATE: US-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 27,341
REGISTRATION NUMBER: 27,341
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: WORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Unknown

NOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-898-860-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 126, Application US/09898860 Publication No. US20030144482A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHODS
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 421792
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEVEN A.
                                                                                                                                 single
                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-344-824-11
                                                                                                                                                                                                                                                                                                                          1 FLPSDYFPSV 10
                                                                                                                                                                                                                                                                                                                                                                  1 FLPSDYFPSV 10
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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APPLICANT: Chesnut, Robert A.
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Emme Response and Methods of Using the Same; FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/10/371,525
CURRENT FILING DATE: 1099-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 86, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: CTLIMM.12CPIC
; CURRENT FILING DATE: 2001-12-07
CURRENT FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR PILICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; RICH RELING DATE: 2000-04-28
; RICH RELING DATE: 2000-04-28
; RICH RELING DATE: 2000-04-28
; RUMBER OF SEQ ID NOS: 89
; SUFTWARE FARTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: HBc 18-27 analog (peptide 941.01)
US-10-371-525-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-10-371-069-226
; Sequence 226, Application US/10371069
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 10; Conservative
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1 FLPSDYFPSV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-026-066-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                 Sequence 25, Application US/10359431
Publication No. US20030171538A1
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                            CORRESPONDERS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTXY: USA
ZIP: 94111-384
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/935,898
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: US 08/591,502
FILING DATE: 01-AUG-1994
APPLICATION NUMBER: US 08/591,502
ATTORNEY/AGENT INFORMATION:
NAME: Lockyer, Jean M.
RESTREMENCE/DOCKET NUMBER: 04/879
TELENCOMMINICATION INFORMATION:
TELENCOMMINICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-10-359-431-25
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Publication No. US20030203869A1
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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1 FLPSDYFPSV 10
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FEATURE: OTHER INFORMATION: HBc 18-27 analog (peptide 941.01)
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Sequence 24, Application US/10117937

Publication No. US2003022039A1

GENERAL INPORMATION:
APPLICANT: CTL IMMUNO THERAPIES CORP.
APPLICANT: DIMAND, David, C.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LILO, Liping
APPLICANT: LILO, Liping
APPLICANT: CTLIMM.027A
CURRENT APPLICATION NUMBER: US/0/117, 937
CURRENT APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-07

PRIOR APPLICATION NUMBER: US 60/337,017

PRIOR FILING DATE: 2001-11-07

PRIOR FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 602

SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 226, Application US/10371260; Publication No. US20030220285A1
GENERAL INFORMATION: APPLICANT: EPIMMIUNE Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLPSDYFPSV 10
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                               1 FLPSDYFPSV 10
                                                                                   1 FLPSDYFPSV 10
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APPLICANT: Fikes, John D.

APPLICANT: Hermanson, Gary G.

APPLICANT: Hermanson, Gary G.

APPLICANT: Hermanson, Gary G.

APPLICANT: Ishioka, Glenn Y.

APPLICANT: Livingston, Brian

APPLICANT: Livingston, Brian

APPLICANT: Epimmune Inc.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an TITLE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 39863-20022.11

CURRENT APPLICATION NUMBER: US 09/078,904

PRIOR APPLICATION NUMBER: US 09/078,904

PRIOR APPLICATION NUMBER: US 06/085,751

PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                    APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Gary G.
APPLICANT: Ishioka, Gary G.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Response and Methods of Using the Same ITILE OF INVENTION: Immune Response and Methods of Using the Same FILE REFERENCE: 39963-2002.10
CURRENT APPLICATION NUMBER: US/10/371,069
CURRENT PILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 55; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:

// OTHER INFORMATION: HBc 18-27 analog (peptide 941.01)

US-10-371-645-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: HBc 18-27 analog (peptide 941.01) US-10-371-069-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 226
LENGTH: 10
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ORGANISM: Artificial Sequence
Publication No. US20030216342A1
GENERAL INFORMATION:
APPLICANT: EPIMMUNE Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                Fikes, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 FLPSDYFPSV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 226
LENGTH: 10
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APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002.13
CURRENT APPLICATION NUMBER: US/10/371,260
CURRENT FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE FastSEQ for Windows Version 3.0
LENGTH: 10
                                                                  Gaps
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Query Match 100.0%; Score 55; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 10; Conservative 0; Mismatches 0; Indels
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Gaps

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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Celso, Scott
APPLICANT: Celso, Esteban
APPLICANT: Celso, Esteban
TITLE OF INVENTION: Inducing Cellular Immune Responses to
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
FTILE REFERENCE: 2060-012-11
FRIOR APPLICATION NUMBER: PCT/US00/33591
FRIOR PILING DATE: 1990-12-11
FRIOR APPLICATION NUMBER: US 09/458,299
FRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SEQ ID NO 4190
LENGTH: 10
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: State, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Blissa
APPLICANT: Keogh, Blissa
TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: 14ER2/neu Using Peptide and Nucleic Acid Compositions
                                                                                                                                                                                      Query Match 100.0%; Score 55; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 0.021; Matches 10; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 2002-06-10
                                                                                                          ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4190, Application US/10149138; Publication No. US20040018971A1; GENERAL INFORMATION:
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; Publication No. US20040018971A1
; GENERAL INFORMATION:
                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
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     LENGTH: 10
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APPLICANT: LANGLADE-DEMOYAN, PIERRE
APPLICANT: LANGLADE-DEMOYAN, PIERRE
APPLICANT: LEMONNIER, FRANCOIS
APPLICANT: VIDER, FRANCOIS
APPLICANT: VOTNA, PARRICIA
TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 02356.0082
CURRENT APPLICATION NUMBER: US/10/448,521
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: CT/FR01/03779
PRIOR PILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 45
SEQ ID NOS: 45
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Sequence 4189, Application US/10149138

Publication No. US20040018971A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sathwood, Scott

APPLICANT: Southwood, Scott

APPLICANT: Glass and Southwood, Scott

APPLICANT: Chesnut, Robert

APPLICANT: Chesnut, Robert

APPLICANT: Calis, Esteban

APPLICANT: Calis, Esteban

APPLICANT: Calis, Esteban

APPLICANT: Calis, Esteban

FILE REFRERCE: 2000-014001

FILE REFRERCE: 2000-014001

CURRENT APPLICATION NUMBER: US/10/149,138

CURRENT FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: US 09/458,299

PRIOR FILING DATE: 1999-12-11

NUMBER OF SEQ ID NOS: 4641

SEQ ID NO 4189
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                                               Query Match
100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/10448521
Publication No. US20040018205A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: human herpesvirus
US-10-448-521-45
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Best Local Similarity 100.
Matches 10; Conservative
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US-10-371-260-226
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## PRIOR APPLICATION NUMBER: PCT/US00/33591
| PRIOR FILING DATE: 2000-12-11 |
| PRIOR FILING DATE: 2000-12-11 |
| PRIOR FILING DATE: 1999-12-11 |
| PRIOR FILING DATE: 1999-12-11 |
| NUMBER OF SEQ ID NOS: 4641 |
| SEQ ID NO 4191 |
| LENGTH: 10 |
| TYPE: PRT |
| OTHER INFORMATION: Artificial Peptide |
| OTHER INFORMATION: AR
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APPLICANT: Boeples M.D., George E.
APPLICANT: Peoples M.D., George E.
APPLICANT: Veshino M.D., Ichiro
APPLICANT: Geodgebuure Ph.D., Peter
TITLE OF INVENTION: Isolated Antigenic Oncogene Peptide
TITLE OF INVENTION: Pragments and Uses
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate, Hall & Stewart
STREET: 53 State Street, Exchange Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/195,075

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Kaplan Esq., Warren A.

REGISCHATION NUMBER: 34,199

REFERENCE/DOCKET NUMBER: 34,199

TELEPOMMUNICATION INFORMATION:

TELEPOMMUNICATION INFORMATION:

TELEPAX: 617:227-566
US-10-266-463A-51
PCT-US92-07218-23
PCT-US94-02195-23
PCT-US95-02121-4
US-09-239-043D-2302
US-09-239-043D-2430
US-09-239-043D-2440
US-09-239-043D-2468
US-09-239-043D-2468
US-09-239-043D-2468
US-08-197-4864-109
US-08-197-4864-109
US-08-197-882-07218-24
US-08-591-5028-75
US-08-591-5028-75
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100.0%; Pred. No. 0.00099;
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MEDLINY TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/08195075; Patent No. 5550214; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617:227-7566
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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COUNTRY: U.S.A.
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: peptide US-08-195-075-12
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Sequence 9, Appli
Sequence 126, App
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Sequence 25, Appli
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2487, Ap
12, Appl
90, Appl
53, Appl
644, Appl
23, Appl
23, Appl
23, Appl
39, Appl
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                                                                                             June 28, 2005, 23:37:59; Search time 18.7363 Seconds (without alignments) 39.842 Million cell updates/sec
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-363-691-9
US-08-417-174-126
US-08-159-3139A-647
US-09-267-439-126
US-08-922-877-1
US-09-311-784A-226
US-09-073-138-126
US-09-073-138-126
US-09-541-608A-43
US-09-541-608A-43
US-08-591-502B-25
US-08-239-043D-2307
US-08-239-043D-2307
US-08-464-235-23
US-08-464-235-23
US-08-464-235-33
US-08-464-235-33
US-08-464-235-33
US-08-158-338A-644
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US-09-239-043D-2521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-913-612A-51
US-09-311-784A-91
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US-08-197-484-4
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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1000.0
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Perfect score:
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Maximum DB
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Sequence 647, Application US/08159339A

GENERAL INFORMATION:
APPLICANT: State Alessandro
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: HAA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Taw Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: CA
COMPUTER: USA
ZIP: 94111-3834
COMPUTER: READABLE FORM:
MEDULUM TYBE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: TESTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: USOS
CONTRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 02-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                             SOFTWATING SISTEM:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 43
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 2026-4124Uf
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 10

"WITH AND ACTERISTICS:
                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
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EDNESS: Unknown
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MOLECULE TYPE: Peptide
US-08-417-174-126
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MEDIUM TYPE:
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Patent No. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA, ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 1; Length 10; 100.0%; Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: User

ZIP: 11753
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordDerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,691
FILING DATE: 23-DEC-1994
CLASSIFICATION NUMBER: 29,281
FILING DATE: Baron, Ronald J.
ATTORNEY/AGENT INFORMATION:
MAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/COCKET NUMBER: 29,430
TELEFAX: (516) 822-3550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                             Sequence 9, Application US/08363691
Sequence 9, Application US/08363691
Sequence 9, Application US/08363691
Sequence 9, S770201
GENERAL INFORMATION:
APPLICANT: Goulany, Els A.J.M.
APPLICANT: Hunt, Donald H.
ITLE OF INVENTION: HA-2 Antigenic Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, ADDRESSEE: Hoffmann & Baron, ADDRESSEE: Hoffmann & Baron, STREET: 350 Jericho Turnpike
CITY: Jericho
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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CITY: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 10; Conservative
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MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
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US-08-417-174-126
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                                                                   US-08-363-691-9
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Sequence 1, Application US/08992877

Sequence 1, Application US/08992877

Sequence 1, Application US/08992877

Patent No. 6340461

Sequence 1, Application US/08992877

TITLE OF INVENTION: SUPERANTIGEN BSED METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: TREATMENT OF INFECTIOUS DISEASE

FILE REFERENCE: superantiqen

CURRENT APPLICATION NUMBER: US/08/992,877

CURRENT APPLICATION NUMBER: US/08/992,877

PRIOR PILING DATE: 1997-12-17

PRIOR PILING DATE: 1997-04-17

NUMBER OF SEQ ID NOS: 78

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 10
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                                                  Gaps
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Sequence 226, Application US/09311784A

Patent No. 6534482

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glann Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Ishioka, Glann Y.
APPLICANT: Ishioka, Glann Y.
APPLICANT: Ishioka, Glann Y.
APPLICANT: Intermed to the standard of the same
FILE REFERENCE: 39963-2002.01
CURRENT APPLICATION NUMBER: US/09/311,784A

PRIOR FILING DATE: 1998-05-15

PRIOR FILING DATE: 1998-05-15
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      100.0%; Score 55; DB 3; Length 10; 100.0%; Pred. No. 0.00099; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 4; Length 10; Pred. No. 0.00099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: HBc 18-27 analog (peptide 941.01)
US-09-311-784A-226
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 226
LENGTH: 10
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                        1 FLPSDYFPSV 10
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      Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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; Sequence 126, Application US/09267439
; Patent No. 6210778
; GENERAL INFORMATION:
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: METHODS
; VINBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
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                                                                                                                                                                                                                                                                                                                                 Length 10;
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PRICATION NATA:
PRILING DATE:
PAPLICATION NATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 22-APR-1995
ATTORNEY/AGBNT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2056-4124US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFANCE: (212) 758-4800
TELEFANCE: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 0186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                          INFORMATION FOR SEQ ID NO: 647:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 10; Conservative 0
                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-647
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STRANDEDNESS: Unk:
TOPOLOGY: Unknown
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AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Reogh, Elissa A.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: HAA Class I A2 Tumor Associated Antigen
TITLE OF INVENTION: Peptides and Vaccine Compositions
FILE REFERENCE: 018623-015710US
CURRENT APPLICATION NUMBER: US/09/543,608A
CURRENT PILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                     COUNTY: U.S.A.

COUNTY: U.S.A.

COMPUTER READABLE FORM:

MEDIUUT TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: THE PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/497,232

FILING DATE: 03-Feb-2000

PRIOR APPLICATION: UNKnown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/074,410

FILING DATE: 08-MAY-1998

APPLICATION NUMBER: US/09/074,410

FILING DATE: 08-MAY-1998

ATTORNY/AGENT INPERMATION:

ATTORNY/AGENT INPERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.00099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 042881/0114
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                     ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-543-608A-43
; Sequence 43, Application US/09543608A
; Patent No. 6602510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                         NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 10
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      Gaps
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                                                            MESULT 8

US-09-073-138-126

i Sequence 126, Application US/09073138

j Patent No. 6537560

i GENERAL INFORMATION:

APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,

ITILE OF INVENTION: MELANOMA ANTICENS AND

TITLE OF INVENTION: HEIR USE IN DIAGNOSTIC AND THERAPEUTIC;

TITLE OF INVENTION: METHODS

TITLE OF INVENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: AGRAWAL, Babita
KRANTZ, Mark J.
REDDISH, Mark A.
LONGENECKER, B. Michael
TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZUPILIATION USA ZUPILATION DATA: USA ZUPILATION DATA: USA ZUPILIATION UNMBER: US/09/073,138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
CLASSIFFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US
TELECHONE: (212) 758-4800
TELECHAN: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09497232
Patent No. 6600012
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 10; Conservative
10; Conservative
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EDNESS: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FLPSDYFPSV 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-497-232-4
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   Matches
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Gaps

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APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
                                                                                                      APPLICANT: Slingluff, Craig L, Jr.
APPLICANT: Engelhard, Victor H.
APPLICANT: Hunt, Donald F.
APPLICANT: Hunt, Donald F.
APPLICANT: Shabanowitz, Jeffrey
APPLICANT: Cox, Andrea L.
TITLE OF INVENTION: PREPTIDES RECOGNIZED BY MELANOWA-SPECIFIC TITLE OF INVENTION: CYTOTOXIC LYMPHOCYTES, AND USES NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 55; DB 4; I
100.0%; Pred. No. 0.00099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,784B
FILING DATE: 29-APR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/197,399
FILING DATE: 16-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: SLINGLUFF=1
TELEPHONE: 202-628-5197
TELEPHONE: 202-628-5197
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                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
                                           ; Sequence 97, Application US/08234784B; Patent No. 6660276; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-239-043D-2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
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Patent No. 6607227
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
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COUNTRY: USA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,502B
FILING DATE: 20-May-1996
CLASSIFICATION: CURROWN>
                                                                                      Query Match 100.0%; Score 55; DB 4; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00099; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.00099; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INPORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32.762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELEPHONE: (415) 576-0300
; FEATURE:
; OTHER INFORMATION: Standard Peptide 941.01
US-09-543-608A-43
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-591-5028-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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Best Local Similarity 100.
Matches 10; Conservative
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Gaps

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Length 10; 0; Indels

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TYPE: PRT
ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
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STREET: 52
"W: Boston
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STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        SEO ID NO 2487
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                                                                                                 PRIOR APPLICATION NUMBER: US 09/189, 702
PRIOR APPLICATION NUMBER: US 08/978, 291
PRIOR FILING DATE: 1998-11-10
PRIOR PILING DATE: 1997-11-25
PRIOR PILING DATE: 1997-11-25
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1997-03-12
PRIOR PILING DATE: 1997-03-13
PRIOR PILING DATE: 1996-03-13
PRIOR PILING DATE: 1996-05-13
PRIOR APPLICATION NUMBER: US 08/461, 603
PRIOR APPLICATION NUMBER: US 08/347, 610
PRIOR APPLICATION NUMBER: US 08/347, 610
PRIOR PILING DATE: 1994-12-01
PRIOR PILING DATE: 1994-11-23
PRIOR PILING DATE: 1994-11-23
PRIOR PILING DATE: 1994-07-21
PRIOR PILING DATE: 1994-07-21
PRIOR PILING DATE: 1994-07-21
PRIOR PILING DATE: 1994-02-16
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TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions PILE REPERRORS: 2060.0060007
CURRENT APPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.00099;
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PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/920,360
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR APPLICATION NUMBER: US 08/820,363
PRIOR PILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-13
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APPLICATION NUMBER: US 08/461,603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2487, Application US/09239043D Patent No. 6689353 GENERAL INFORMATION: APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: HBV analog peptide US-09-239-043D-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Livingston, Brian D.
Celis, Esteban
Kubo, Ralph T.
Grey, Howard M.
Chesnut, Robert
Epimmune Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sidney, John
Southwood, Scott
Vitiello, Maria A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
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LENGTH: 10
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PRIOR FILING DATE: 1995-06-05

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR PILING DATE: 1994-11-01

PRIOR PILING DATE: 1994-11-23

PRIOR PILING DATE: 1994-01-02

PRIOR PILING DATE: 1994-07-02

PRIOR PILING DATE: 1994-07-01

PRIOR PILING DATE: 1994-07-04

PRIOR PILING DATE: 1994-03-04

PRIOR FILING DATE: 1994-03-04

PRIOR FILING DATE: 1994-03-04

PRIOR PILING DATE: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Standard peptide that binds to HLA A*0201, HLA ; OTHER INFORMATION: A*0202, HLA A*0203, HLAA*0206, HLA A*0207 US-09-239-043D-2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: Eberlein M.D., Timothy J.
APPLICANT: Peoples M.D., George E.
APPLICANT: Yoshino M.D., Ichiro
TITLE OF INVENTION: Isolated Antigenic Oncogene Peptide
TITLE OF INVENTION: Fragments and Uses
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Choate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 55; DB 4; Length 10; 100.0%; Pred. No. 0.00099;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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RR: 092662-003
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GENERAL INFORMATION:
APPLICANT: Eberlein M.D., Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Kaplan Esq., Warren A.
REGISTRATION NUMBER: 34,199
REPRENCE/DOCKET NUMBER: 09266
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617:227-5020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-01672-12
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0; Gaps
Query Match 100.0%; Score 55; DB 5; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00099; Matches 10; Conservative 0; Mismatches 0; Indels
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¹ FLPSDYFPSV 10 ||||||||| 1 FLPSDYFPSV 10

Search completed: June 29, 2005, 01:44:31 Job time: 19.7863 secs

juis bade Blank (nsbto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-76

1 YLEPAIAKY 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOMMERTES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	38	80.9	:	-	J00855	hypothetical 36.8K
8	38	80.9		~	AI0926	
m	38	80.9		~	A11037	
4	37	78.7		7	C84364	porting
S	37	78.7		~	T16763	hypothetical prote
9	35	74.5		~	T41008	hypothetical prote
7	34	72.3	108	~	JN0695	υ
æ	34	72.3		N	B69063	O-antigen transpor
σ	34	72.3		~	T18776	hypothetical prote
10	34	72.3	-	~	C84547	
11	33	70.2	286	~	F89796	hypothetical prote
12	33	70.2		~	AC3567	ㄷ
13	33	70.2		N	T00158	amidase (EC 3.5
14	33	70.2		~	T43895	t-complex-type mol
15	33	70.2	1168	~	S76195	hypothetical prote
16	33	70.2		~	T07584	Н
17	32	68.1	156	N	A97841	
18	32	68.1		N	G87495	hypothetical prote
19	32	68.1		~	D75471	probable proline d
20	32	68.1	440	~	T50912	hypothetical prote
21	32	68.1		N	S55106	
22	32	68.1		~	S38011	hypothetical prote
23	32	68.1		~	S76197	
24	32	68.1	1286	-	S38058	
25	31	0.99		~	AH2575	
26	31	99		~	C71184	
27	31	99	17	~	D86696	pantothenate metab
28	31	99	7	~	G84043	
59	31	66.0	230	~	F95083	transcription acti

hypothetical prote	coenzyme F420 hydr	head size determin	head size determin	MG068 homolog D02	ketopantoate hydro	probable membrane	ribose-phosphate d	ribose-phosphate d	ribose-phosphate d	ribose-phosphate d	hypothetical prote	hypothetical prote	probable fructose-	hypothetical prote	NADH2 dehydrogenas
B97951	S16723	GSBPP4	F42465	S73587	AF1312	AC0489	KIHUR1	KIRTR1	S46824	860393	T04826	T20728	B95949	AB2226	T13815
~	0	Н	~	N	~	~	Н	н	N	~	N	N	N	~	0
230	243	244	244	265	277	309	318	318	320	321	323	334	347	350	368
0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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hypotherical 36.8K protein - Bscherichia coli retron Ec67
NyAlternate names: gpQ protein homolog
NyAlternate names: gpQ protein homolog
SpSecies Bscherichia coli retron Ec67
C;Dscession: JQ0855
Hssquence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0855
Hssu, W.Y.; Innouye, M.; Innouye,
```

щар A; Note: insertion site is equivalent to 19 min of E. coli K12 genetic

Gaps ö Query Match 80.9%; Score 38; DB 2; Length 326; Best Local Similarity 87.5%; Pred. No. 3.4; Matches 7; Conservative 1; Mismatches 0; Indels

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||||:||| LEPALAKY 133 2 LEPAIAKY 9 126 ð g

Probable capsid portal protein [imported] - Salmonella enterica subsp. enterica serovar 1920 C; Species: Salmonella enterica subsp. enterica serovar Typhi G; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C; Accession: A10926 K; Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Alaure 413, 848-852, 2001
A; Alaurence: Parker Complete genome sequence of a multiple drug resistant Salmonella enterica serc A; Reference number: AB0502; MUD:21534947; PMID:11677608
A; Accession: A10926
A; Status: preliminary
A; Residues: 1-345 c.PAR.

A; Cross-references: GB: AL513382; PIDN: CAD09435.1; PID:g16504552; GSPDB: GN00176 C; Genetics:

Score 38; DB 2; Length 345; Pred. No. 3.6; 80.9%; Query Match Best Local Similarity

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A;Cross-references: UNIPROT:Q21994; EMBL:U00036; NID:g458996; PID:g459000; PIDN:AAA5065.
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypotherical protein SPCC1494.07 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41008
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, June 1998
A;Reference number: Z21963
A;Reference number: Z21963
A;Recession: T41008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Roleutle type: DNA
A;Residues: 1-152 < WOO>
A;Residues: 1-152 < WOO>
A;Residues: 1-152 < WOO>
A;Residues: UNIPROT:O60081; EMBL:AL023776; PIDN:CAA19305.1; GSPDB:GN00067; SPDB:A;Residuestal Bource: Strain 972h-; cosmid c1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tributyltin chloride resistant protein - Alteromonas sp. (strain M-1)
C;Species: Alteromonas sp.
C;Species: Alteromonas sp.
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
C;Accession: UN0695
R;Fukagawa, T.; Suzuki, S.
Biochem Elophyse Res. Commun. 194, 733-740, 1993
A;Title: Cloning of gene responsible for tributyltin chloride (TBTC1) resistance in TBTA.
A;Reference number: UN0695; MUID:93343930; PMID:8343157
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:R151.2
A;Introns: 11/1; 63/3; 235/2; 293/2; 346/3
C;Superfamily: ribose-phosphate pyrophosphokinase catalytic chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.5%; Score 35; DB 2; Length 1502; 100.0%; Pred. No. 83; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.7%; Score 37; DB 2; Length 377; 77.8%; Pred. No. 6.6; tive 0; Mismatches 2; Indels
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                   C;Accession: T16763
R;Fulton, L.
submitted to the EMBL Data Library, February 1994
A;Description: The sequence of C. elegans cosmid R151.
A;Reference number: $44639
A;Accession: T16763
                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-377 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 72.3%; Score 34; DB 2; Best Local Similarity 87.5%; Pred. No. 7.2; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 7; Conservative
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A;Residues: 1-108 «FUK»
Keywords: membrane protein
F;87-92/Region: hydrophilic
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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. P. Leithauser, B.; Faller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: C84364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:Q9HNE1; GB:AE004437; NID:g10581556; PIDN:AAG20279.1; GSPDB:G
C,Genetics:
                                                                                                                                                                                                                                               probable capsid portal protein [imported] - Salmonella enterica subsp. enterica serovar probable capsid portal protein [imported] - Salmonella enterica serovar Typhi d.Note: this species has also been called Salmonella typhi c.pare: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C.Accession: Al1037 C.pares, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Athiches: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; MUID:1534947; PMID:11677608
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A;Cross-references: GB:AL513382; PIDN:CAD06750.1; PID:g16505401; GSPDB:GN00176
C;Genetics:
A;Gene: STY4628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H+-transporting ATP synthase subunit C [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Species: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 6.1;
0; Mismatches 2; Indels
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           Indels
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C;Superfamily: H+ transporting ATP synthase C subunit
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hypothetical protein R151.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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Pred. No. 3.7;
1; Mismatches
        Mismatches
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Best Local Similarity 87.5
Matches 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-348 <PAR>
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Matches 7; Conserv
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                                                           2 LEPAIAKY
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           7;
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Gaps

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Nature 402, 761-768, 1999
Nature and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84547
A;Accession: C84547
A;Residues: preliminary
A;Residues: DAA
A;Residues: 1-1169 <STO>
A;Coss=references: UNIPROT:Q7XJL8; GB:AE002093; NID:g6598360; PIDN:AAF18598.1; GSPDB:GCGenetics:
A;Genetics: At2g17030
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89796
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K., C.; Sibiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-286 -(XIIX>
A;Cross-references: UNIPROT:Q99WR0; GB:BA000018; PID:g13700231; PIDN:BAB41529.1; GSPDB:
A;Experimental source: strain N315
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: ACJS67
C;Accession: ACJS67
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
Nazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A;Reference number: ADJ252; PMID:11756688
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A;Molecule type: DNA
A;Residues: 1-339 <KUR>
A;Cross-references: UNIPROT:Q8YCR8; GB:AE008918; PIDN:AAL53702.1; PID:g17984624; GSPDB:
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-nitropropane dioxygenase (EC 1.13.11.32) [imported] - Brucella melitensis (strain 16
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146
A,Accession: F89796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Staphylococcus aureus (strain N315)
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Pred. No. 35;
2; Mismatches 2; Indels
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Pred. No. 1e+02;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.3%;
66.7%;
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Matches 5; Conservative
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252 YIEPKVAHY 260
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C; Keywords: oxidoreductase
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Best Local Similarity
Matches 6; Conserv
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A; Gene: BMEII0460
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A;Reference number: Z19020
A;Accession: T18776
A;Atatuer: preliminary; translated from GB/EMBL/DDBJ
A;Hotlecule type: DNA
A;Residues: 1-564 <WIL>
A;Residues: 1-564 <WIL>
A;Cross-references: UNIPROT:045228; EMBL:Z82256; PIDN:CAB05117.1; GSPDB:GN00022; CESP:BdC;Genetics:
                                                                                                                                                                                                                                                                                O-antigen transporter homolog - Methanobacterium thermoautotrophicum (strain Delta H) (5) Species: Methanobacterium thermoautotrophicum (5) Species: Methanobacterium thermoautotrophicum (5) Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004 (5) Accession: B69063 (8) Accession: B69063 (8) Accession: B69063 (8) Accession: B69063 (8) Accession: B69063 (9) Accession: B69063 
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2 Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84547
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:027516; GB:AE000908; GB:AE000666; NID:g2622579; PIDN:AAB8594
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH1472
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18776
R;Matthews, L.
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A;Introns: 125/3; 160/2; 245/3; 359/2; 427/3; 494/3
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Pred. No. 9;
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Pred. No. 45;
2; Mismatches
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87.5%;
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Similarity 75.0%;
6; Conservative 2
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Matches 7; Conservative
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344 YLQPAISK 351
                                                                                             LTPAIAKY 75
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Best Local Similarity
Matches 6; Conserv
                                  LEPAIAKY
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A;Molecule type: DNA
A;Residues: 1-484 <KAN>
A;Cross-references: UNIPROT:080064; EMBL:AB009866; NID:d1204727; PIDN:BAA31898.1; PID:d1
C;Keywords: hydrolase
                                                                                                                                                                                                                                                    Middle (EC 3.5...) - Staphylococcus aureus phage phi PVL
NiAlternate names: peptidoglycan hydrolase
Cispecies: Staphylococcus aureus phage phi PVL
Cispecies: Staphylococcus aureus phage phi PVL
Cipate: 32-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CiAccession: T00158
RiKaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
A; Kineko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
A; File: Panton-Valentine leukocidin genes in a phage-like particle isolated from mitomy A; Reference number: Z14119; MUID:98067870; PMID:9404084
A; Accession: T00158
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R;Iijima, M.; Shimizu, H.; Tanaka, Y.; Urushihara, H.
R;Iijima, M.; Shimizu, H.; Tanaka, Y.; Urushihara, H.
R;Iijima, M.; Shimizu, H.; Tanaka, Y.; Urushihara, H.
R;IIII-10-106, 1998
A;Title: A Dictyostelium discoideum homologue to Tcp-1 is essential for growth and devel
A;Reference number: Z22716; MUID:98296288; PMID:9630545
A;Accession: T43895
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-548 <113>
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C;Genetics:
A;Gene: Tcp-1
C;Superfamily: molecular chaperone t-complex-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t-complex-type molecular chaperone TCP1 homolog [imported] - slime mold (Dictyostellum C;Species: Dictyostellum discoideum C;Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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  Length 339;
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Pred. No. 63;
1; Mismatches
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100.0%; Pred. No. 72;
ive 0; Mismatches
    5;
  Score 33; DB Pred. No. 42; 2; Mismatches
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Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity luu...
A: Conservative
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Best Local Similarity 66...
Secondary 61...
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208 YITPNIAKY 216
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hypothetical protein all1527 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 876195
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

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O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud. DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti. S.; Reference unalysis of the genome of the unicellular cyanobacterium Synechocysti. S.; Reference unaber: S74132; MUID:97061201; PMID:8905231
A;Accession: S76195
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1168 cKAN>
A;Residues: 1-1168 cKAN>
A;Residues: UNIPROT:P74359; EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA184
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s111527
Query Match
Best Local Similarity 55.6%; Pred. No. 1.78+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
D) 343 YLKPGLAKF 351
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salmonella
burkholderi
burkholderi
burkholderi
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                                                                                                                                                                                                        June 28, 2005, 23:28:22; Search time 54.2473 Seconds (without alignments) 84.958 Million cell updates/sec
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Q8zms9
Q6mkg4
O60081
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1612378 seqs, 512079187 residues
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Q7NJS9
Q8ZMS9
Q6MKG4
O60081
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Gapop 10.0 , Gapext 0.5
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Wang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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66.7%; Pred. No. 15;
iive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buell R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC092211; AAN05003.1; -.
HSSP; Q40577; 1HX9.
                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
Putative aristolochene synthase, 3'-partial (Fragment)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                            (TrEMBLrel. 22, (TrEMBLrel. 22,
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199 YLEPGLARY 207
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01-0CT-2002
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Parkhill J., Dougan G., James K.D., Thomson N.R., Fickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Barooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Dowle R., Dowle L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CTI8.";
J. Bacteriol. 185:2330-2337(2003).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Enterobacteriaceae; Salmonella.
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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Last annotation update)
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Last annotation update)
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EMBL; AE016845; AAO70939.1; -.
Pfam; PF04860; Phage_portal; 1.
TIGRFAMS; TIGR01540; portal_PBSK; 1.
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                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=STY3674, t3416;
1;
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                                                                                                                                                                                                                    Q82359; Q7C655;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:848-852(2001).
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Matches 7; Conservative
7; Conservative
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                                                                                    117 LEPALAKY 124
                                          2 LEPAIAKY 9
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                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CT18;
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                                                                                                                                                STRAIN-01:NM / CL-1;
MEDLINE=91067724; PubMed=1701261;
Hsu M.-Y., Inouye M., Inouye S.;
"Retron for the 67-base multicopy single-stranded DNA from Escherichia coli: a potential transposable element encoding both reverse transcriptase and Dam methylase functions.";
Proc. Natl. Acad. Sci. U.S., 87:9454-9458(1990).
-: SIMILARITY: Strong, to the phage P2 presumed portal vertex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANN=ATCC 23344;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Nierman W.C., DeShazer D., Konning C.M., Brinkac L.M., Daugherty S.C.,
Pavidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madipu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Structural flexibility in the Burkholderia mallei genome.";
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
EMBL; CP000010; AAU48679:1;
-. SEQUENCE 337 AA; 38300 MW; AC77382B0D4776F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                       Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Burkholderiaceae; Burkholderia.
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InterPro; IPR006944; Phage portal.
InterPro; IPR006430; Portal PBSX.
Pfam; PF04860; Phage portal; 1.
TIGRPAMs; TIGR01540; portal PBSX; 1.
Hypothetical protein; Transposable element.
SEQUENCE 326 AA; 36819 MW; 80A67F9A238173E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical 36.8 kDa protein (ORF5) (Retron EC67)
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Pred. No. 24;
1; Mismatches
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Pred. No.
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Burkholderia mallei ATCC 23344.
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348 AA; 39710 MW; 68F1A713B73778A4 CRC64;
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STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
MEDLINE=22531367; PubMed=12644504;
DOI=10.1128/JB.185.7.2330-2337.2003;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                              STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;
MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Carer S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Stevenl T., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
SEQUENCE 345 AA; 39126 MW; PE41C15B20DB0D28 CRC64;
                                                                                                                                                                                                                         of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U. S.A. 99:17020-17024 (2002).

EMBL; AC16758; AMT9920.1;
InterPro; IPR0069027; L9 Nike.

InterPro; IPR006944; Phage portal.

InterPro; IPR00640; Portal PBSX.

Pfam; PF04660; Phage_Dortal. 1.

Pfam; PF04660; Phage_Dortal. 1.
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01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
02-MAR-2002 (TYEMBLrel. 28, Last annotation update)
Probable capsid portal protein.
OrderedLocusNames=STY4628, t4321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 38; DB 2;
87.5%; Pred. No. 26;
iive 1; Mismatches
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EMBL; AE016848; AAO71777.1; -.
Pfam; PF04860; Phage portal; 1.
TIGREAMS; TIGR01540; portal PBSX; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 87.5%;
les 7; Conservative
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127 LEPALAKY 134
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NCBI_TaxID=217992;
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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Davidson T.D., Deboy R.T., Dimitrov G., Dadson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Selengut J., Shamblin C., Sullivan B.A., White O., Yu Y., Zafar N.,
Proc. In Praser C.M.;
Perc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

EMBL; CP000010; AAU482611;
EMBL; CP000010; AAU482611;
EMBL; CP000010; AAU482611;
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Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chilingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Reith K.E., Maddison M., Moule S., Price C., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
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Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
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Burkholderiaceae, Burkholderia.
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87.5%; Pred. No. 26;
tive 1; Mismatches 0; Indels
                             Length 348;
                                                                                     Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Phage portal protein, PBSX family.
ORFNames=BWA2691,
Burkholderia mallei ATCC 23344.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                          351 AA
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                             80.9%; Score 38; DB
87.5%; Pred. No. 26;
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Query Match
Best Local Similarity 87.5,
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Best Local Similarity 87.5-
T. Conservative
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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ORFNames=BPSS1062;
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131 LEPALAKY 138
                                                                                                                                                                                               129 LEPALAKY 136
                                                                                                                                       2 LEPAIAKY 9
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Query Match
Best Local Similarity 66./v,
Best a 6; Conservative
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Best Local Similarity 87.5
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115 YLEPGLARY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=OSJNBb0049A16.6;
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Ry PubMcd=1537794;

Atkins T. Crossman L.C., Pitt T., Churcher C., Mungall K.,

Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,

Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,

Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,

Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,

Reitwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,

Reitwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,

Robinowitsch E., Rutherford K., Sanders M., Simmonds M.,

Songsivilai S., Stevens K., Tunapa S., Vesaratchavest M.,

Whitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

"Genomic plasticity of the causative agent of melioidosis,

Burkholderia pseudomallei.",

"Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).

RBBL; BSZ1965; CAH34160.11; -.

SEQUENCE 351 AA; 39441 MW; BB5D1A854843ED6A CRC64;
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                                                                                                                              Gaps
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DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DF Probable portal protein.
3N ORNames=BPELOII.
S Burkholderia pseudomallei K96243.
C Burkholderia pseudomallei Betaproteobacteria; Burkholderiales;
C NCBI_TAXID=272560;
V NCBI_TAXID=272560;
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitchead S., Yacto F.C.F., Parkhill J.; Grenomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei."; Burkholderia pseudomallei."; Burkholderia St. U.S. A. 101:14240-14245 (2004). EMBL; BX571966; CAH38528.1; - SEQUENCE 351 AA, 39489 MW; EADDB3CC39BA2BED CRC64;
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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                                                                                                    DB 2; Length 351;
26;
                                                                                                                             0; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative phage portal vertex protein.
ORFNames=BPSL0173;
                                                                                                  Score 38; DB 2; Pred. No. 26; 1; Mismatches
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87.5%;
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Best Local Similarity 87.5.
Best Local 7; Conservative
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nes 7; Conservative
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131 LEPALAKY 138
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131 LEPALAKY 138
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Q63YL4;
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PubMed=1537739;
PubMed=1537739;
Athin=K96243;
PubMed=1537739;
Athin T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Athin T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Athin T.G., Titball R.W., Thomson N.K., Bason N., Beacham I.R., Benches K., Brown K.A., Brown K.P., Challing G.L., Cherevach I., Choillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Rabbinowitech E., Rutherford K., Sanders M., Sinmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Molitehead S., Yeate C., Barrell B.G., Oyston P.C.F., Parkhill J.; Genomic plasticity of the causative agent of melioidosis, Burkholderia pseudomallei."; Burkholderia pseudomallei."; Proc. Nall. Asad. Scil. U.S.A. 101:14240-14245 (2004).
REMBL; BX511965; CAH34096.1; -. REQUENCE 370 AA; 41640 MW; E9F5FF9F77AEF86B CRC64;
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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87.5%; Pred. No. 28;
iive 1; Mismatches 0; Indels
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Submirted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO90120; AAL31055.1; -.
HSSP; O81192; INIZ.
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GO; GO:0008152; P:metabolism; IEA.
Pfam; PF01397; Terpene Synth; 1.
SEQUENCE 468 AA; 53441 MW; 81D9E5B891305C05 CRC64;
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STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736 (03)12659-1;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";

Lancet 361:743-749(2003).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Capsid protein (Fragment).
Turkey astrovirus 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
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Vibrionaceae; Vibrio.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein VP2909.
                                                                                                                                                                                                                                                                                                                      80.9%; Score 38; DB 2;
66.7%; Pred. No. 38;
ive 2; Mismatches
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                             InterPro; IPR005630; Terpene, synth C. InterPro; IRR008949; Terpenoid synth. InterPro; IPR008930; Terpenoid synth. InterPro; IPR001906; Terp synth-like. Pfam; PR01397; Terpene synth; 1. Pfam; PR0396; Terpene synth; 1. SEQUENCE 505 AA; 57549 MW; DE64AS.
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GO:0008152; P:metabolism; IEA
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Conservative
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152 YLEPGLARY 160
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Best Local Similarity
6; Conserv?
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Best Local Similarity
7; Conserve
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NCBI_TaxID=246343;
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                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton I.L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
White O., Salberg S.L., Fraser C.M.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017107, AAPS4380.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 468
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC146481; AAR87368.1; ~.
GO; GO:0016829; F:lyase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936; Terpene_synth_C; 1.
468 AA; 53441 MW; 81D9E5B891305C05 CRC64;
                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
1-ORT-2004 (TrEMBLrel. 26, Last annotation update)
Putative monoterpene synthase.
ORFNames=OSJNBb0049A16.6;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative terpene synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 2;
Pred. No. 35;
                                 468 AA
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                                                                                                     Created)
                                 PRT;
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66.7%;
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                                                                                                 (TrEMBLrel. 25,
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                          PRELIMINARY;
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Matches 6; Conserv
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                                                                                                 01-OCT-2003
01-OCT-2003
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                             Q7XD63
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RESULT 13

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RP SEQUENCE FROM N.A.
RA Guy J.S., Miles A., Smith L.G., Fuller F., Schultz-Cherry S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

BEBL; AX320042; AAQ88297.1; -.
FT NON TER 261 261
SQ SEQUENCE 261 AA; 29740 MW; 8E36C789F52D733D CRC64;

Query Match
Rest Local Similarity 77.8; Pred. No. 31;
Best Local Similarity 77.8; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
| | | | | | | | | |
| Db 110 YTEPAIQKY 118

Search completed: June 29, 2005, 01:34:54
Job time: 57.2473 secs
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Sequence 78 Sequence 13

Sequence 6219, Ap Sequence 14967, Sequence 14967, Sequence 164967, Sequence 258227, Sequence 27227, Sequence 177259, Sequence 177259, Sequence 177259, Sequence 177259, Sequence 27613, Sequence 177251, Sequence 27673, Sequence 27673, Sequence 177252, Sequence 2, Appli Sequence 15052, Sequence 15053, Sequence 15053, Sequence 15053, Sequence 15053, Sequence 15053, Sequence 15053, Sequence 121286, Sequence 121286, Sequence 121286, Sequence 2567, A

Scoring table:

Searched:

Database

Title: Perfect score:

Seguence:

OM protein

Run on:

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APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
TITLE OF INVENTION: HIA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSEE: Townsend and Townsend Khourie and Crew STREET: One Market Plaza, Steuart Street Tower, 20th STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPETANTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPELICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION NUMBER: US 08/278,634
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REPREBRICE/DOCKET NUMBER: 34,774
REPREBRICE/DOCKET NUMBER: 34,774
REPREBRICE/DOCKET NUMBER: 34,774
REPREBRICE/DOCKET NUMBER: 14137-80-1
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4 US-10-076-157-13
5 US-10-369-493-6219
5 US-10-369-493-10443
6 US-10-437-963-149025
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6 US-10-425-115-296016
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US-10-424-59-161628

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US-10-732-923-15052
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US-10-437-963-17266
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US-09-815-242-12173
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US-10-437-963-177254
US-10-437-963-133630
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. Sequence 10. Application US/08344824
. Publication No. US20030152580A1
. GENERAL INFORMATION:
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STATE: California
COUNTRY: USA
RESULT 1
Sequence 10, Appl
Sequence 2115, Ap
Sequence 2175, Ap
Sequence 2486, Ap
Sequence 117, App
Sequence 117, App
Sequence 14226,
Sequence 48180, A
Sequence 5776, App
Sequence 5776, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                   (without alignments)
64.268 Million cell updates/sec
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                                                                                                                                                                           June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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(cgn2 6/ptodata1/pubpaa/USO7 PUBCOMB.ppp:*

(cgn2 6/ptodata1/pubpaa/PCT_NEW_PUB.pep:*

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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1717557 seqs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Score

Result No.

Sequence 177254, Sequence 133630,

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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Mosey, Esteban
APPLICANT: Mosey, Esteban
APPLICANT: Celis, Esteban
APPLICANT: APPLICATION NUMBER: US/10/149,138
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 1209-12-11
PRIOR APPLICATION NUMBER: US/12-11
PRIOR APPLICATION NUMBER: US/12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE: PatentIn version 3.1
LENGTH: 9
LENGTH: 9
MAGE2/3 Using Peptide and Nucleic Acid Compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 47; DB 15; 100.0%; Pred. No. 1.5e+06;
              THIER COTINGENIALY: TAKABLY SELING PEDFLOCATION CURRENT APPLICATION NUMBER: US/10/149,135
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: PCT/US00/3345
PRIOR PILING DATE: 2000-12-11
PRIOR PELING DATE: 1999-12-10
PRIOR PELING DATE: 1999-12-10
PRIOR PELING DATE: 1998-11-10
PRIOR PELING DATE: 1998-11-10
PRIOR PELING DATE: 1998-11-20
PRIOR PELING DATE: 1993-04
PRIOR FILING DATE: 1993-04
PRIOR PELING DATE: 1993-04
PRIOR PELING DATE: 1993-11-29
PRIOR PELING DATE: 1993-06-04
PRIOR PELING DATE: 1993-03-05
NUMBER OF SEQ ID NOS: 2479
SOFTWARE: PACENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Artificial Peptide US-10-149-138-4188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificial Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4188, Application US/10149138 Publication No. US20040121946A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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| Publication No. US20040018971A1 |
| GENERAL INFORMATION: |
| APPLICANT: Sette, Alessandro |
| APPLICANT: Sette, Alessandro |
| APPLICANT: Southwood, Scott |
| APPLICANT: Southwood, Scott |
| APPLICANT: Chesnut, Robert |
| TITLE OF INVENTION: Inducing Cellular Immune Responses to |
| TITLE OF INVENTION: 10001 |
| TITLE OF INVENTION NUMBER: US/10/149,138 |
| CURRENT APPLICATION NUMBER: PG00-12-11 |
| PRIOR APPLICATION NUMBER: US 09/458,299 |
| PRIOR APPLICATION NUMBER: US 09/458,299 |
| PRIOR FILING DATE: 1999-12-11 |
| NUMBER OF SEQ ID NOS: 4641 |
| SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                100.0%; Score 47; DB 8; Length 9; 100.0%; Pred. No. 1.5e+06;
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APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
TITLE OF INVENTION: Inducing Cellular Immune Responses to
                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Artificial Peptide US-10-149-138-4188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2175, Application US/10149135
Publication No. US20040053822A1
                          TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERIFYICS:
LENGTH: 9 amino acids
(415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                          single
                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YLEPAIAKY 9
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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1 YLEPAIAKY
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TELEPHONE:
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LENGTH: 9
                                                                                                                                                                                                                                                          US-08-344-824-10
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APPLICANT:
APPLICANT:
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Sequence 142246, Application US/10437963
Sequence 142246, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Early Songwei
APPLICANT: Cao, Yongwei
APPLICANT: W. Wei
APPLICANT: Bunkharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 240653, Application US/10425115

Sequence 240653, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Applicant Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REPERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 240653

LENGTH: 129
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US-10-425-115-240653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 17; 100.0%; Pred. No. 1.5e+06;
                             CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR PILING DATE: 2000-08-18
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-09-16
NUMBER: OF SEQ ID NOS: 163
SEQ ID NO 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity 100.0
....hes 9; Conservative
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Matches 7; Conservative
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; ORGANISM: Homo sapiens
US-10-751-845-117
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19 YLQPAIAKW 27
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US-10-425-115-240653
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APPLICANT: Livingston, Brian D.
APPLICANT: Calis Esteban
APPLICANT: Calis Esteban
APPLICANT: Calis Esteban
APPLICANT: Chesuk, Raibh T.
APPLICANT: Chesuk, Robert
TITLE OF INVENTION: Unducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Unducing Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.006007
CURRENT PRILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-01-27
PRIOR PLILING DATE: 1999-11-10
PRIOR PLILING DATE: 1999-11-125
PRIOR PLILING DATE: 1999-11-125
PRIOR PLILING DATE: 1999-11-13
PRIOR PLILING DATE: 1997-13-13
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR PLILING DATE: 1997-01-13
PRIOR PLILING DATE: 1997-01-13
PRIOR PLILING DATE: 1997-01-13
PRIOR PLILING DATE: 1997-12-01
PRIOR PLILING DATE: 1997-12-01
PRIOR PLILING DATE: 1994-12-01
PRIOR PLILING DATE: 1994-11-23
PRIOR PLILING DATE: 1994-11-21
PRIOR PRILING DATE: 1994-03-04
PRIOR PLILING DATE: 1994-
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APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPITOES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
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US-10-654-601-2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 17; Length 9; 100.0%; Pred. No. 1.5e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                            Sequence 2486, Application US/10654601
Publication No. US20050063983A1
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: Sequence 117, Application US/10751845
: Publication No. US20050100928A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sidney, John
Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D.
Cells, Esteban
Kubo, Ralph T.
Grey, Howard M.
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                                                                                                                                                                                                                             Publication No. US20050063983A
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
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1 YLEPAIAKY 9
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Best Local Similarity
Matches 9; Conserv
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1; Mismatches
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ORGANISM: Caenorhabditis elegans
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77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Turkey astrovirus
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Matches 7; Conservative
     7; Conservative
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204 YAEPAILKY 212
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                                                                                                        106 YLVPALARY 114
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Best Local Similarity
Matches 7; Conserv
                                                        1 YLEPAIAKY
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US-10-437-963-172470
                                                                                                                                                                                          RESULT 10
US-10-369-493-5776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-5776
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US-10-684-129-9
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCES: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: (0/191,078

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-24

PRIOR PLING DATE: 2000-10-24

PRIOR PLING DATE: 2000-10-27

PRIOR PLING DATE: 2000-10-27

PRIOR PLING DATE: 2000-10-24

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Pred. No. 53;
                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_43270C.1.pep
US-10-437-963-142246
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 142246
LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-282-122A-48180
; Sequence 48180, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Yeskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamanco, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Burkholderia cepacia
US-10-282-122A-48180
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77.8%;
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SEQ ID NO 48180
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Best Local Similarity 66.7;
...... 6; Conservative
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                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YLEPAIAKY 9
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Best Local Similarity
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Sequence 5776, Application US/10369493
; Sequence 5776, Application US/10369493
; Publication No. US20030233675A1
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Gldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Chen, Xianfeng
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
    TITLE OF INVENTION PLANTS WITH IMPROVED
    TITLE OF INVENTION OF MICROBIAL PROTEINS
    TITLE OF INVENTION WOWBER: US 60/360,039
    PRIOR APPLICATION NUMBER: US 60/360,039
    PRIOR PILING DATE: 2002-02-21
    NUMBER OF SEQ ID NOS: 47374
    SEQ ID NO 5776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10684129;
Publication No. US20050079485A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schultz-Cherry,
APPLICANT: Koki, Matchew,
TITLE OF INVENTION: Method to Detect Antibodies Specific for Type-2 Turkey Astroviru,
FILE REFERENCE: 800.039US1
CURRENT APPLICATION NUMBER: US/10/684,129
CURRENT FILING DATE: 2003-10-10
NUMBER OF SEQ ID NOS: 28
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 15; Length 377;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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APPLICANT: Pompejus, Markus
APPLICANT: Suelberger, Harald
APPLICANT: Suelberger, Harald
APPLICANT: Joeffken, Hans Wolfgang
APPLICANT: Joeffken, Hans Wolfgang
APPLICANT: Joeffken, Hans Wolfgang
APPLICANT: Jamenez, Alberto;
APPLICANT: Jamenez, Alberto;
APPLICANT: Garcia, Maria Angeles Santos
TITLE OF INVENTION: microbial riboflavin synthesis
TITLE OF INVENTION: microbial riboflavin synthesis
FILE REPRENCE: 48664DIV
CURRENT APPLICATION NUMBER: US/10/076,157
CURRENT APPLICATION NUMBER: US 2002-02-15
PRIOR APPLICATION NUMBER: US 998-12-16
MUMBER OF SEQ ID NOS: 21
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WS-10-1369-493-6219

WS-10-1369-493-6219

Sequence 6219, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED

TITLE OF INVENTION: WIMBER: US/10/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 6219
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Pred. No. 3.9e+02;
2; Mismatches 0; Indels
                                                                                                                                                                          Sequence 13, Application US/10076157; Publication No. US20030027309A1; GENERAL INFORMATION:
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ORGANISM: Caenorhabditis elegans
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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US-10-076-157-13
                    227 YLEPNLARY 235
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149 YAEPSVVKY 157
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Best Local Similarity
5; Conserve
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                                                                                                                RESULT 14
US-10-076-157-13
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GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Exovalic, David K.

APPLICANT: Exovalic, David K.

APPLICANT: APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Butharov, Andrey A.

APPLICANT: Butharov, Andrey A.

APPLICANT: Butharov, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: US/10/437,963

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 172470
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APPLICANT: Cooper, Bret
APPLICANT: Glazebrock, Jane
APPLICANT: Glazebrock, Jane
APPLICANT: Gragiti, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: APLOSANT: Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
TITLE OF INVENTION: 10ENTIFICATION WUMBER: US/10/259,194A
CURRENT APPLICATION NUMBER: US 60/325,277
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTHARE: PATENTIFIED NOS: 662
NUMBER OF SEQ ID NOS: 662
CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTRACTOR OF THE CONTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 16; Length 527;
Pred. No. 1.4e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT4530_70602C.1.pep
US-10-437-963-172470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 78, Application US/10259194A; Sequence 78, Application US/10259194A; Publication No. US20040010815A1; GENERAL INFORMATION:
APPLICANT: Lange, Markus B.
APPLICANT: Ghassemian, Majid
APPLICANT: Grasemian, Majid
APPLICANT: Gooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Glazebrook, Jane
APPLICANT: Gazebrook, Jane
APPLICANT: Katagiri, Fumiyaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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159 YLEPNLARY 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-194A-78
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Search completed: June 29, 2005, 05:48:16

1 YLEPAIAKY 9

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Job time : 53.8517 secs

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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
Sequence 13, Appl
Sequence 45328, A
Sequence 2, Appli
Sequence 54202, A
Sequence 5453, Ap
Sequence 2410, A
Sequence 279, App
Sequence 13629, A
Sequence 13629, A
Sequence 3374, Ap
Sequence 3784, Ap
Sequence 3784, Ap
Sequence 3784, Ap
Sequence 3569, A
Sequence 3569, A
Sequence 54786, A
Sequence 54786, A
Sequence 54786, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Appli
Sequence 126, App
Sequence 42, Appl
Sequence 2486, Ap
Sequence 62, Appl
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5, Appli
11677, A
2824, Ap
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                                                                                                                             (without alignments)
39.842 Million cell updates/sec
                                                                                                          June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
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Sequence
Sequence
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-159-339A-126

US-09-239-043D-2486

US-09-200-920-62

US-09-212-247C-13

US-09-212-247C-13

US-09-212-247C-13

US-09-213-299C-5453

US-09-270-767-38985

US-09-270-767-54202

US-09-270-767-54202

US-09-213-999C-6819

US-09-213-999C-6819

US-09-213-999C-6819

US-09-134-000C-3784

US-09-134-000C-3784

US-09-270-767-38370

US-09-270-767-3887

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                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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882, App
7474 App
17382, Ap
41519, Ap
43819, Ap
932, Ap
8245, Ap
10455, Ap
10455, Ap
10608, Ap
3811, Ap
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Sequence 9
Sequence 7
Sequence 1
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US-09-248-796A-21348
US-09-107-433-4980
US-09-270-76-59221
US-09-538-092-882
US-09-949-016-7474
US-09-249-016-7474
US-09-249-016-7474
US-09-270-767-41519
US-09-134-0016-8245
US-09-270-767-43819
US-09-270-767-43819
US-09-270-767-43819
US-09-270-767-43819
US-09-270-767-43819
US-09-270-767-43819
US-09-270-767-43819
US-09-249-016-8245
US-09-348-016-8245
US-09-349-016-10455
US-09-949-016-10455
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US-09-949-016-10455
US-09-949-016-10455
US-09-949-016-8245
US-09-949-016-825
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us-08-186-266-3
; Sequence 3, Application US/08186266
; Patent No. 5652907
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPTIOPES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCES: 20
; CORRESPONDENCES: 20
; CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 0....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US 2110-1143
ZIP: 94105-1443
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,266
FILING DATE: 25-JAN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339
FILING DATE: 29-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-WAR-1993
PRIOR APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1993
PRIOR APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1993
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-50-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
```

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APPLICANT: Calis, Esteban
APPLICANT: Calis, Esteban
APPLICANT: Calis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060,0060007
CURRENT FILING DATE: 1999-01-27
CURRENT FILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-11-25
PRIOR PELICATION NUMBER: US 08/978,291
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR PILING DATE: 1994-12-01
                                                                                                                                                                         APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Southwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa A.
APPLICANT: Epimmun Robert
APPLICANT: Epimmun Robert
APPLICANT: Epimmun Robert
APPLICANT: Peptides and Vaccine Compositions
TITLE OF INVENTION: Peptides and Vaccine Compositions
FILE REFERENCE: 018623-01571008;
CURRENT APPLICATION NUMBER: US/09/543,608A
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Standard Peptide 944.02
US-09-543-608A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2486, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
                                                                                                                  ; Sequence 42, Application US/09543608A; Patent No. 6602510; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sidney, John
Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D.
Celis, Esteban
Kubo, Ralph T.
Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
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Best Local Similarity luv...
Best Conservative
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1 YLEPAIAKY
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                                                                                         US-09-543-608A-42
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                                                                                                                                         100.0%; Score 47; DB 1; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 126, Application US/08159339A
Sequence 126, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Celis, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTRY: USA
ZIP: 94111-3834
COMPUTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 32,762
TELEPHONE: (415) 576-0300
                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                Query Match
Best Local Similarity 10v...
9, Conservative
  LENGTH: 9 amino acids
                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-186-266-3
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Best Local Similarity
Matches 9; Conserve
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US-08-159-339A-126
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1 YLEPAIAKY 9

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Gaps

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US-09-876-221-2

Sequence 2, Application US/09876221

Sequence 2, Application: Thomas

APPLICANT: Rea, Stephen

APPLICANT: Rea, Stephen

APPLICANT: Estenhaber, Frank

APPLICANT: Estenhaber, Frank

APPLICANT: Correctly Donal

TITLE OF INVENTION: dependent chromosome stability

TITLE OF INVENTION: dependent chromosome stability

FILE REFERENCE: 0652.2240001

CURRENT APPLICATION NUMBER: US/09/876,221

CURRENT FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: TOS/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45328
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%; Score 33; DB 4; Length 187; 55.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                        ZIP: 20036
COMPUTER READABLE FORM:
COMPUTER: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM AT-compatible, Pentium processor OPERAPING SYSTEM: Windows 95
SOFFWARE: WordPerfect version 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 3;
Pred. No. 44;
2; Mismatches
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/212,247C
FILING DATE: 16-Dec-1998
CLASSIFICATION: «Unknown»
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
             STREET: 1101 Connecticut Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-767-45328
; Sequence 4538, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.3%;
                                    CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 55.6
Matches 5; Conservative
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149 YAEPSVVKY 157
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162 YYRPSVAKY 170
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Matches 5; Conservat
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TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use thereof in microbial riboflavin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR PILIG DATE: 1994-07-21
PRIOR PILIG DATE: 1994-07-21
PRIOR PILING DATE: 1994-07-30-04
PRIOR PILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2486
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Standard peptide that binds to HLA A*0101
US-09-239-043D-2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.7%; Score 37; DB 4; Length 724; 77.8%; Pred. No. 25; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 47; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 62, Application US/09900920; Patent No. 6696562; Patent No. 6696562; GENERAL INFORMATION: APPLICANT: Schultz-Cherry, Stacey; APPLICANT: Relley, Laura; APPLICANT: Relley, Laura; APPLICANT: Relley, Laura; APPLICANT: Real, Bruce; TITLE OF INVENTION: No. 6696562el Avian Astrovirus; TITLE OF INVENTION: No. 6696562el Avian Astrovirus; FILE REFERENCE: turkeyastrovirus; CURRENT APPLICATION NUMBER: US/09/900,920; CURRENT FILING DATE: 2001-07-10; PRIOR FILING DATE: 2000-07-10; PRIOR FILING DATE: 2000-07-10; NUMBER OF SEQ ID NOS: 65; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09212247C Patent No. 6391603 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Turkey astrovirus
US-09-900-920-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Gaps

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Gaps

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RESULT 12

US-09-248-796A-24410

US-09-248-796A-24410

Sequence 24410, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC?

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1999-02-13

PRIOR PILING DATE: 1999-02-13

PRIOR PILING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 24410

LENGTH: 174
                                                                                                                                                                          GENERAL 13-999C-5453
; Sequence 5453, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Dunals Milne Edwards, J.B.
; APPLICANT: Dunals Milne Edwards, J.B.
; APPLICANT: Dunals Milne Edwards, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PILE REFERENCE: 59.012.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 32; DB 4; Length 104; 75.0%; Pred. No. 35;
                         Indels
                         2;
      Pred. No. 30;
2; Mismatches
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    Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 75.0
Matches 6; Conservative
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95 YFDPSIQKY 103
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TYPE: PRT
ORGANISM: Homo sapiens
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45 YLQPMIGRY 53
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59 LKPAIAEY 66
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US-09-248-796A-18090
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Patent No. 6703491
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54202, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT PAPLICATION DAYS: 1099-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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55.6%; Pred. No. 30;
tive 2; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-38985
PRIOR APPLICATION NUMBER: EP 00 112 345.4

PRIOR FILING DATE: 2000-06-09

PRIOR PRILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 2000-06-09

PRIOR PILING DATE: 2000-08-09

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 2

SEQ ID NO 2

SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Drosophila melanogaster
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; OTHER INFORMATION: Xaa means any
US-09-270-767-54202
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Best Local Similarity 75.۰
امات 6، Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            186 LOPAIAEY 193
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LENGTH: 90
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LENGTH: 90
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RESULT 15
US-09-513-999C-6819
; Sequence 6819-7 Application US/09513999C
; Patent No. 678361
; GENERAL INFORMATION:
; APPLICANT: Duclert, A.;
; APPLICANT: Duclert, A.;
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.;
; Patent No. 6783661
; FILE REFERENCE: 59.US2.REG
; CURRENT PILING DATE: 2000-02-24
; PRIOR PAPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SCOTTARRE: Patent.pm
; SEQ ID NO 6819
LENGTH: 72
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Pred. No. 38;
2; Mismatches 2; Indels
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Pred. No. 35;
1; Mismatches 1; Indels
i LOCATION: -53...-1
i IDENTIFICATION METHOD: Von Heijne matrix
i OTHER INFORMATION: score 8.8
i OTHER INFORMATION: seq ILLLLTVLPCIXM/GQ
US-08-905-223-279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 29, 2005, 01:44:30 Job time: 17.9126 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%;
                                                                                                                                               Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 55.64
....nea 5, Conservative
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; ORGANISM: Homo sapiens
US-09-513-999C-6819
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56 EPGVAKY 62
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             Sequence 18090, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR PELLON NUMBER: US 60/074,725

PRIOR PELLON NUMBER: US 60/074,725

PRIOR PELLON NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18090

LENGTH: 744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 279, Application US/08905223
Sequence 279, Application US/08905223
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Lacroix, Bruno
ITILE OP INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUWTRY: USA
ITILIANS
INVENTIONAL SECONDERS
STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: 18TSELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELEFONMUNICATION INFORMATION:
TELEFAX: (619) 235-0176
INFORMATION POR SEQ ID NO: 279:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Flogpy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18090
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 YLEPDLSKF 478
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US-08-905-223-279
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                         - protein search, using sw model
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US-08-170-344-75 45 1 ATELOTTIH 9 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: Total number of hits satisfying chosen parameters:

283416

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description a Query Score Match Length DB No. Result

	protein E6 - human	Holliday junction	lamin-like protein	cytochrome c-type	conserved hypothet	hypothetical prote	pulmonary surfacta	probable histidino	conserved hypothet	bolA protein - Esc	probable regulator	probable murein ge	hypothetical profe	-	_	_		hypothetical prote	u	histidinol dehydro	peptide-chain-rele	glycosyltransferas	hypothetical prote	probable protein k	outer capsid prote	retrovirus-related	protein F46F5.2 [i	hypothetical prote	
	WEWLHS	A72217	159767	H82168	AD2742	C97523	LNDGPS	A70544	F83310	BVECBA	A90690	E85540	C95022	F97893	T34436	D81919	G81182	T26298	T45246	C87066	AC2353	E97092	H70108	T06576	VPXRMN	A26718	H88028	T45713	T15104
1	н	N	0	~	~	~	-	~	~	н	~	~	~	N	N	0	~	N	N	~	~	~	N	~	Н	4	~	~	7
	158	334	138	394	2155	2155	248	438	1317	116	116	116	189	189	108	201	201	259	431	449	540	769	773	982	280	335	381	591	617
	91.1	90.0	•		77.8		75.6				73.3	73.3	73.3	73.3	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1		71.1	68.9	68.9	6.89	68.9	68.9
	41	36	32	32	32	32	34	34	34	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31
	1	01	м	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

DNA topoisomerase	outer layer protei	outer layer protei	hypothetical prote	PARIS-1 protein -	TonB-dependent rec	probable outer mem	vacuolar protein-s	hypothetical prote	probable calcium-t	retrovirus-related	line-1 protein ORF	reverse transcript	reverse transcript	hypothetical prote	hypothetical prote
E22930	VPXRWT	VPXRW9	T31818	JC7799	E81076	G81865	556936	T19727	T40737	GNHUL1	B28096	I38588	S65824	B34087	139917
-	-	-4	~	~	~	N	~	~	~	4	N	~	~	~	7
638	774	116	881	917	921	922	944	1117	1258	1259	1275	1275	1275	1280	2032
68.9	68.9	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8
	_	7	31	31	31	31	31	31	31	31	31	31	31	31	31
31	m	,			•										

ALIGNMENTS

protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A03682, T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
J; Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Reference number: Z17014; MUID:91162763; PMID:1848319 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
A;Gene: E6 C; Keywords: DNA binding; early protein; zinc finger F;37-73/Region: zinc finger CCCC motif F;110-146/Region: zinc finger CCCC motif C; Superfamily: papillomavirus E6 protein

Gaps ö Query Match 91.1%; Score 41; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.19; Matches 8; Conservative 0; Mismatches 0; Indels

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TELOTTIH 31 TELOTTIH 9 N 24

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RESULT 2
47217
Holliday junction DNA helicase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72217
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.
Nature 399, 323-329, 1999
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72217

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conserved hypothetical protein Atul348 [imported] - Agrobacterium tumefaciens (strain C C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                           CjAccession: AD2742
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AGR_C_2490 [imported] - Agrobacterium tumefaciens (strain C58, Cer C; Species: Agrobacterium tumefaciens
C; Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: C97523
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tule, Reference number: A97359, WUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: C97523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2155 <KUR>
A;Cross-references: UNIPROT:Q8UFP9; GB:AE007869; PIDN:AAK87140.1; PID:g15156408; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulmonary surfactant protein A precursor - dog
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 16-Jul-1999
C;Accession: A22296; A61227; A60142
R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:QBUFP9; GB:AE008688; PIDN:AAL42354.1; PID:g17739760; GSPDB:
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                             A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AD2742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%; Score 35; DB 2; Length 2155; 66.7%; Pred. No. 71;
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Pred. No. 71;
2; Mismatches
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A, Map position: circular chromosome
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Best Local Similarity 66.,
Laga 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.8
Best Local Similarity 66.7
Matches 6; Conservative
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A; Residues: 1-2155 < KUR>
ELQTTVH 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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65
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셤
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Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Jul-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-334 <ARN>
A;Cross-references: UNIPROT:O56313; GB:AE001812; GB:AE000512; NID:g4982302; PIDN:AAD3679
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 159767
R;Bloom, D.C.; Massung, R.F.; Savage, L.; Morrison, D.K.; Moyer, R.W.
Virology 169, 115-126, 1989
A;Title: Recruitment to the cytoplasm of a cellular lamin-like protein from the nucleus A;Reference number: 159767; MUD:89163245; PMID:2538026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Reaidues: 1-138 <RES.
A;Kesidues: 1-138 <RES.
A;Cross-references: UNIPROT:Q14755; GB:M24732; NID:g187176; PIDN:AAA36178.1; PID:g187177
C;Superfamily: pol polyprotein
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A,Experimental source: serogroup O1; strain N16961; biotype El Tor
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C;Superfamily: membrane-bound tetraheme cytochrome TorC/YecK; nirT
                                                                                                                                                                                                                                            Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 138;
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                                                                                                                                                                                                                                                                                                 1; Indels
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Pred. No. 3.3;
1; Mismatches (
                                                                                                                                                                                                                                         DB 2;
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                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lamin-like protein - human (fragment)
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87.5%;
                                                                                                                                                                                                                                         80.0%;
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Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                                         Query Match 80.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                               C,Genetics:
A,Gene: TM1730
C,Superfamily: ruvB protein
                                                                                                                                                                                                                                                                                                                                                                                                     72 ASELOTNIH 80
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124 ATEIQTTI 131
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A, Molecule type: DNA
A, Residues: 1-394 <HEI>
  A;Status: preliminary
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P.; Hickey, M.J.; B
A.; Larbig, K.; Lim
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Mature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
A,Residues: 1-1317 <STO>
A,Cross-references: UNIPROT:Q910F4; GB:AE004696; GB:AE004091; NID:g9948750; PIDN:AAG060
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R;Lindquist, S.; Weston-Hafer, K.; Schmidt, H.; Pul, C.; Korfmann, G.; Erickson, J.; Sa
Mol. Microbiol. 9, 703-715, 1993
A;Title: AmpG, a signal transducer in chromosomal beta-lactamase induction.
A;Reference number: S37389; MUID:94049112; PMID:8231804
A;Accession: S37389
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A;Status: not. 53.70.
A;Status: not. 53.70.
A;Residues: DNA
A;Residues: 1-10.
A;Residues: 1-10.
A;Residues: 1-10.
A;Cross-references: GB:S67816; NID:9459274; PIDN:AAB28882.1; PID:9459275
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (Science 277, 1453-1462, 1397
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     triggers transcription of bolA,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved hypothetical protein PA2684 [imported] - Pseudomonas aeruginosa (e C;Species: Pseudomonas aeruginosa C;Species: Es-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: F93310 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hick adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxh. Nature 406, 959-964, 2000
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Dacession: 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: JS0356; S37389; G64773
R;Aldea, M.; Garrido, T.; Hernandez-Chico, C.; Vicente, M.; Kushner, S.R.
EMBO J. 8, 3923-3911, 1989
A;Title: Induction of a growth-phase-dependent promoter triggers transcripti
                                                           Gaps
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                                                           Indels
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Pred. No. 68;
2; Mismatches
             Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain PAO1
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         66.78;
                                                           6; Conservative
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1008 ARELRTTVH 1016
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C;Superfamily: rhsF protein
                                                                                                                                                                                                                                293 AGQLOTTVH 301
             Best Local Similarity
Matches 6; Conserv
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A; Status: preliminary
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Best Local S:
Matches 6
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Maure 325, 490, 1987

Mature 325, 490, 1987

Mature 325, 490, 1987

Mydeference number: 493389; MUID:87115834; PMID:3808053

A;Contents: annotation; animal lectin domain homology

C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers the C;Comment: This protein is a slaloglycoprotein synthesized by alveolar type II cells. It pendent on the presence of calcium ions.

C;Superfamily: mannose-binding lectin, C-type lectin homology

C;Reywords alveolar proteinosis; calcium; disulfide bond; gaseous exchange; hydroxyprol F:1-17/Domain: signal sequence #status predicted <SIGs

F:18-248/Product: pulmonary surfactant protein A #status experimental <MPT>

F:28-102/Region: collagen-like
                                                                                                                                                                             A Molecule type: mRNA

**Residues: 1-248 <BRN>

**A/Note: the authors translated the codon TTG for residue 60 as Pro

**A/Note: part of the sequence, including the amino end of the mature protein, was confirm

**R.Liau, D.F.; Ryan, S.F.

**Residues: D.F.; Ryan, S.F.

**A/Hitle: Purification of surfactant protein A from dog lung by reconstitution with surfa

**A/Ritle: Purification of surfactant protein A from dog lung by reconstitution with surfactant and the surfa
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Reference number: A70500; WUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable histidinol dehydrogenase (EC 1.1.1.23) hisD [similarity] - Mycobacterium tuberc
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 18-32 <LIA>
R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Bjochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification A;Reference number: A60142; MUID:86159848; PMID:3006781
                                                      apoprotein: cDNA and complete amino
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C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
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F:20,207/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:30/Modified site: 4-hydroxyproline (Pro) #status experimental
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Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985
Affilie: Structure of canine pulmonary surfactant apopro
A;Reference number: A25296; MUID:86016705; PMID:3863100
A;Accession: A25296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: protein
A,Residues: 24-34;95-101,'X',103-108 <ROS>
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85.7%;
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Best Local Similarity
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Matches

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A;Cross-references: GB:AE000149; GB:U00096; NID:91786628; PIDN:AAC73538.1; PID:91786638 A;Experimental source: strain K-12, substrain MG1655

A, Molecule type: DNA A, Residues: 1-116 < BLAT>

C;Superfamily: Histidinol dehydrogenase; histidinol dehydrogenase homology C;Keywords: histidine biosynthesis; oxidoreductase F;37-437/Domain: histidinol dehydrogenase homology <HID>

hisD

Length 438;

75.6%; Score 34; DB 2;

Query Match

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hypotherical protein spr0174 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004
C;Accession: F97893
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
F;Hoskins, J.A.; Alborn Jr., W.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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A;Gene: spr0174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q978X2; GB:AE005672; PIDN:AAK74372.1; PID:g14971659; GSPDB:
A;Experimental source: strain TIGR4
                                                                                                                                                                                                     hypothetical protein SP0191 [imported] - Streptococcus pneumoniae (strain TIGR4)
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C;Species: Caenorhabditis elegans
C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34436
C;Bradshaw, H.
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AEELSTTVH
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-189 <KUR>
1 ATELOTTIH
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A, Status: preliminary
A, Molecule type: DNA
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Best Local S:
Matches 7
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C;Species: Inc. School #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: E85540
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Recence number: A85480; MUD:21074935; PMID:11206551
A;Accession: E85540
A;Accession: 
                                                                                                                A;Description: involved in the morphogenetic pathways; probably involved in the inductic (S. Superfamily: bolA protein (S. Superfamily: bolA protein (S. Reywords: DNA binding; transcription regulation (S. Reywords: DNA binding; transcription predicted <DBI>
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*Residues: 1-116 <HAY>
A;Cross-references: UNIPROT:Q8XE61; GB:BA000007; PIDN:BAB33912.1; PID:g13359946; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A90690
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Fitle: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable regulator of murein genes [imported] - Escherichia coli (strain 0157:H7, substr
protein causes round morphology of the organism when overexpressed.
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submitted to the EMBL Data Library, February 1997

A; Description: The sequence of C. elegans cosmid K11H12.

A; Reference number: 221526

A; Accession: T34436

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residuses: 1-108 - BRA>

A; Cross-references: UNIPROT:P91375; EMBL:U88168; PIDN:AAC24398.1; GSPDB:GN00022; CESP:K1

A; Residuses: 1-108 - RRA>

A; Cross-references: WIPROT:P91375; EMBL:U88168; PIDN:AAC24398.1; GSPDB:GN00022; CESP:K1

A; Reperimental source: strain Bristol N2; clone K11H12

C; Genetics:
A; Map position: 4

A; Introns: 22/3; 61/3

C; Superfamily: bolA protein

Query Match

G; Superfamily: bolA protein

G; Superfamily: bolA protein

Best Local Similarity 66.7%; Pred: No. 11;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATBLQTTH 9

71 AKELATTWH 79
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Search completed: June 29, 2005, 01:38:52 Job time : 13.2747 secs



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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBJ, PR04694; AAL01345.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Q919B6;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Copyright (c) 1993 - 2005 Compugen Ltd.
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MEDLINE=21046229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart P.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart P.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874 (2002).

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:005677; F:DNA binding; IEA.

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MEDLINE=9743744; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Buonaguro G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
Gen. Virol. 78:2199-2208 (1997).
GO; GO:0042025; C:host cell nucleus; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                    SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 1.2;
ive 0; Mismatches (
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100.0%; Pred. No. 1.2;
ative 0; Mismatches
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EMBL; AF404702; AAL01361.1; -. 60; GO:0042025; C:host cell nucleus; IEA. 60; GO:00367; F:DNA binding; IEA. Pfam; PF00518; E6; 1.
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Best Local Similarity 100...
8; Conservative
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9 TELOTTIH 16
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NCBI_TaxID=10581;
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Beth-Giraldo E., Giraldo G.;

Beth-Giraldo E., Giraldo G.;

Sequence avaiations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";

J. Gen. Virol. 78:2199-2208 (1997).

EMBL, AF003016; AAB70733.1;

GO, GO:0003677; F:DNA binding; IEA.

InterPro; IPR00134; E6.

InterPro; IPR00134; E6.

SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6DBA CRC64;
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
D.2. and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
GO; GO:0003677; F:DNA binding; IBA.
InterPro; IPR001334; B6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 1.3;
iive 0; Mismatches
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MEDLINE-20112892; PubMed=10644829; Van Bulline-20112892; PubMed=10644829; Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walbooners J.M.; Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).

EMBL; AJ88063; CAB45118.1; -. GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

InterPro; IPR001334; E6.

Pfam; PP00518; E6; 1.

SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CFIF CRC64;
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Martins C.R.F.;
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MEDLINE=20112892; PubMed=10644829;
van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
van Duin M., Shijders P.J., Vossen M.T., Walboomers J.M.;
"Analyais of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6 variant (Transforming protein E6).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang.";
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Pred. No. 1.3;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A31287851; AAG459401; -.
EMBL; AJ388069; CAB45106.1; -.
Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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100.0%; Pred. No. 1...
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Mol. Evol. 55:491-499(2002)
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Best Local Similarity 100.1
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NCBI_TaxID=10581;
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05-JUL-2004
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WARDLINE-20112892; PubMed=10644829;
WARDLINE-20112892; PubMed=10644829;
WARDLINE-20112892; PubMed=10644829;
Wardline W.H., Helmerhorst T.J., Majler C.J., Walbcomers J.M.;
Verheijen R.H., Helmerhorst T.J., Majler C.J., Walbcomers J.M.;
Waller M. Waller M. Majler M. 
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                             to the EMBL/GenBank/DDBJ databases.
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05-UL-2004 (TrEMBLrel. 27, Created)
05-UL-2004 (TrEMBLrel. 27, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
E6 oncoprotein (E6 protein).
Human papillomavirus type 16.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                Pfam; PF00518; E6; 1.
SEQUENCE :151 AA; 18292 MW; 35012A9E01993C35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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                   Submitted (Aug-1995) to the EMBL/GenBank/DDI
EMBL; U34114; AAA91661.1; -
EMBL; U34125; AAA91672.1; -
EMBL; U34130; AAA91677.1; -
EMBL; U34131; AAA91677.1; -
GO: 000402055; C:host cell nucleus; IEA.
GO; GO: 0003677; F:DNA binding; IEA.
InterPro: IPR001334; E6.
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nes 8; Conservative
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SEQUENCE FROM N.A.
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05-JUL-2004 (
05-JUL-2004 (
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Q77E16
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MEDLINE=20112892; PubMed=10644829;

MEDLINE=20112892; PubMed=10644829;

MAT Dulin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.,

J. Gen Virol. 81:317-325 (2000).

B. KMEL, AF003014; AAB70731.1, -

B. KMEL, AF003017; AAB70734.1, -

R. EMBL, AF038088; CAB45128.1, -

R. EMBL, AF038088; CAB45128.1, -

R. EMBL, ALONGONIS, AAB70730.1, -

C. GO:00042025; C:host cell nucleus; IEA.

R. O. GO:0042025; C:host cell nucleus; IEA.

R. InterPro, C. IPR001334; E6.
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
  populations characterized by nucleotide sequence analysis of the E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q80966 PRELIMINARY; PRT; 151 AA.
Q80966; Q12650; Q12651; Q12652; Q12925; Q12926; Q12927; Q80962;
Q80964; Q80965;
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Pred. No. 1.3;
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                     Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34122; AAA91669.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPRON01334; E6.
Fam; PP00518; E6; 1.
SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
                                                                                                                                                                                                                                                                                                                   91.1%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                        L2, and L1 coding segments."
J. virol. 69:7743-7753(1995)
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Best Local Similarity 100.
Matches 8; Conservative
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nes 8; Conservative
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NCBI_TaxID=10581;
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
Sequence variations and vixal genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:199-2208(1997).
EMBL; AF003019; AAB70736.1;
CGO, GO:0042025; Chost cell nucleus; IEA.
GO; GO:0042025; Chost cell nucleus; IEA.
InterPro; IPR001334; E6.
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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"Human papillomavirus type 16 variant lineages in United States
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Pred. No. 1.3;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Early transforming protein 86.
Human papillomavirus.
Viruses, daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
EMBL; AY089951; AAM11875.1; -.
EMBL; AX089954; AAM11881.1; -.
EMBL; AX112665; AAM51884.1; -.
GO; GO:004205; C:host cell nucleus; IEA.
GO; GO:005077; F:DNA binding; IEA.
InterPro; IPRO01334; E6.
SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;
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SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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100.0%; Pred. No. 1.3;
ive 0; Mismatches
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100.0%; Pred. No. ...
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nes 8; Conservative
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Matches 8; Conserv
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NCBI_TaxID=10581;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96079021; PubMed=7494284;
MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
Li., and Ll coding segments.";
J. Virol. 69:7743-7753(1995).
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C 989648; 012653; 012654; 012229;
T 01-NOV-1996 (TrEMBLrel. 01, Created)
T 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
T 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E Early transforming protein E6.
S Human papillomavirus.
Viruses; dabNa viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
(NILL TAXID=10566;
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                                                                                                                                                                                                                     Early transforming protein E6.

Human papillomavirus.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10566;
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;
                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                              151 AA
                                                                                                              PRT;
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Matches 8; Conservative
                                                                                                           PRELIMINARY;
17 TELQTTIH 24
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Q89640;
                                                                 RESULT 13
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                                                                                                              DORRAR REPORT TO DESCRIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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Farmer A.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34110; AAA91657.1; -.
EMBL; U34113; AAA91660.1; -.
REMBL; U34113; AAA91660.1; -.
REMBL; U34113; AAA91682.1; -.
REMBL; U34113; AAA91682.1; -.
REMBL; U34135; AAA91682.1; -.
REMBL; U34105; AAA91682.1; -.
REMBL; U34135; AAA91682.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.1%; Score 41; DB 2; Length 151; 100.0%; Pred. No. 1.3; ive 0; Mismatches 0; Indels
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EMBL; U34128; AAA91675.1; -.
EMBL; U34117; AAA91664.1; -.
EMBL; U34118; AAA91665.1; -.
GO; GO:0004205; C:host cell nucleus; IEA.
GO; GO:0005677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
Human papillomavirus.
Viruses, debnay viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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Matches 8; Conservative
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nes 8; Conservative
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Sequence 3

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| Sequence 3, Application US/07909122
| Sequence 3, Application US/07909122
| Patent No. 5415995
| Patent No. 5415995
| Patent No. 5415995
| Patent No. 5415996

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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DatentIn Release #1.0, Version #1.25
SURRENT PAPLICATION DATE: 19920706
CLASSIFICATION NUMBER: US/07/909,122
FLING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 28600-20105.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US93-08528-256
US-09-489-039A-12134
US-09-252-991A-22090
                       US-09-557-034-38

US-09-031-485-23

US-08-847-429-23

US-09-557-034-23

US-09-557-034-139

US-09-557-034-139

US-09-05-144-139

US-09-05-180A-4

US-09-031-485-33

US-09-031-485-33

US-09-031-485-33

US-09-05-474-33

US-09-557-034-33

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100.0%; Pred. No. 0.055;
tive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 494 0792
TELEX: 706141
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
302
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US-07-909-122-3
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8; Conserv
  Query Match
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Sequence 165, App
Sequence 165, App
Sequence 3797, Ap
Sequence 38, App
Sequence 38
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4, Appli
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Sequence 14, Appl
Sequence 31032, A
Sequence 4167, Ap
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Sequence 102, App
Sequence 248, App
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                                                                                                                                                                              June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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Sequence 4, Ap
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Sequence 10,
Sequence 10,
Sequence 10,
Sequence 11,
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Sequence 3
Sequence 4
Sequence 1
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-934-915-159

US-09-980-523A-4

US-09-980-523A-2

US-09-316-239B-3

US-09-316-239B-4

US-08-316-239B-4

US-08-316-239B-4

US-08-316-239B-4

US-08-316-239B-4

US-08-359-33B-14

US-08-359-33B-14

US-09-359-38B-16

US-09-485-885-10

US-09-252-91A-3103

US-09-107-413-4185

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165

US-09-055-474-165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   - protein search, using sw model
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seq length: 200000000
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45
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Match 1
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                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
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Maximum DB
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No.
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Gaps

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GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GOILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: PERRIES, ESTELLE
ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: POT/FR00/01513
FRIOR APPLICATION NUMBER: POT/FR00/01513
FRIOR PLING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 30
LENGTH: 30
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91.1%; Score 41; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels
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STATE: D.C.

CUMURKY: USA

ZIP: 20005-3115

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: BLM PC compatible

COMPUTER: Ploppy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/363,586

FILING DATE: 23-DEC-1994

CLASSIFICATION ADATA:

APPLICATION NUMBER: US 07/909,296

FILING DATE: 09-JUL-1992

APPLICATION NUMBER: B 9111720.8

FILING DATE: 13-JUL-1991

ATCANSY AGINT INFORMATION:

NAME: Wadler, Linda A.

REGISTRATION NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 33,218

REFERENCE/DOCKET NUMBER: 33,218

REFERENCE COMMUNICATION INFORMATION:

TELEPPAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 TELOTTIH 24
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Patent No. 5629161

GENERAL INPORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Deptides for the Diagnostic Purpose
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 91.1%; Score 41; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 0.081; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.081;
                                           INFORMATION FOR SEQ ID NO: 159: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 TELOTTIH 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-934-915-159
                                         US-08-934-915-159
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US-08-363-586-4
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Gaps

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APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 41; DB 1; Length 162; 100.0%; Pred. No. 0.83; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             91.1%; Score 41; DB 1; Length 162; 100.0%; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 30-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: JGGIAILAI, AJBY A.

REGISTRATION NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: UNME-0001

TELEPAX: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acid

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
  UNME-0001
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COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08316239B Patent No. 5679509
GENERAL INFORMATION:
                                         TELEPHONE: (703) 817-9453
TELEPRAX: (703) 803-9387
INFORMATION FOR SEG ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                     TELECOMMUNICATION INFORMATION
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
                                                                                                                                                                                   SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: not relevant not relevant
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
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Matches 8; Conservative
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Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheelar, Cosette M.
APPLICANT: Wheelar, Cheryl A.
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Jagtiani & Associates
STREET: G126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                        APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
ITILE OF INVENTION: PROTEINE OF THE E6 AND E7
ITILE OF INVENTION: PROTEINEN OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION
FILE REPERENCE: WOBI AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
FRIOR APPLICATION NUMBER: F99/07012
FRIOR APPLICATION NUMBER: F8 99/07012
FRIOR APPLICATION NUMBER: F8 99/07012
FRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver: 2.1
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ZIP: 20120-3400

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: DATE PROME SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/316,239B
                                                                                                                                                        Sequence 2, Application US/09980523A Patent No. 6783763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Jagtiani, Ajak A.
REGISTRATION NUMBER: 35,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human Papillomavirus US-09-980-523A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                     US-09-980-523A-2
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APPLICANT: Boursnell, Michael B.
APPLICANT: Inglis, Stephen C.
APPLICANT: Inglis, Stephen C.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: A Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLCOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.1%; Score 41; DB 1; Length 182; 100.0%; Pred. No. 0.94; tive 0; Mismatches 0; Indels
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the open reading frame."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: VC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRICATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: 4,190
REFERENCE/DOCKET NUMBER: 4,190
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-398-3249
TELEREX: 910-277299
TELEFAX: 415-398-3249
TELEREX: 910-277299
TELEFAX: 415-398-3249
TELEFAX: 415-398-3249
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TELEFAX: 415-398-3249
TELEFAX: 910-277299
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           ; Sequence 10, Application US/08117083; Patent No. 5719054; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 100.
Matches 8; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
93 TELQTTIH 100
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
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COUNTRY: US
ZIP: 94111
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US-08-860-165-10
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                                                                                                                  US-08-117-083-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09359382
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA
FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT APPLICATION NUMBER: US/09/22
; BARLIER PILING DATE: 1997-09-22
; BARLIER PILING DATE: 1995-12-20
; EARLIER PILING DATE: 1995-12-20
; BARLIER PILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTHARE: PALENTIN UVET: 2.0
; SOFTHARE: PALENTIN UVET: 2.0
                                                                                                                                        US-08-860-165-14

| Sequence 14, Application US/08860165A
| Sequence 14, Application US/08860165A
| Patent No. 6004557
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: FRAZER, Ian 1722/1A
| TITLE OP INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
| TILE REFERENCE: 1722/1A
| CURRENT APPLICATION NUMBER: US/08/660,165A
| CURRENT APPLICATION NUMBER: PCT/AUS/00668
| BARLIER FILING DATE: 1995-12-20
| EARLIER FILING DATE: 1995-12-20
| EARLIER FILING DATE: 1994-11-20
| NUMBER OF SEQ ID NOS: 12
| SOOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 91.1%; Score 41; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.88; Matches 9; Indels Matches 0; Indels
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US-09-359-382-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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24 TELOTTIH 31
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LENGTH: 172
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TYPE: PRT

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Pred. No. 1.5;
Mismatches 0: Indele
                                                                                                                                                                                                                                    DB 4; Length 266;
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITLLE OF INVENTION: Vaccine
FILE REFERENCE: B49107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FRASEQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR PELICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                    91.1%; Score 41; DB 100.0%; Pred. No. 1.4 ive 0; Mismatches
                                                                                                                                                                    ORGANISM: Human papillomavirus type 16
         PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO I
LENGTH: 266
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US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
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                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                             24 TELQTTIH 31
                                                                                                                                                                                                                                                                                                                                2 TELOTTIH 9
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LENGTH: 273
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                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09359382

Sequence 10, Application US/09359382

Retent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARDAN, Stirling John

APPLICANT: EDWARDAN, Stirling John

APPLICANT: ENARER, Islizabeth Ann

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1995-07-23

EARLIER PELICATION NUMBER: US 08/860,165

EARLIER PELICATION NUMBER: PCT/AU95/00868

EARLIER PELING DATE: 1995-12-20

MUMBER OF SEQ ID NOS: 27

SOFTHARE: PAPLICATION NUMBER: AU PN0157/94

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 2.0
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; Sequence 1, Application US/09367309A
; Sequence 1, Application US/09367309A
; GENERAL INCORNATION:
; APPLICANT: MALLIAROS, JM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR FILING DATE: 1998-02-13
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91.1%; Score 41; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Qy 2 TELOTTIH 9

Cy 2 TELOTTIH 9

Db 149 TELOTTIH 156

Search Completed: June 29, 2005, 01:44:29
JOb time: 17.9126 secs
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us-08-170-344-75.rapb

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Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 8, Appli
Sequence 53, Appli
Sequence 4, Appli
Sequence 9, Appli
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64.268 Million cell updates/sec
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Sequence 6
Sequence 2
Sequence 2
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                                                                                                            June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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"Cgn2_6/ptodata/1/pubpaa/US07_WW PUB.pep:"

"Cgn2_6/ptodata/1/pubpaa/US06_WW PUB.pep:"

"Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:"

"Cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:"

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"Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:"

"Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:"

enCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-476-570-21
US-10-476-570-22
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US-10-476-570-9
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US-10-476-570-19
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 ATELQTTIH 9
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1-858-384-	-10-367-0	2-724-	09-367-30	-10-000-0	-10-899-7	-10-000-9	-10-899-771-	-10-000-903-	899-771-	-000	899-771-1		368-046-1	367-367-1	US-10-918-337-10	US-10-484-063-2		US-10-767-701-52305	2	US-09-815-242-5118	US-10-282-122A-43495	-437-963-12697	US-10-425-115-223782	10-425-115-26458	10-425-115-24043	10-156-761-876	10-474-776-	10-472-928-192	10-264-237-148	-10-094-749-262	LO-275-026A	-10-369-493-15948	-115-2231
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158	158	171	266	273	273	292	292	371	371	390	390	536	536	536	536	10	126	120	472	1317	1317	47	74	74	121	176	189	189	258	995	201	222	267
91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	91.1	80.0	77.8	75.6	75.6	75.6	75.6	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	71.1	71.1	71.1
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	36	35	34	34	34	34	33	33	33	33	33	33	33	33	33	32	32	32
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42		44	45

ALIGNMENTS

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 17-31 US-10-476-570-20
                                                                                                                  ## APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
## APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
## APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
## APPLICANT: MAILLERER, Bernard
## APPLICANT: MAILLERER, Bernard
## APPLICANT: BOUNGAULT-VILLADA, Isabelle
## APPLICANT: BOUNGAULT-VILLADA, Isabelle
## APPLICANT: BOUNGAULT-VILLADA, Sandra
## APPLICANT: MAILLER Sandra
## APPLICANT: Jean-Gerard
## TITLE OF INVENTION: MAILLER of peptides derived from E6 and/or E7
## TITLE OF INVENTION: MAILLER SOUS-10-04
## PILE REFERENCE: 45636-5071-US
## CURRENT APPLICATION NUMBER: DET/FR02/01533
## PRIOR APPLICATION NUMBER: PR 01 05980
## PRIOR PAPLICATION NUMBER: FR 01 05980
## PRIOR PAPLICATION NUMBER: FR 01 05980
## PRIOR PAPLICATION NUMBER: FR 01 05980
## PRIOR FILING DATE: 2002-05-04
## NUMBER OF SEQ ID NOS: 63
## SEQ ID NO 20
## SEQ ID NO 20
## LENGTH: 15
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                                Sequence 20, Application US/10476570 Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 8; Conservative
US-10-476-570-20
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Query Match 91.1
Best Local Similarity 100.
Matches 8; Conservative
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
US-10-476-570-22
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                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BERTHARG
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REPERENCE: 45545-6701-US
CURRENT PILING DATE: 2003-11-04
FRIOR PILING DATE: 2002-05-03
FRIOR FILING DATE: 2002-05-03
FRIOR PELICATION NUMBER: FC 01 05980
FRIOR PELICATION DATE: 2001-05-04
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGALLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPL
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91.1%; Score 41; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10476570
Publication No. US20040170644A1
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ORGANISM: artificial sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
LENGTH: 15
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2 TELOTTIH 9
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LENGTH: 15
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Query Match

91.18, Scored 1, DB 16; Length 15;

Matchee 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

02 2 FELOTH 8

1 TELOTH 9

1 TELOTH 19

1 TELOTH 19

1 TELOTH 19

2 TELOTH 19

2 TELOTH 19

3 SEQUENCE 8, APPLICANT

4 MERITAL MISCARLIAN

MARILOMY COMMISSARIA A.L.EMBGIE ATOMIQUE

APPLICANT

MARILOMY ENGARIAN

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MARILOMY ENGARLY MARKET

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45 US-10-476-570-9
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| Sequence 6, Application US/1017390
| Publication No. US20030143743A1
| GENERAL INFORMATION:
| APPLICANT: Schuler, Gerold
| APPLICANT: N.V. Antwerps Innovatiecentrum
| TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
| TITLE OF INVENTION: Polynuclectides by Blectroporation
| TITLE OF INVENTION: Polynuclectides by Blectroporation
| TITLE OF INVENTION: Polynuclectides by Blectroporation
| CURRENT APPLICATION NUMBER: US/10/177,390
| CURRENT FILING DATE: 2002-06-20
| NUMBER OF SEQ ID NOS: 34
| SOFWARE: Patentin Ver. 2.1
| SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLEER, Mernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: BOUNGAULT-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR FILING DATE: 2003-11-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 19
LENGTH: 33
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100.0%; Pred. No. 0.64;
tive 0; Mismatches 0
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US-10-476-570-19
Sequence 19, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
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                                          SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 32
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
           NUMBER OF SEQ ID NOS: 63
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US-10-177-390-6
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                                                                                                           OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUVELLE-WORATILLE, Sandra
APPLICANT: GUILLE-MORATILLE, Sandra
APPLICANT: GUILLE-MORATILLE, Sandra
APPLICANT: GUILLE-MORATILLE, Sandra
APPLICANT: GUILLE-MORATILLE, Sandra
APPLICANT: MUNENTION: MAILLE SANDRANTION: MAILLE OF INVENTION: MAILLE DE SANDRANTION: PAPILICANTION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-013
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10858384

Publication No. US20050033025A1

Publication No. US20050033025A1

GENERAL INFORMATION:

APPLICANT: GHOPPIN, JEANNINE

APPLICANT: GHOPPIN, JEANNINE

APPLICANT: GOUNGAULT VILLADA, ISABELLE

APPLICANT: GOUNGAULT VILLADA, ISABELLE

APPLICANT: GOUNGAULT VILLADA, ISABELLE

APPLICANT: GOUNDA, PRANCINE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRACMENTS OF THE B6 PROTEIN

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

TITLE OF INVENTION: DARTICULARLY IN VACCINATION

TITLE OF INVENTION: DARTICULARLY IN VACCINATION

CURRENT PAPLICATION NUMBER: B7 9907012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SEO ID NO 4

SEO ID NO 4

SEO ID NO 4

SEO ID NO 4

SEO ID NO 6

SEO ID 
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                                                                                                                                                                                                                           91.1%; Score 41; DB 16; Length 30;
100.0%; Pred. No. 0.6;
tive 0; Mismatches 0; Indels
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; Publication No. US20040170644A1
; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                           ; OTHER INFURM
US-10-476-570-53
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US-110-808-384

| Sequence 2, Application US/10858384
| Sequence 2, Application No. US20050033025A1
| GENERAL INFORMATION:
| APPLICANT: CHOPPIN, JEANNINE
| APPLICANT: GUILLET, JEAN-GERARD
| APPLICANT: FERRIES, ESTELLE
| TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
| TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
| FILE REPERENCE: 0508-103-1.
| CURRENT FILING DATE: 1999-06-03
| NUMBER OF SEQ ID NOS: 24
| SOFTWARE: PATENTIN VET: 3.2
| SEQ ID NO 2
| LENGTH: 158
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91.1%; Score 41; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels
91.1%; Score 41; DB 17; Length 151; 100.0%; Pred. No. 3.4; ive 0; Mismatches 0; Indels
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| Sequence 16, Application US/10367057
| Publication No. US20050100554A1
| GENERAL INFORMATION:
| APPLICANT: Cuthill, Scott;
| APPLICANT: Lewin, David A.;
| APPLICANT: Lewin, David A.;
| APPLICANT: Lewin, Complexes and Methods of Using Same:
| TITLE OF INVENTION: Complexes and Methods of Using Same:
| TITLE OF INVENTION: Complexes and Methods of Using Same:
| TILLE OF INVENTION: Complexes and Methods of Using Same:
| FILE REFERENCE: 21402-559
| CURRENT APPLICATION NUMBER: US/10/367,057
| CURRENT FILING DATE: 2002-02-14
| PRIOR FILING DATE: 2002-02-14
| NUMBER OF SEQ ID NOS: 198
| SOFTWARE: Curasequist version 0.1
| SEQ ID NO 16
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     Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-367-057-16
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; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REPERBENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFFWARR: Patentin Ver. 2.1
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US-10-484-063-20

i Sequence 20, Application US/10484063

i Publication No. US20050048467A1

i GENERAL INFORMATION:

i APPLICANT: SASTRY, K. JAGANNADHA

i APPLICANT: TORTCLERO-LUNA, GUILLERMO

i TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

i TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

i CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2004-01-16

i PRIOR FILING DATE: 2001-07-19

i PRIOR PELING DATE: 2001-07-20

i NUMBER OF SEQ ID NOS: 27

i SOFTHARE: Patentin Ver: 2.1

i ENGTH: 151
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; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
                           TYPE: PRT ; ORGANISM: Human papillomavirus type 16 US-10-177-390-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human papillomavirus
US-10-484-063-20
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Best Local Similarity 100.
Matches 8; Conservative
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          LENGTH: 151
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RESULT 14

US-10-472-724-2

Sequence 2, Application US/10472724

; Publication No. US20040171806A1

; GENERAL INFORMATION:

APPLICANT: Cid-Arregui, Angel

; APPLICANT: Cid-Arregui, Angel

; APPLICANT: Cid-Arregui, Angel

; APPLICANT: Law Farregui, Angel

; APPLICANT: Angel

; TILE REFERENCE: 4121-154

; CURRENT APPLICATION NUMBER: US/10/472,724

; CURRENT PILING DATE: 2003-09-17

; PRIOR APPLICATION NUMBER: EP 01107271.7

; PRIOR PILING DATE: 2001-03-23

; NUMBER OF SEQ ID NOS: 27

; SEQ ID NO 2

; LENGTH: 171

LENGTH: 171
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Sequence 1, Application US/09367309A

Publication No. US20020081329A1

GENERAL INFORMATION:

APPLICANT: MACENALIAN,

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING INMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: DY/AU98/00080

PRIOR PAPLICATION NUMBER: AU PO 5178

PRIOR PELING DATE: 1998-02-13

PRIOR PELING DATE: 1997-02-19

NUMBER OF SEQ 1D NOS: 6

SOFTWARE: Patentin Ver: 2.1

SEQ 1D NO 1

LENGTH: 266

TYPE: PRT

ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
91.1%; Score 41; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels
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91.1%; Score 41; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
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ORGANISM: Artificial Sequence
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29 TELQTTIH 36
  24 TELOTTIH 31
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24 TELOTTIH 31
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US-09-367-309A-1
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Sequence:

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075f99 ashbya goss

06wu90 lactobacill

06x377 human papil

08xv6 lactobacill

08xv6 lactobacill

08iv5 plasmodium

08re78 fusobacteri

07re2 bacteriopha

08gj20 escherichia

07udn7 shigella fl

06a8f3 propionibac

08gj19 escherichia

08gj14 escherichia
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100.0%; Pred. No. 0.026;
tive 0; Mismatches 0; Indels
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitred (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF465198; AAOLS594.1;
InterPro; IPR000148; Papvi_E7.
Pfam:_PF00527;_E7; 1.__
                                                                                                                                                                                                                                                                                                                                                                                                               Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF546023; AA016240.1; -..
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
NON TER
SEQÜENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;
                                                                                                                                                                                                                                                                          Q8B563;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
E7 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
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Last sequence update)
Last annotation update)
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06ANS6
075F99
06W90
06W90
VE7 HPV31
08K7V6
08K7V6
08HE78
0716C2
0716C2
08G320
07UDN7
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Best Local Similarity 100.vv
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01-JUN-2003 (TrEMBLrel.
E7 protein (Fragment).
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NCBI_TaxID=10566;
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SEQUENCE
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Q8B5P5
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Q8B563
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Q9qdh4 human papil
Q9qdh8 human papil
Q8b5p6 human papil
Q8b5p6 human papil
Q1150 human papil
Q11513 human papil
Q12137 human papil
Q8qrd3 human papil
Q778h3 human papil
Q91821 xenogus lae
Q91821 xenogus lae
Q91821 xenogus lae
Q91822 bacillus an
Q91802 pacillus an
Q91803 pacillus an
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Q8b5p5 human papil
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                                                                                                (without alignments)
84.958 Million cell updates/sec
                                                                                June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9QDH4
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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49
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SEQUENCE FROM N.A.

Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;

Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;

Submitted (SEPP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF1879666, AAF13333.1;

InterPro; IPR000148; Papvi_E7.

InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; 1.

NON TER

93

SEQUENCE 93 AA, 10452 MW; 83281BBEZAEZCBAIF CRC64;
                                                                                                                                                                                                                                                             Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187867; AAF13395.1; -.
InterPro; IPR000148; Papvi E7.
Pfan; PF00527; E7; 1.
NON TER
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JMA-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
E7 oncoprotein (Fragment).
Human papillomavirus type 16.
Viruses; dsDMA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
                                                                                                                              Humān papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Lue H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1879669, AAR13399.1; -.
InterPro; IPR000148; Papvi_F7.
InterPro; IPR000148; Papvi_F7.
NON TER 93
SEQÜENCE 93 AA; 10452 MW; 83281BB2AEZCBAIF CRC64;
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SEQUENCE FROM N.A.
Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, FN187868; AMF13397.1;
InterPro; IPRO00148; Papvi_E7.
Pfam: _PF00527; E7; 1.
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100.0%; Pred. No. 0.031; wismatches 0; Indels
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01-MAY.2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN 2010 (Tremment).
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JW-2001 (TrEMBLrel. 17, Last annotation update)
01-Trepein (Fragment).
Human papillomavirus type 16.
Viruses; dsNA viruses, no RNA stage; Papillomaviridae;
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93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
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                                            Conservative
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Matches 9; Conservative
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Matches 9; Conserv
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NCBI_TaxID=10581;
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SEQUENCE
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MEDLINE=90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
"Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
J. Gen. Virol. 71:809-817(1990).
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                                                                                                                                                                                                                                           ;
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Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.,
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                                                                                                       100.0%; Score 49; DB 2; Length 94; 100.0%; Pred. No. 0.039;
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469197; AA015692.1; -.
InterPro; IPR000148; Papvi_E7.
Pfam: PF00527; E7; 1.
                                                                                                                                                                                                                                           0; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                           SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
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(Rel. 45, Last annotation update)
                                                                                                                                                                                                                                           0; Mismatches
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MEDLINE=88223347; PubMed=2836062;
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Matches 9; Conservative
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49 RAHYNIVTF
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21-JUL-1986 (
25-OCT-2004 (
E7 protein.
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P03129;
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SEQUENCE FROM N.A.
MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplassa in southern China.";
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Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
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MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
                                                                                                                                                      PIR; A03689; W7MLHS.
InterPro; IPR000148; Papvi_E7.
Efan; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Trans-acting factor; Transcription regulation.
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U76404; AAC58243.1; -.
EMBL; AF472509; AAO15706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEWBLrel. 04, Created)
01-JUL-1997 (TrEWBLrel. 04, Last sequence update)
05-JUL-1997 (TrEMBLrel. 27, Last annotation update)
butative transforming protein E7.
Human papillomavirus type 16.
Viruses, debny viruses, no RNA stage, Papillomaviridae,
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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C-XX-C motif-2.
9BD612534CD2C9EB CRC64;
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EMBL; U76413; AAB18964.1; -.
EMBL; AF003020; AAB70737.1; -.
EMBL; AF003024; AAB70740.1; -.
EMBL; AF003024; AAB70741.1; -.
EMBL; AF003026; AAB70742.1; -.
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EMBL, AF486330; AAL96635.1; --
EMBL, AF486331; AAL96636.1; --
EMBL, AF486332; AAL96636.1; --
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MEDLINE=2182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.R.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:656-700(2002). EMBL, FA8486345; AAL96501.; -.. InterPro; IPR000148; Papvi_E7.

Fram; PF00527; E7; 1. SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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                                                                          SEQUENCE FROM N.A.
Jinhu X., Xinxing W., Yun T.;
Jinhu Y., Xinxing W., Yun T.;
Jinhu Y., Xinxing W., Yun T.;
Jinhu X., Xinxing W., Xinxing W., Yun Y., Xinxing W., Xinxi
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Viruses; dapNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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SEQUENCE FROM N.A.
MEDIENCE-9437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
EMBL, AR003021; AAB707381; -.
InterPro; IPR00148; Papvi_E7.
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Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                        EMBL; AF486346; AAL96651.1; --
EMBL; AF486350; AAL96655.1; --
EMBL; AF48631; AAQ196656.1; --
EMBL; AF534061; AAQ10404.1; --
INTERPPC; IPRO00148; Papvi_E7.
SPÉam; PF00527; E7: 1.
SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00527; E7; 1. -
SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;
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012338
ID 012338
AC 012338,
DT 01-UUL-1997 (TYEMBLrel. 04, Created)
DT 01-UUL-2004 (TYEMBLrel. 27, Last sequence update)
DE 87 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E7 protein.
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  AF486333; AAL96639.1; -. AF486334; AAL96639.1; -. AF486336; AAL96641.1; -. AF486338; AAL96643.1; -.
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SEQUENCE FROM N.A.
MEDLINE-2182962, PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Chenng A.F.;
Thuman papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
BMBL, FAR96529; AAL96634-1;
InterPro; IPR000148; Papvi_B7.
SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;
                                                                                                                                              Gaps
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Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                  Q8QRD4 PRELIMINARY; PRT; 98 AA.
Q8QRD4;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
F7 procein.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Jinhu X., Xinxing W., Yun T.;
Jinhu X., Xinxing W., Yun T.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, PR461264; AAL66736.1; -.
Ffam; PF00527; E7; 1.
SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;
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Viruses; deDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus.
NCBI_TAXID=10581;
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
EMBL; AF486344; AAL96649.1; -.
PlearPro; IPR000148; Papvi_E7.
Pfam; PR00527; B7; 1.
SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E7 protein.
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Best Local Similarity 100.
Matches 9; Conservative
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49 RAHYNIVTF 57
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NCBI_TaxID=10581;
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Qy 1 RAHYNIVTF 9
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Db 49 RAHYNIVTF 57
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Search completed: June 29, 2005, 01:34:51 Job time : 56.2473 secs and spank (napto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-74 Title: Perfect score: Sequence:

1 RAHYNIVTF 9

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	E7 protein - human	alanyl-tRNA synthe	p69Eg3 protein - A	glutamine-fructose	glutamine-fructose	polymorphic antige	probable membrane	nonstructural prot	segment S4 protein	E7 protein - human	response regulator	alpha-galactosidas	hypothetical prote	adenosinetriphosph	formylmethanofuran	formylmethanofuran	formylmethanofuran	probable glucosylt	hypothetical prote	gene 13 protein -	hypothetical prote	hypothetical serin	probable membrane	probable adenosine	probable porin VC0	iojap-related prot	conserved hypothet	probable cytochrom	hypothetical prote
SUMMARIES	ID	W7WLHS	G75027	S52244	B81246	H82022	T29107	S57139	A45342	A58457	W7WL31	G82244	A44819	S18623	T18515	H69490	S57458	A69075	C71402	T16237	S30958	T33418	T40137	S64926	T30869	B82256	C95203	C98070	E82448	D64147
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	Query Match Length	86	405	651	612	612	1452	279	727	727	98	447	720	735	1149	421	424	437	456	579	593	658	891	893	1149	349	117	117	181	245
æ	Query	100.0	79.6	77.6	75.5	75.5	75.5	73.5	73.5	73.5	69.4	69.4	69.4	69.4	69.4	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	66.3	65.3	65.3	65.3	65.3
	Score	49	39	38	37	37	37	36	36	36	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	32.5	32	32	32	32
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conserved hypothet	hypothetical prote	hypothetical prote	signal sequence pe	Muramoyltetrapepti	phosphoprotein pho	probable aspartate	hypothetical prote	SOF1 protein - yea	hypothetical prote	conserved hypothet	probable glycyl-tR	probable aldehyde	hypothetical prote	stripe a/b protein	hypothetical prote
AG2950	D98332	D82154	F69456	E64865	B55346	C69672	T32673	835323	H71933	D64578	C72544	A83348	T31795	869205	C72779
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264	278	281	290	304	305	392	440	489	495	495	583	771	870	1180	107
65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	63.3
32	32	32	32	32	32	32	32	32	32	32	. 32	32	32	32	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

W/WLISS

E/Species: human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Accession: A03688; S12367; T10428

R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

V;Yicology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03688

A;Molecule type: DNA

A;Residues: 1-98 <SEB.

A;Cross-references: UMRPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333031

R;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 lax

A;Reference number: S12367; MUID:90107938; PMID:2153075

A;Accession: S12367

A;Accession: Breliminary

A;Molecule type: protein

A;Residues: 1-98 <BAR>

B;Residues: 1-98 <BAR>

A;Residues: 1-98 <BAR>

A;Residues: 1-98 <BAR>

A;Residues: 1-98 <BAR>
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A;Residues: 1-98 <BAR>
A;Residues: 1-98 <BAR>
A;Residues: 1-98 <BAR

A;Accession: T10428 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-98 <KEN> A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033 C;Genetics:

A,Gene: E7 C,Superfamily: papillomavirus E7 protein C,Keywords: DNA binding, early protein; transcription regulation; zinc finger F,58-94/Region: zinc finger CCCC motif

Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels

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0 1 RAHYNIVTF 셤

RESULT 2

alanyi-tRNA synthetase related protein PAB1190 - Pyrococcus abyssi (strain Orsay) (C.Species: Pyrococcus abyssi (C.Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004 (AAccession: G79027

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75.5%; Score 37; DB 2; Length 1452; 75.0%; Pred. No. 46; tive 2; Mismatches 0; Indels
                                                                                                                               75.5%;
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Best Local Similarity 75.0°
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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9 RAHHNVVDF 17
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DéBEG3 protein - African clawed frog
C,Species: Xenopus laevis (African clawed frog)
C,Species: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 16-Aug-2004
C,Accession: S5224
K,Roghi, C.; 1e Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
Sk,Roghi, C.; 1e Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
Submitted to the EMBL Data Library, October 1992
A,Description: Eg3, selected by differential screening encodes a new Xenopus protein kir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMB0031 [similar N;Alternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer] (S;Species Neisseria meningitidis (S;Species Neisseria meningitidis (S;Species 1.00 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 (S;Accession: B81246 (S;Accession: Balzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Fi, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 (Sill, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-405 «KAM»
A;Cross-references: UNIPROT:Q9UXV2; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5066
A;Experimental source: strain Orsay
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A;Cross-references: UNIPROT:Q9X1P9; GB:AE002361; GB:AE002098; NID:g7225245; PIDN:AAF4050
A;Experimental source: serogroup B, strain MC58
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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A75001
A;Accession: G75027
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Pred. No. 4.7;
1; Mismatches
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75.0%; Pred. No. 12;
iive 1; Mismatches
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;Keywords: ATP
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85.7%;
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Best Local Similarity 75.v.
6, Conservative
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558 RAHYNVTT 565
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A,Molecule type: mRNA
A,Residues: 1-651 <ROG>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S52244
                                                                                                                                                                                                                                                                                            A;Gene: PAB1190
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                                                                                                                                                                                                                                                                      Genetics
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Matches
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C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred:
F;2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMA0276 [simila N,Alternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer] (Speciaes Neisseria maningitidis C;Speciaes Neisseria maningitidis C;Accession: H82022 (Speciaes)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: glms; NNA0276
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
C;Keywords: aminotransferase; isomerase
F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred
F;2/Active site: Cys #status predicted
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C;Species: Theileria parva
C;Species: Theileria parva
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29107
C;Accession: T29107
C;Accession: K.P.; Macklin, M.D.; Gobright, E.
submitted to the EMBL Data Library, September 1995
A;Description: Characterisation of a polymorphic 150 kilodalton antigen of Theileria pa A;Reference number: Z20571
A;Accession: T29107
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Sclession: T29107
A;Status: DNA
A;Docidang.
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A;Cross-references: UNIPROT:Q27028; EMBL:L47230; NID:g986990; PID:g986991; PIDN:AAA7542.
A;Experimental source: strain Muguga; ssp. parva
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A;Note: P150
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-1452/Product: polymorphic antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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2
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Gaps

us-08-170-344-74.rpr

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C,Accession: B32444
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
R;Goldsborough, M.D.; 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assc A;Reference number: A94398; MUID:89299478; PMID:2545036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
A, Residues: 1-98 (GOL>
A, Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g45991
C, Comment: This protein may be involved in the oncogenic potential of this virus.
C; Superfamily: papillomavirus E7 protein
C; Keywords: DNA binding; early protein; transcription regulation; zinc finger
F; 58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
C;Accession: 682244
R;Heidelberg, U.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, N. R.Y., Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:AE004189; GB:AE003852; NID:g9655541; PIDN:AAF94246.1; GSPDB:GN00
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: VC1087
A;Map position: 1
C;Superfamily: response regulator with HD-GYP domain; response regulator homology; sens
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C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                 Gaps
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                         A;Molecule type: mRNA
A;Residues: 1-727 <ZHA>
A;Cross-references: UNIPROT:Q85436
C;Superfamily: wound tumor virus nonstructural protein Pns4
C;Reywords: GTP binding; nucleotide binding; P-loop; zinc finger
F;33-40/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 447;
Pred. No. 53;
1; Mismatches 2; Indels
                                                                                                                                                                                                                       73.5%; Score 36; DB 2; Length 727; 66.7%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 1; Length 98;
Pred. No. 11;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              2; Mismatches
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75.0%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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A, Status: translation not shown
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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84 RQHWNIMTF 92
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A; Status: preliminary
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C,Superfamily: wound tumor virus nonstructural protein Pns4
C;Keywords: glycoprotein; nonstructural protein
F;2,94,138,161,176,283,402,537,600,644/Binding site: carbohydrate (Asn) (covalent) #stat
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R;Zhao, X.; Li, Y.; Liu, Y.; Liang, X.; Chen, Z.
Acta Microbiol. Sin. 36, 93-102, 1996
A;Title: Sequencing and function analysis of the deduced protein of rice dwarf virus gen A;Reference number: A58457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Suzuki, N.; Watanabe, Y.; Kusano, T.; Kitagawa, Y.
Virology 179, 446-454, 1990
A;Title: Sequence analysis of rice dwarf phytoreovirus genome segments S4, S5, and S6.
A;Reference number: A45342, MUID:91021049; PMID:2219732
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: Genomic RNA
A;Cross-references: UNIPROT:P22474; GB:X54622; NID:g61469; PIDN:CAA38442.1; PID:g61470
C;Genetics:
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C;Species: rice dwarf virus
C;Date:.30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                              probable membrane protein YJR116w - yeast (Saccharomyces cerevisiae)
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C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change
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C;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change
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R;Rose, M.; Koetter, P.; Entian, K.D.
Rsubmitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S57139
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71.4%; Pred. No. 13;
tive 2; Mismatches
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Pred. No. 35;
2; Mismatches
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A,Crose-references: SGD:S0003877
A,Map position: 10R
C,Keywords: transmembrane protein
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Best Local Similarity 71.3.
For Si Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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84 RQHWNIMTF 92
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836 AHFNILTF 843
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101 HYNVVTY 107
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A; Residues: 1-279 <ROS>
2 AHYNIVTF
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R;Williamson, P.; Halleck, M.
submitted to the EMBL Data Library, January 1999
**Reference number: Z18940
**A;Reference number: Z18940
**A;Reference number: Z18940
**A;Residues: preliminary; translated from GB/EMBL/DDBJ
**A;Molecule type: mRNA
**A;Molecule type: mRNA
**A;Residues: 1-1149 < WIL>
**A;Cross-references: UNIPROT:Q29449; EMBL:U51100; NID:g4115340; PID:g4115341; PIDN:AADD3
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cormylmethanofuran dehydrogenase (tungsten) chain B homolog (fwdB-2) - Archaeoglobus fulcingly formylmethanofuran dehydrogenase (tungsten) chain B homolog (fwdB-2) - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Caccession: H69490
C;Caccession: H69490
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso, J. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S:Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Atthors: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Accession: H69490
A;Accession: H69490
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C;Superfamily: formylmethanofuran dehydrogenase (molybdenum) beta chain
C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin
                                                                                                                                                                                                                                                                                                                                                       69.4%; Score 34; DB 2; Length 1149; 75.0%; Pred. No. 1.4e+02; ive 1; Mismatches 1; Indels
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Matches 6; Conservative
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57 AKYNIITF 64
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A; Residues: 1-421 <KLE>
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A, Residues: 1-720 <ADU>
A, Cross-references: UNIPROT: P27756; GB: M77351; EMBL: M60777; NID: 9153734; PIDN: AAA26933.1
A, Notes sequence extracted from NCBI backbone (NCBIN: 70487, NCBIP: 70488)
R, Aduse-Opoku, J.; Tao, L.; Ferretti, J.J.; Russell, R.R.B.
J. Gen. Microbiol. 137, 757-764, 1991
A, Title: Biochemical and genetic analysis of Streptococcus mutans alpha-galactosidase.
A, Reference number: A44673; MUID: 91311378; PMID: 1649890
A, Contents: annotation
A, Note: this sequence has been revised in reference A44810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein 1 (ntrC 3' region) - Azorhizobium caulinodans C;Species: Azorhizobium caulinodans C;Species: Azorhizobium caulinodans C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 C;Accession: S18623 #Sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 R;Pawlowski, K.; Klosse, U.; de Bruijn, F.J. Mol. Gen. Genet. 231, 124-138, 1991 A;Pitle: Characterization of a novel Azorhizobium caulinodans ORS571 two-component regulation: S18622; MUD:92092954; PMID:1661370
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A;Molecule type: DNA
A;Residues: 1-735 <PAW>
A;Cross-references: UNIPROT:Q04855; GB:X63841; GB:S71362; NID:g38734; PIDN:CAA45329.1;
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N;Alternate names: chromaffin granule ATPase II; P-type ATPase
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18515
                                                                                                                                                                                                                                                                                          alpha-galactosidase (EC 3.2.1.22) - Streptococcus mutans
C;Species: Streptococcus mutans
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A44819; A44673
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Pred. No. 89;
2; Mismatches 1; Indels
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A;Reference number: A44819; MUID:92085044; PMID:1660918
A;Contents: erratum; strain Ingbritt
A;Accession: A44819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Gene: aga
C;Superfamily: alpha-galactosidase II
C;Keywords: glycosidase; hydrolase
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Best Local Similarity 62.5
Matches 5; Conservative
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182 SHYDVITF 189
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123 SHYGVVIF 130
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Sequence 93, Appl Sequence 93, Appl Sequence 93, Appl Sequence 331, Appl Sequence 49, Appl Sequence 48, Appl Sequence 15, Appl Sequence 15, Appl Sequence 22, Appli Sequence 22, Appli

Sequence 109 Sequence 22, Sequence 32,

54, 68, 55,

Sequence Seq

Sequence 62, Sequence 64, Sequence 74, Sequence 16, Sequence 16, Sequence 14,

Sequence 57, A Sequence 73, A Sequence 107,

Sequence 149,

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Similarity 100.0%; Score 49; DB 9; Length 9; Similarity 100.0%; Pred. No. 1.6e+06; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.; APPLICANT: Winnett, Mark T.; APPLICANT: Goldstone, Stephen E.; APPLICANT: Slagel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003301
; CURRENT PILING DATE: 2000.10-19
; PRIOR APPLICATION NUMBER: US/09/891,823
; CURRENT PILING DATE: 2000.06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FRAESEQ for Windows Version 4.0
         US-10-367-658-93

US-10-367-668-93

US-10-367-668-93

US-10-367-67-93

US-10-777-053-331

US-10-871-138-49

US-10-871-138-49

US-10-871-138-49

US-10-871-138-49

US-10-871-138-49

US-10-844-701-9

US-10-844-701-9

US-10-751-845-109

US-10-751-845-109

US-10-751-845-109

US-10-654-200-52

US-10-654-200-53

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US-10-654-200-55

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US-10-306-541-64

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US-10-306-541-16
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US-10-306-541-107
US-09-870-759-149
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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ORGANISM: Human papilloma virus
            RAHYNI VTF
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             SEQ ID NO 48
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                                                                                     June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds (without alignments) 64.268 Million cell updates/sec
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Sequence 4, Ag
Sequence 1, 7
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Sequence 4
Sequence 5
Sequence 5
Sequence 6
Sequence 6
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| Cgn2_6/ptodata/1/pubpaa/USO5_MW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO6_MW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.ppp:*
                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-888-721-4
US-09-07-439A-1
US-10-227-789-3
US-10-115-620-3
US-10-365-908-48
US-10-367-580-93
US-10-367-580-93
US-10-367-593-93
US-10-367-593-93
US-10-367-594-93
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                    1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Sequence No. US20020132990A1

Sequence No. US20020132990A1

GENERAL INFORMATION:

APPLICANT: Huston, James S.

APPLICANT: Huston, James S.

APPLICANT: Laurent, Olivier

APPLICANT: Laurent, Olivier

APPLICANT: Baresco, Wayne A.

TITLE OF INVENTION: DELIVERY

TITLE OF INVENTION: DELIVERY

FILE REFERENCE: 23611-A USA

CURRENT FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATENTION OF SEQ ID NOS: 45

SOFTWARE: PATENTION OF SEQ ID NOS: 45

SOFTWARE: PATENTION OF SEQ ID NOS: 45
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Publication No. US2003020299A1

GENERAL INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Blanke, Steven R.

APPLICANT: Balard, Jill C.

APPLICANT: Ballard, Jimy D.

APPLICANT: Starnbach, Michael N.

CURRENT APPLICANTON: Handles for Delivering Compounds into Cells

FILE REFERENCE: 1999-04-08

FRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-06-07

PRIOR FILING DATE: 1996-12-13

NUMBER OF SEQ ID NOS: 26

SSOTWARE: FRACESO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 49; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Human papillomavirus
US-09-888-721-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Sequence 3, Application US/10115620
; Sequence 3, Application US/20030118588A1
; GENERAL INFORMATION:
; APPLICANT: WELIEF. Cornelius
; APPLICANT: Schoenberger. Stephen
; APPLICANT: Offinga, Rienk
; APPLICANT: Offinga, Rienk
; APPLICANT: Toes, Rene
; TILL OF INVENTION: CD-40 Binding Molecules and CTL Peptides for Treating Tumors
; FILE REPERENCE: TNX 98-04
; CURRENT APPLICATION NUMBER: US/10/115,620
; CURRENT PLING DATE: 1999-05-22
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NOS: 3
; SEQ ID NOS: 3
; SEQ ID NO 3
; TUMORER PATENTION OF SEQ ID NOS: 3
; SEQ ID NO 3
; SEQ ID NO 3
                                                            GENERAL INFUGUATION:
GENERAL INFUGUATION:
GENERAL INFUGUATION:
APPLICANT: Schoenberger, Stephen
APPLICANT: Schoenberger, Stephen
APPLICANT: Offitings, Rienk
APPLICANT: Toes, Rene
TITLE OF INVENTION: Thuncrs
TITLE OF INVENTION: Thuncrs
TITLE REPERBNCE: TAX 98-04
CURRENT PAPLICATION NUMBER: US/10/227,789
CURRENT PILING DATE: 1999-05-22
PRIOR PILING DATE: 1999-05-22
PRIOR PILING DATE: 1999-05-22
PRIOR PILING DATE: 1999-05-32
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 9
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human Papilloma Virus Type 16 E7 derived peptide
US-10-227-789-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human Papilloma Virus Type 16 B7 derived peptide
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100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+06;
iive 0; Mismatches 0;
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APPLICANT: Noefe, John R.
APPLICANT: Winnett, Mark T.
; Sequence 3, Application US/10227789; Publication No. US20030022860A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
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Matches 9; Conservative
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US-10-115-620-3
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APPLICANT: Mayhew, Mark

TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/461061

CURRENT APPLICATION NUMBER: US/10/367,580

CURRENT FILING DATE: 2003-02-14

FRIOR APPLICATION NUMBER: US 09/794,832

FRIOR APPLICATION NUMBER: US 09/794,832

FRIOR APPLICATION NUMBER: US 09/7011,645

FRIOR APPLICATION NUMBER: PCT/US96/13363

FRIOR FILING DATE: 1998-02-13

FRIOR FILING DATE: 1995-08-18

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100.0%; Score 49; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
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100.0%; Score 49; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: synthetic peptide
US-10-367-580-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: synthetic peptide
US-10-367-593-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Publication No. US20040005711A1
GENERAL INFORMATION:
APPLICANT: Regies, Geesje D.
APPLICANT: Holtrop, Marijke
APPLICANT: Wilschut, Christiaan J.
APPLICANT: Daemen, Arnoldine C.
APPLICANT: Daemen, Arnoldine C.
APPLICANT: Barent Arnoldine C.
APPLICANT: Paemen, Arnoldine C.
APPLICANT: Paemen, Arnoldine C.
APPLICANT: Paemen, Arnoldine C.
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        APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
FILE REPERENCE: 12011-003001
CURRENT APPLICATION NUMBER: US/10/365,908
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/891,823
PRIOR PILING DATE: 2001-10-19
PRIOR FILING DATE: 2000-06-26
NUMBER: OF SEQ ID NOS: 140
SOFTWARR: FASESEQ for Windows Version 4.0
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/406,818
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: PCT/NL01/00740
PRIOR FILING DATE: 2001-10-08
PRIOR FILING DATE: 2001-10-08
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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1 RAHYNIVTF 9
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US-10-367-668-93
                                                                                                                                                                                                                                                                                                                          US-10-367-658-93
                                                                                                          FEATURE:
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                                                                                              GENERAL INFORMATION:

APPLICANT: Rothman, James E.

APPLICANT: Rothman, James E.

APPLICANT: Hartl, F. Ulrich

APPLICANT: How, Mee H.

APPLICANT: How, Mee H.

APPLICANT: How, Mee H.

APPLICANT: Takechi, Yoshizumi

APPLICANT: Maybew, Mark

ITILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

FILE REFERENCE: 11746/461041

CURRENT APPLICATION NUMBER: US/10/367,594

CURRENT APPLICATION NUMBER: US 09/680,806

FRIOR APPLICATION NUMBER: US 09/011,645

FRIOR PILING DATE: 1996-02-13

FRIOR PILING DATE: 1996-02-13

FRIOR PILING DATE: 1996-08-16

FRIOR PILING DATE: 1995-08-16

FRIOR PILING DATE: 1995-08-16

FRIOR APPLICATION NUMBER: US 60/002,479

FRIOR APPLICATION NUMBER: US 60/002,479

FRIOR APPLICATION NUMBER: US 60/002,479
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: synthetic peptide US-10-367-594-93
                                                                          Sequence 93, Application US/10367594
Publication No. US20040071722A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 9; Conservative
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1 RAHYNIVTF 9
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1 RAHYNIVTF
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US-10-367-654-93
                                                              US-10-367-594-93
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## SERVERAL IN FORMATION:
## SAPLICANT: Rothman, James E.
## APPLICANT: Rothman, James E.
## APPLICANT: Hoe, Mee H.
## APPLICANT: Hoe, Mee H.
## APPLICANT: Hoedhton, Alan
## APPLICANT: Takechi, Yoshizumi
## APPLICANT: Takechi, Yoshizumi
## APPLICANT: Takechi, Yoshizumi
## APPLICANT: Takechi, Yoshizumi
## APPLICANT: Mark
## ITILE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
## FILE REFERENCE: 1746/461051
## CURRENT APPLICATION NUMBER: US/10/367,658
## CURRENT APPLICATION NUMBER: US 09/794,529
## PRIOR APPLICATION NUMBER: US 09/794,529
## PRIOR APPLICATION NUMBER: PCT/US96/1363
## PRIOR APPLICATION NUMBER: PCT/US96/1363
## PRIOR PLING DATE: 1996-08-18
## PRIOR PLING DATE: 1996-08-18
## PRIOR PLING DATE: 1995-08-18
## NUMBER OF SEQ ID NOS: 349
## NUMBER OF SEQ ID NOS: 349
## NUMBER OF SEQ ID NOS: 349
## INVENTIOR OF SEQ ID NOS: 349
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100.0%; Pred. No. 1.6e+06;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 49; DB 15; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 93
                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic peptide US-10-367-654-93
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Publication No. US20040071725A1
GENERAL INFORMATION:
APPLICANT: Rothman, James E.
APPLICANT: Hart!, F. Ulrich
APPLICANT: Hoe, Mee H.
APPLICANT: Houghton, Alan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 93, Application US/10167658
Publication No. US20040071724A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FITLE REFERENCE: 11746/461072
CURRENT PILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 09/794,517
PRIOR APPLICATION NUMBER: US 09/011,645
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-02-16
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR SEQ ID NOS: 349
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JAPLICANT: Rothman, James E.
APPLICANT: Rothman, James E.
APPLICANT: Rothman, James E.
APPLICANT: Hartl, F. Ulrich
APPLICANT: Howe, Mee H.
APPLICANT: Howelven, Alan
APPLICANT: Takechi, Yoshizumi
APPLICANT: Takechi, Yoshizumi
APPLICANT: Mayhew, Mark
TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
FILE REFERENCE: 11746/4610211
CURRENT APPLICATION NUMBER: US 10/10/38
PRIOR APPLICATION NUMBER: US 10/170,738
PRIOR APPLICATION NUMBER: US 09/552,868
PRIOR APPLICATION NUMBER: US 09/011,645
PRIOR APPLICATION NUMBER: US 09/011,645
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR APPLICATION NUMBER: US 60/002,490
PRIOR PILING DATE: 1996-08-16
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR PILING DATE: 1995-08-18
PRIOR SED ID NOS: 349
NUMBER OF SED ID NOS: 349
SOFTWARE: WordPerfect 8:0 for Windows
TINNG DATE: 1905-08-18
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100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-668-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-674-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-367-674-93
; Sequence 93, Application US/10367674
; Beblication No. US20040127684A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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1 RAHYNIVTF 9
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100.0%; Score 49; DB 16; Length 9;

Query Match

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Sequence 331, Application US/1077053

Publication No. US20040132088A1

Publication No. US2004013208BA1

APPLICANT: Simard, John J. L.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Diamond, David C.

APPLICANT: Lei, Xiang-Dong

TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF

TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN

FILE REFERENCE: MANNK. 022C1

CURRENT APPLICATION NUMBER: US/10/777, 053

CURRENT FILING DATE: 2004-02-10

PRIOR FILING DATE: 2001-11-07

PRIOR PAPLICATION NUMBER: 60/336, 968

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 979

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 331

LENTH: 9
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                         0; Indels
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100.0%; Score 49; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
  100.0%; Pred. No. 1.6e+06; vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 29, 2005, 05:48:15
Job time: 53.8517 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human Papillomavirus 16
                      9; Conservative
                                                                    1 RAHYNIVTF 9
                                                                                         1 RAHYNIVTF 9
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Best Local Similarity
Matches 9; Conserv
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US-10-777-053-331
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1, Appli 4, Appli 4, Appli 19, Appli 11, Appli 11, Appli 11, Appli 12, Appli 12, Appli 12, Appli 12, Appli 12, Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence 3

Sequence

Sequence

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APPLICANT: Subo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
SUBRESSEE: Townsend and Townsend and Crew LLP
STREET: Yow Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette COMPUTER: DOS SOFTWARE: FASTESE (For Windows Version 2.0 CURRATY APPLICATION NUMBER: US 08/02/39A FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-AMR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1992
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGESTRATION NUMBER: 32,762
REGENANCE (A15) 576-0300
US-08-075-541D-42
US-09-382-616A-1
US-08-944-368A-4
US-09-813-303-8
US-09-613-303-8
US-09-986-118A-4
US-09-986-118A-4
US-09-986-118A-4
US-10-201-764-19
US-10-201-764-19
US-09-637-746-3
US-09-637-746-3
US-09-637-746-3
US-09-637-746-3
US-09-613-303-12
US-09-613-303-12
US-09-613-303-12
US-08-613-303-12
US-08-613-303-12
US-08-613-303-12
US-08-613-303-12
                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
     1000.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA
USA
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US-08-159-339A-138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: CA
       Sequence 138, App Sequence 5, Appli Sequence 5, Appli Sequence 32, Appli Sequence 4, Appli Sequence 4, Appli Sequence 26, Appli Sequence 279, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 15, Appli Sequence 20, Appli Sequence 21, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 8, Appli
                                                                                                                     June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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Sequence
Sequence
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-159-339A-138

US-09-501-097A-5

US-09-501-097A-5

US-10-365-908-48

US-10-365-908-48

US-08-075-541D-49

US-08-075-541D-56

US-08-075-541D-29

US-08-075-541D-29

US-08-075-541D-29

US-08-075-541D-29

US-08-075-541D-30

US-08-075-541D-20

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US-08-075-541D-8
US-09-501-097A-6
US-09-390-027-6
US-08-406-248-6
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                               1 RAHYNIVTF 9
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                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB
Maximum DB
                                                                                        OM protein
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100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 49; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
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Sequence 48 Application US/10365908
GENERAL INFORMATION:
APPLICANT: Boux, Leslie J.
APPLICANT: Winnet, wark T.
APPLICANT: Siegel, Marvin B.
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT;
TITLE REPERENCE: 12071-003001;
CURRENT APPLICATION NUMBER: US/10/365,908
                  FILING DATE: 21-JUL-1995
APPLICATION NUMBER: US 60/007,184
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: US 66,286
FILING DATE: 01-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAITON, Alexis
REGISTRATION NUMBER: 22,702
REGISTRATION NUMBER: 22,702
TELEPHONE: (215) 923-4466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TZYY-CHOOU WU

APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICANTION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 9
APPLICATION NUMBER: US 60/001,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                            TELEPHONE: (215) 923-4466
TELEFAX: (215) 923-2189
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09501097A; Patent No. 6734173; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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1 RAHYNIVTF 9
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US-09-501-097A-5
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US-09-000-003A-5
US-09-000-003A-5
Fatent No. 6652850
Fatent No. 6652850
Fatent No. 6652850
TELECANT: Philip, Ramila
TILE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
THER USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
SPECIFIC IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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US-09-593-870A-25
Sequence 25. Application US/09593870A
Factor No. 6548643
FILE OF INVENTION: We fail an Title OF INVENTION: We fail Immunotherapy
FILE REFRENCE: 2368-MCKenzie
CURRENT APPLICATION NUMBER: US/09/593,870A
CURRENT APPLICATION NUMBER: 09/223,043
FRICR APPLICATION NUMBER: 09/223,043
FRICR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 3.0
EMEGTH: 2548-MCM NUMBER OF SEQ ID NO 25
FACTOR NO 25

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CORRESPONDENCE ADDRESS:
ADDRESSE: ALEXIS Barron, Esq.
STREET: Suite 2600 Aramark Tower, 1101 Market Street
                                                     100.0%; Score 49; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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COUNTRY: United States of America
ZIP: 1910.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 49; DB 4; I 100.0%; Pred. No. 4.1e+05; attive 0; Mismatches 0;
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FILING DATE: 19-JUL-1996
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                         Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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1 RAHYNIVTF 9
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US-08-159-339A-138
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CORRENT AFFLICATION DATA CONTROL APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-JUN-1993
CLASSFITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU Pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S.
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: 215-567-2020
                           ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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STRANDEDNESS: single
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         COUNTRY:
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| Sequence 4, Application US/08075541D |
| Patent No. 6183745 |
| Fatent No. 6183745 |
| APPLICANT: TINDLE, ROBERT |
| APPLICANT: FERNANDO, GERMAIN |
| APPLICANT: FERNANDO, GERMAIN |
| TITLE OF INVENTION: SUBGNIT PAPILLOMA VIRUS VACCINE AND |
| TITLE OF INVENTION: PEPTIDES FOR USE THEREIN |
| NUMBER OF SEQUENCES: 56 |
| CORRESPONDENCE S. 56 |
| ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. |
| STRRET: 1601 MARKET STREET, 36TH FLOOR |
| COLLY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 49; DB 4; Length 10; 100.0%; Pred. No. 0.0026; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                         100.0%; Score 49; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
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APPLICANT: Neefe, John R.
APPLICANT: Neefe, John R.
APPLICANT: Minnett, Mark T.
APPLICANT: Minnett, Mark T.
APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marrin
TITLE OF INTENTION: HUMAN PAPILLOMA VIRUS TREATMENT
FILE REFERENCE: 12071-003001
CURRENT APPLICATION NUMBER: US/09/891,823
FRIOR PILING DATE: 2003-02-13
PRIOR PILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/214,202
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3: SEQ ID NOS: 140
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/891,823
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/214,202
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
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US-10-355-908-32
Sequence 32, Application US/10365908
; Patent No. 6797491
                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Human papilloma virus
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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1 RAHYNIVTF 9
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Fatent No. 6183745
GENERAL INPORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FERNANDO, GERMAIN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: BEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESSE:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STREET: 19103-2398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 49; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.0038; Matches 9; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UNN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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100.0%; Score 49; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-09-601-729-279
; Sequence 279, Application US/09601729
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   ; MOLECULE TYPE: peptide US-08-075-541D-56
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| Sequence 56, Application US/08075541D |
| Sequence 56, Application US/08075541D |
| Patent No. 6183745 |
| Patent Sequence 56, Application US/08075541D |
| APPLICANT: TINDLE, ROBERT |
| APPLICANT: FERNANDO, GERMAIN |
| TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND |
| TITLE OF INVENTION: PEPTIDES FOR USE THEREIN |
| NUMBER OF SEQUENCES: 56 |
| CORRESPONDENCE ADDRESS: 56 |
| ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 49; DB 3; Length 14; 100.0%; Pred. No. 0.0038; ative 0; Mismatches 0; Indels
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
COMPUTRY: USA
ZIP: 19103-2398
COMPUTRY: USA
COMPUTRY: IBM PC COMPACINDE
COMPUTRY: IBM PC COMPACINDE
COMPUTRY: IBM PC COMPACINDE
COMPUTRY: IBM PC COMPACINDE
SOFTWARE: PARCHININ RELEASE #1.0, Version #1.25
CURRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: 10-UUN-1993
CILASSIFICATION NUMBER: US/08/075,541D
FILING DATE: 10-UUN-1993
CILASSIFICATION NUMBER: AU Pk 3876
FILING DATE: 12-DEC-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: AU Pk 3876
FILING DATE: 12-DEC-1990
FRIOR APPLICATION NUMBER: 27,363
ATTORNEY/ADATE 12-DEC-1991
FILING DATE: APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                  NAME: NADEL, ALANS
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
REBRENCE/DOCKET NUMBER: 8795-
TELEPHONE: 215-567-202
TELEPHONE: 215-567-2991
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-075-541D-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Sequence 16, Application US/09980523A

Sequence 16, Application US/09980523A

BORGANION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOURGAUTY VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAN, FRANCINE

APPLICANT: CONNAN, FRANCINE

APPLICANT: FERRIES, ESTELLE

TITLE OF INVENTION: PROTEINE PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINES OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION NUMBER: US/09/980,523A

CURRENT APPLICATION NUMBER: PCT/FR00/01513

FRIOR PLING DATE: 2000-05-31

FRIOR PLING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PATENTIN VET. 2.1

SEQTURARE: PATENTIN VET. 2.1

SEQTURARE: PATENTIN VET. 2.1
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Fatent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FERNANDO, GERMAIN
TITLE OF INVENTION: SUBNUIT PAPILLOWA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES POR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEBE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                          100.0%; Score 49; DB 3; Length 17; 100.0%; Pred. No. 0.0046; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 49; DB 4; Length 17; 100.0%; Pred. No. 0.0046;
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                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human Papillomavirus
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                        ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-075-541D-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RAHYNIVTF 9
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US-08-075-541D-30
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       GENERAL INFORMATION:
APPLICANT: THIAM, KADER
APPLICANT: THIAM, KADER
APPLICANT: AURIAULT, CLAUDE
APPLICANT: AURIAULT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: USING, ESTELLE
APPLICANT: WINDER: USPOPPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT PILING DATE: 1999-02-05
PRIOR PILING DATE: 1999-02-05
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SEQ ID NO 279
LENGTH: 15
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUUNTRY: USA

ZIP: 19103-2398

COUNTRY: USA

ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D

FILING DATE: 10-JUN-1993

CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: AU pk 3876

FILING DATE: 12-DEC-1990

PRIOR APPLICATION NUMBER: pct/au91/00575

FILING DATE: 12-DEC-1991

RILING DATE: 12-DEC-1991

RILING DATE: 12-DEC-1991

RILING DATE: 12-DEC-1991

ATPLICATION NUMBER: pct/au91/00575

FILING DATE: 12-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 WARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
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Matches 9; Conserv
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Gaps

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Search completed: June 29, 2005, 01:44:28
Job time : 16.9126 secs
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Sequence 3, Application US/08075541D

Patent No. 6183745

GENERAL INFORMATION:

APPLICANT: TINIE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                          COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
FILING DATE: 12-DEC-1990
FILING DATE: 12-DEC-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PC/Au91/00575
FILING DATE: 12-DEC-1991
ATPORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 8795-4
FELEFRANCE/DOCKET NUMBER: 8795-4
TELEPHONE: 215-567-2020
TELEFRAX: 215-207-2020
TELEFRAX: 215-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                     PENNSYLVANIA
: USA
PHILADELPHIA
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Gaps
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100.0%; Score 49; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/aug1/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27, 363
REGISTRATION NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2991
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acide
"VOR: amino acide"
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 RAHYNIVTF 14
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 28, 2005, 23:32:21; Search time 11.2747 Seconds

(without alignments)

76.805 Million cell updates/sec

Title:

US-08-170-344-73

Sequence:

1 RFHNIRGRW 9

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum Match 04

Maximum Match 1004

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Description	:	cern Eo	E6 protein - human		E6 protein - human			E6 protein - human	E6 protein - human	E6 protein - rhesu	branched-chain ami	probable outer mem	major outer membra	E6 protein - human	probable pseudouri	E6 protein - human	E6 protein - human	HHRF6 protein - hu	conserved hypothet	hypothetical prote	glucosyltransferas	glucosyltransferas	hypothetical prote		lysozyme (EC 3.2.1	cytochrome c bioge				
SUMMARIES		CHIMOM	A61237	S36573	W6WL33	W6WL58	S15614	S36497	W6WL31	W6WL35	W6WL51	S36544	S15621	W6WLR1	E69423	H71479	H81742	836567	B75366	W6WL8	836538	QQBED6	H72222	F81302	T30857	T30552	H71155	W6WL18	S18463	B83847
Length DB			•	148 2	149 1	149 1	159 1	159 2	149 1	149 1	151 1	150 2	153 1	191 1	274 2	340 2	340 2	138 2	321 2	155 1	157 2	197 1		466 2	1449 2		114 2	158 1	211 2	556 2
% Query Match		TOO. 0	89.3	89.3	89.3	89.3	89.3	89.3	87.5	87.5	78.6	71.4	71.4	71.4		9.69	9.69	67.9	67.9	66.1	66.1	66.1	66.1	66.1	66.1	66.1	64.3	64.3	64.3	64.3
Score		0	20	20	20	20	20	20	49	49	44	40	40	40	39	39	39	38	38	37	37	37	37	37	37	37	36		36	36
Result No.		٠,	7	m	4	2	9	7	Φ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

116 2 A57096 99 2 AE0343 131 1 R4FP17 154 2 G82980 124 2 G82981 124 2 E85513 124 2 E85513 124 2 E85513 124 2 E85513 124 2 E85513 125 2 A33497 111 2 A89724 111 2 D64905 146 2 JC4798 146 2 JC4798 147 2 T39936	64.3 2616 2 A5/1096 62.5 132 2 RE0343 62.5 131 1 R4FP17 62.5 131 2 R36491 62.5 154 2 G82980 62.5 324 2 G82981 62.5 324 2 G8513 62.5 387 1 RSBFF 62.5 387 2 A34497 62.5 511 2 A99083 62.5 511 2 A99083 62.5 511 2 A90083 62.5 510 2 D64905 62.5 510 2 D64905 62.5 510 2 D64905 62.5 1040 2 T39936	2616 2 9 9 2 1 131 1 131 1 154 2 324 2 334 2 387 2 511 2 511 2 526 2 1040 2	nudel protein prec	phage integrase (p	hypothetical prote	ribosomal protein	conserved hypothet	E6 protein - human	probable integrase	probable integrase	integrase - phage	prophage DLP12 int	hypothetical prote	hypothetical prote	probable sugar tra	seizure-related me	SNF2 helicase homo	probable helicase
116 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		6666666666666666 4666666666666666 £ £ £ £ £ £ £ £ £ £ £ £ £ £ £ £ £ £ £	A57096	AE0343	E75006	R4FF17	G82980	S36491	E85513	G90662	RSBPIP	A33497	Н90893	A85724	D64905	JC4798	D70066	T39936
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ALIGNMENTS

RESULT 1
nomins protein B6 - human papillomavirus type 16
C;Species: human papillomavirus type 16 C:Date: 28-Mav-1986 #semmence revision 28-Mav-1986 #text change 09-Jul-2004
C;Accession: A03682; T10427
R;Seedort, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G. Virology 145, 181–185, 1985
A,Titles Human papillomavirus type 16 DNA sequence.
A;Accession: A03682
A;Molecule type: DNA A;Residues: 1-158 <see></see>
A; Cross-references: UNIPROT: P03126; GB: K02718; NID: 9333031; PIDN: AAA46939.1; PID: 933303
k;kennedy, 1.m.; Haddow, J.K.; Clemencs, J.B. J. Virol. 65, 2093-2097, 1991
A,Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A; Accession: 110427
A;Status: preliminary; translated from GB/EMBL/DDBJ
Ajmolecule Lype: DNA AjResidues: 1-158 <ken></ken>
A;Cross_references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics: A;Gene: E6
C;Superfamily: papillomavirus B6 protein C:Kavmorda: DNA hinding: parly protein: zing finger
1
Query Match 100.1%; Score 56; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.0044; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RPHNIRGRW 9
Db 131 RFHNIRGRW 139
RESULT 2 846127 Ed protein - human papillomavirus type 52 C;Species: human papillomavirus type 52 C;Species: human papillomavirus type 52 C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996 C;Accession: A61237 R;Takami, Y:; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, Int. J. Cancer 48, 516-522, 1991 A;Title: Cloning and characterization of human papillomavirus type 52 from cervical car A;Accession: A61237 A;Accession: A61237 A;Status: preliminary A;Molecule type: DNA

Query Match

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Virology 185, 424-427, 1991
A; reference number: A36779; MUD:92024102; PMID:1656594
A; Reference number: A36779; MUD:92024102; PMID:1656594
A; Reference number: A36779; MUD:92024102; PMID:1656594
A; Status: translation not shown
A; Status: translation not shown
A; Molecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
A; Rolecule type: DNA
C; Superfamily: papillomavirus R6 protein
C; Superfamily: papillomavirus R6 protein
C; Superfamily: papillomavirus R7
C; Reywords: DNA binding; early proteif; zinc finger
F; 30-66/Region: zinc finger CCCC motif
F; 103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
S15614
E protein - human papillomavirus type 2a
C;Species: human papillomavirus type 2a
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: 815614
E;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: 815614; MUID:91188699; PMID:1964523
A;Accession: 815614
A;Molecule type: DNA
A;Residues: 1-159 <HIR>
A;Cross-references: UNIPROT:P25484; EMBL:X55964
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;35-11/Region: zinc finger CCCC motif
F;108-144/Region: zinc finger CCCC motif
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Es protein - human papillomavirus type 27

Es protein - human papillomavirus type 27

C;Species: human papillomavirus type 27

C;Species: 10-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: Sistant H.; Hofmann, B.

C;Accession: Sistant Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: Sistant Sista
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Pred. No. 0.054;
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88.9%; Pred. No. 0.057;
iive 0; Mismatches
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Y.; Iwamoto, S.; Matsukura, T.
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Best Local Similarity 88.5
Thes 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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C;Species: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
R;Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh A;Reference number: A93020; MUID:86200464; PMID:3009002
A;Reference number: A93020; MUID:86200464; PMID:333049; PIDN:AAA46958.1; PID:9463177
A;Residues: 1-149 <CCL
S;Superfamily: papillomavirus Ef protein
C;Superfamily: papillomavirus Ef protein
C;Superfamily: papillomavirus Ef protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148 cDEL>
A;Residues: 1-148 cDEL>
A;Cross-references: UNIPROT: P36814; EMBL: X74481; NID: 9397038; PIDN: CAA52585.1; PID: 93970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar.1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein - human papillomavirus type 52
Species: human papillomavirus type 52
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2
C;Accession: 836573
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
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88.9%; Pred. No. 0.054;
iive 0; Mismatches 1; Indels
                                                                                                               Length 148;
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                                                                                                           Score 50; DB 2;
Pred. No. 0.053;
0; Mismatches
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88.9%; Pred. No. 0.053;
iive 0; Mismatches
A,Residues: 1-148 <TAK>
C,Superfamily: papillomavirus E6 protein
                                                                                                               88.3%;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                               Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
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124 RFHNIMGRW 132
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A,Molecule type: DNA
A,Residues: 1-150 < DBLD:
A,Cross-references: UNIPROT: P36807; EMBL:X74472; NID:g396956; PIDN:CAA52530.1; PID:g396
C,Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger
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C;Species: 10-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15621
C;Accession: S15621
C;Accession: Holis, H.; de Villiers, E.M.
Virus Res. 18, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: S15614; MUID:91188699; PMID:1964523
                                                                                                                                                                 WGWL51

BG protein - human papillomavirus type 51

C;Species: human papillomavirus type 51

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E40415

J; Virol. 65, 4216-4225, 1991

A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus the A;Reference number: A40415; MUDE:91303675; PMID:1649326

A;Accession: E40415
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B6 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Spacesion: S36544
B;Delius, H.; Hofmann, B.
Bubmitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Reference number: S36469
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A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-151 - LUNDNA
A; Cross-references: UNINNAT: P26554; GB: M62877
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA binding; early procein; zinc finger
C; Region: zinc finger CCCC motif
F; 103-139/Region: zinc finger CCCC motif
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Pred. No.
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77.8%;
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Matches 6; Conservative
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         124 RFHNIGGRW 132
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-153 <HIR>
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S15621
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                                                                                                                                                                                                                                                                                                                                        C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A3244
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoctation and the sequence of human papillomavirus type 31: a cervical neoplasia-assoctation and the sequence of human papillomavirus type 31: a cervical neoplasia-assoctations associated sequence of human papillomavirus type 31: a cervical neoplasia-assoctation and the sequence of human papillomavirus type 31: a cervical neoplasia-associated sequence number: A;Reference number: A;Ref
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C;Species: human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E40824; S36521
E;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
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A,Status: translation not shown
A,Status: translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
R,Delius, H.; Hofmann, B
R,Delius, H
R,Deliu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Accession: A3244
A)Status: translation not shown
A)Molecule type: DNA
A)Residues: 1-149 <GOL>
A)Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
C)Comment: This protein may be involved in the oncogenic potential of this virus.
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A;Molecule type: DNA
A;Residues: 1-149 <-DBL>
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAAS2561.1; PID:g396998
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C, Superfamily: papillomavirus E6 protein
C, Reywords: DNA binding; early protein; zinc finger
E, 30-66 Region: zinc finger CCCC motif
F, 103-139/Region: zinc finger CCCC motif
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C;Keywords: DNA binding; early protein; zinc finger
E;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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Pred. No. 0.082;
0; Mismatches
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Pred. No. 0.082;
0; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                129 RFHNISGRW 137
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A; Accession: $36521
1 RFHNIRGRW 9
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C;Species: rhesus papillomavirus
C;Species: rhesus papillomavirus
C;Species: necaus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
A;Title: Characterization of the complete RhPV 1 genomic sequence and an integration location of the complete RhPV 1 genomic sequence and an integration location number: A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Cross-references: UNIPROT:P22158; EMBL:X55965; NID:g60882; PIDN:CAA39430.1; PID:g60883
C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus P6 protein
F;Psy-e4-groun: pinding; early protein; transforming protein; zinc finger
F;29-65/Region: zinc finger CCCC motif
F;102-138/Region: zinc finger CCCC motif
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, P. Peleschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
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A; Residues: 1-274 «KLE>
A; Cross-references: GB:AE001008; GB:AE000782; NID:g2689331; PIDN:AAB89855.1; PID:g264918
C; Superfamily: ATP-binding cassette homology
C; Keywords: ATP, nucleotide binding; Ploop
F; 36-241/Domain: ATP-binding cassette homology «ABC>
F; 53-60/Region: nucleotide-binding motif A (P-loop)
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Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-191 <0ST>
A; Cross-references: UNIPROT: P222159; EMBL: M37717
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA blinding; aarly protein; transforming protein; zinc finger
F; 60-96/Region: zinc finger CCCC motif
F; 133-169/Region: zinc finger CCCC motif
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A;Status: translation
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Job time: 12.2747 secs
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Best Local Similarity 62.5%;
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319 FYNVEGRW 326
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Haceger L G., Galutira D.F., Younghusband B.H.;
Haceger L G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1; -.
GO; GO:0003677; F:DNS cell nucleus; IEA.
GO; GO:0003677; F:DNS binding; IEA.
InterPro; IPR001334; E6.
NOW TER 1 1
NOW TER 91 91
SEQÜENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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09W931
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
E6 protein (Fragment)
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Papillomavirus
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404700; AAL01357.1;
GO; GO:0002675; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-87(2022).
EMBL; AF404659; AAL01355.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
FPfam; PF00518; E6; 1.
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SEQÜENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OFC-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein (Fragment)
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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100.0%; Pred. No. 0.014;
Live 0; Mismatches 0;
                                                                                                           100.0%; Score 56; DB 2; 100.0%; Pred. No. 0.014;
                                                                                                                                                                      0; Mismatches
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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Pfam; PF00518; E6; 1.
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NCBI_TaxID=10581;
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MEDLINE=21846229; PubWed=11857370;
MATLE K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868=874(2002).
EMBL, AR404701; AAL01359.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubWed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, AR404703; AL01363.1;

GO; GO:00042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
EMBL, AF404692; AAL01342.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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SEQÜENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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76 RFHNIRGRW 84
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer 19:868-874(2002).
EMBL, J. Cancer 97:868-874(2002).
EMBL, AF404694; AAL01345.1;
GO, GO:0003677; F:Dost cell nucleus; IEA.
GO, GO:0003677; F:DNA binding; IEA.
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EMBL, FA0407102; AAL01361.1; ---
EMBL, FA0407025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

PEam; PF00518; E6; 1.
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Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
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Papillomavirus.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE-21846229; PubMed=11857370;
MATER K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AP404696; AL01349-1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868 =874(2002).
EMBL; AR4046595; AAL01347.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
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Human papillomavirus type 16.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
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NCBI_TaxID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Pred. No. 0.014;
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Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF046698; AAL01353.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Beth-ciraldo E., Giraldo G.,

Beth-ciraldo E., Giraldo G.,

Sequence variations and viral genomic state of human papillomavirus

type 16 in penile carcinomas from Ugandan patients.";

J. Gen. Virol. 78:2199-2208[1997].

GO, GO:0042025; C:host cell nucleus; IEA.

GO, GO:0003677; F:DNA binding; IEA.

InterPro; IPR00138; E6; 1.

SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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124 RFHNIRGRW 132
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL, AP0031016; AAB70733.1; -.
EMBL, AP0031016; AAB70733.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
J. virol. 69:7743-7753(1995).
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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100.0%; Pred. No. 0.017;
tive 0; Mismatches 0; Indels
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34114; AAA91661.1; -.
                                                                                       Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBL_TaxID=10581;
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Human papillomavirus.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IRR001334; E6.
Pfan; PF00518; E6; 1.
SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches 9; Conservative
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Query Match 100.0%; Score 56; DB 2; Length 151; Best Local Similarity 100.0%; Pred. No. 0.017; Matches 9; Conservative 0; Mismatches 0; Indels
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Search completed: June 29, 2005, 01:34:49 Job time : 54.2473 secs

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Sequence 41, P
Sequence 56, P
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Sequence 40,
Sequence 5,
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Sequence 2, A
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-476-570-40
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Maximum Match 100%
Listing first 45 summaries
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US-10-425-114-36574
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OTHER INFORMATION: Description of the artificial sequence: peptide E6 130-144
                                                                                         APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: MAILIERE, BETTART
APPLICANT: MAILIERE, BETTART
APPLICANT: MAILIERE, BETTART
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOUVEGLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
FRIOR FILING DATE: 2002-05-03
FRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE PATENTING VET: 2.1
Sequence 43, Application US/10476570; Publication No. US20040170644A1; GENERAL INFORMATION:
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ORGANISM: artificial sequence
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Gaps

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TYPE: PRT
ORGANISM: Artificial Sequence
                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 23
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, OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
US-10-476-570-56
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                                                                                                                                                                                                                                                  APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MATLIERE, Bernard
APPLICANT: MATLIERE, Bernard
APPLICANT: MATLIERE, Bernard
APPLICANT: MATLIERE, Bernard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: MATLIERE APPLICANTION: MATLIERE APPLICANTION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN Ver. 2.1
IENGTH: 20
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Publication No. US20040170644A1

GENERAL INFORMATION

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MAILLERE, BERNAR

APPLICANT: MAILLERE, Bernard

APPLICANT: MAILLERE, Sandra

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: POUVELLE-MORATILLE, Sandra

TITLE OF INVENTION: MAXLURE of peptides derived from E6 and/or E7

TITLE OF INVENTION: Papillomavirus proteins and uses thereof

TITLE OF INVENTION: DADIILOMAVIRUS proteins and uses thereof

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT APPLICATION NUMBER: PCT/FR02/01533

PRIOR PILING DATE: 2003-01-05-03

PRIOR FILING DATE: 2002-05-03

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VOICE SEQ ID NOS: 63
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; Sequence 41, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
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RFHNIRGRW 10
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11 RFHNIRGRW 19
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1 RFHNIRGRW 9
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LENGTH: 22
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Sequence 27, Application US/10484063

Sequence 27, Application US/10484063

Publication No. US20050048467A1

GENERAL INFORMATION:

APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORYOLERO-LUNA, GUILLERMO

APPLICANT: FOLLEN, MICHELB

TITLE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

CURRENT APPLICATION NUMBER: PCT/US02/23198

PRIOR APPLICATION NUMBER: PCT/US02/23198

PRIOR PILING DATE: 2002-01-16

PRIOR PILING DATE: 2002-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PALENT Ver. 2.1

SEQ ID NO 27

LENGTH: 151
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; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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ORGANISM: Human Papillomavirus
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Best Local Similarity 100...
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Matches 9; Conservative
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                                               ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140 US-10-476-570-40
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; Sequence 20, Application US/10484063
; Publication No US20050048467A1
; GENERAL INFORMATION:
    APPLICANT: SAGTRY, K. JACANNADHA
; APPLICANT: TORIOLENCLINA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-20
; NUMBER OF SEQ ID NOS: 27
; SOGTWARE: PATENTIN VEY: 2.1
; SEQ ID NO 20
ILENCETH: SEQ ID NOS: 27
; SUCTWARE: PATENTIN VEY: 2.1
; SEQ ID NO 20
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Sequence 6, Application US/10177390
Publication No. US2030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear
TITLE OF INVENTION: Polynuclecides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT FAPRICATION NUMBER: US/10/177,390
CURRENT FAPRICATION DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 202-06-20
NUMBER OF SEQ ID NOS: 2.1
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                                                                                                                         Query Match
100.0%; Score 56; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-484-063-20
ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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14 RFHNIRGRW 22
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Gaps

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Sequence 2, Application US/10858384

Publication No. US20050033025A1

GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUINENTION: PRATICULARLY IN VACCINATION
TITLE OF INVENTION: OR ET OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 1999-06-03
FRIOR PILLING DATE: 1999-06-03
FRIOR PILLING DATE: 1999-06-03
FRIOR FILING DATE: 1999-06-03
FRIOR PILLING DATE: 1999-06-03
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Gaps

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Sequence 4, Application US/1089971
Sequence 4, Application US/1089971
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 56; DB 9; Length 266; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10000903
; Publication No. US2002018221A1
; GENERAL INFORMATION:
APPLICANT: Banck, Claudine
; APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Delisse, Anne-Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVEXTYION: Vaccine
; TITLE OF INVEXTYION: Vaccine
; TITLE OF INVEXTYION: Vaccine
; FILE REFERENCE: B45.10
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT APPLICATION NUMBER: PCT/EP98/05285
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1998-08-17
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOSTWARE: FASELEQ FOR Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 RFHNIRGRW 245
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LENGTH: 266
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US-10-899-771-4
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Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Sequence 2, Application US/10402724

Sequence 2, Application US/10402724

GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
CURRENT APPLICANTON NUMBER: US/10/472,724

CURRENT APPLICATION NUMBER: PCT/EP02/03271

PRIOR FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: EP 01107271.7

PRIOR APPLICANTON NUMBER: EP 01107271.7

SOFTWARE: PatentIn version 3.2
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100.0%; Score 56; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels (
  RESULT 10
US-10-367-057-16

Sequence 16, Application US/10367057

Publication No. US20050100554A1

GENERAL INFORMATION:

APPLICANT: Cuthill, Scott;

APPLICANT: Jackson, Amanda;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

PILE REFERENCE: 21402-559

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US/10/367,057

CURRENT FILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEC ID NOS: 198

SOFTWARE: CuraseqList version 0.1

SEC ID NO 16

LENGTH: 158
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APPLICANT: MALLIRROS, JIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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131 RFHNIRGRW 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Bapiens
US-10-367-057-16
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LENGTH: 171
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                                                                                                                                                                                                                                               FEATURE:
CTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type;
CTHER INFORMATION: 16)
US-10-899-771-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Score 56; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/1000903
Publication No. US2002018221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45.10'
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1996-12-18
PRIOR PILING DATE: 1996-12-24
NUMBER OF SEQ ID NOS: 28
SOUTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 RFHNIRGRW 245
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256 RFHNIRGRW 264
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US-10-000-903-10
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LENGTH: 292
TYPE: PRT
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US-10-000-903-10
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Search completed: June 29, 2005, 05:48:15 Job time : 53.8517 secs

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June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                              - protein search, using sw model
                                                                                              OM protein
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	(without alignments) 76.805 Million cell updates
Title:	US-08-170-344-72
Sequence:	ol 1 CYSLYGITL 9
Scoring table: BLOSUM62	BLOSUM62

283416 segs, 96216763 residues

Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	protein E6 - human	E6 protein - human	probable L-fuculos	probable membrane	probable exonuclea	Ca2+-transporting	hypothetical prote		_	protein -	E6 protein - human	E6 protein - human		pleiotropic drug r			coprotein	E6 protein - human	probable transcrip			E6 protein - rhesu	hypothetical prote	Ω	G protein-coupled	probable transport	probable resistanc	probable resistanc	hypothetical prote
ΩI	MEWLHS	W6WL31	H95900	S51256	G82450	T31688	T24836	E86512	D72109	A61237	836573	W6WL58	S41690	S64015	T24439	D82181	S35783	W6WL33	D83290	W6WL56	A44890	W6WLR1	T22399	PABY	B55733	S40819	C86075	D91228	H89914
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Length	158	149	232	473	1013	1160	323	91	91	4	148	149	255	1068	262	429	4	149	S	2	155	191	345	348	354	421	421	421	604
% Query Match	100.0	76.5	-:	74.5	74.5	74.5	72.5	70.6	70.6	9.07	70.6	70.6	70.6	70.6	68.6	68.6	9.89	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
Score	51	39	38	38	38	38	37	36	36	36	36	36	36	36	35	32	32	34	34	34	34	34	34	34	34	34	34	34	34
Result No.	-	0	ю	4	ഗ	9	7	œ	0	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

UDP-sugar hydrolas	probable outer mem	outer membrane pro	omega-agatoxin III	omega-agatoxin III	omega-agatoxin III	conserved hypothet	hypothetical prote	hypothetical prote	,	E6 protein - human	_	hypothetical prote		_	hypothetical prote
C84295	C71982	A64523	A54252	D54252	A42335	H71270	G82424	F72747	W6WL35	836503	AF2088	T25724	T34008	T40323	H97756
0	~	~	7	7	~	7	7	7	Н	~	~	7	~	7	7
682	069	711	16	9/	92	91	105	124	149	153	202	234	271	277	284
66.7	66.7	66.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7
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ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SEE>
A; Residues: 1-158 <SEE>
A; Residues: 1-158 <SEE>
A; Cross-references: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G33303
A; Cross-references: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G33303
B; Kennedy, I.m.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Virol. 65, 2093-2097, 1991
A; Fitle: A negative element in the human poapillomavirus type 16 genome acts at the lev
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
A; Accession: T10427
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protein B6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Rossidues: 1-158 <KEN>
A;Cross-references: EMBL:KO2718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 51; DB 1; Length 158; larity 100.0%; Pred. No. 0.024; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: papillomavirus B6 protein
Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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Best Local Similarity
Matches 9; Conserv
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CYSLYGITL 95 83

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RESULT 2

WGWL31.

WGWL31.

E protein - human papillomavirus type 31

E protein - human papillomavirus type 31

S,Species: human papillomavirus type 31

A,Note: host Homo sapiens (man)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C;Accession: A3244

R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assc

A;Reference number: A94398; MUD:89299478; PMID:2545036

A;Referension: A32444

A;Status: translation not shown

Length 473;

DB 2;

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A; Cross-references: EMBL: Z48758; NID: g747879; PID: g747880; MIPS: YDR105c
                                                                                                                                                                                                                                               F122-138/Domain: transmembrane #status predicted CTM4-
F150-166/Domain: transmembrane #status predicted CTM5-
F1200-218/Domain: transmembrane #status predicted CTM6-
F1228-312/Domain: transmembrane #status predicted CTM7-
F1296-312/Domain: transmembrane #status predicted CTM7-
F401-417/Domain: transmembrane #status predicted CTM9-
F441-459/Domain: transmembrane #status predicted CTM9-
                                                                                                      A,Cross-references: SGD:S0002512
A;Map position: 4R
C;Keywords: transmembrane protein
F;4-20/Domain: transmembrane #status predicted <TM1>
F;4-60/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1160 <ELW>
                                                                                                                                                                                                                                F;90-106/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB Pred. No. 20; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%;
75.0%;
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Best Local Similarity 75.v-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.5
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 CYALYGWTV 457
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              A; Molecule type: DNA
A; Residues: 1-473 < MUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Gene: VCA0521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YDR105c - yeast (Saccharomyces cerevisiae)
NyAlternate names: probable membrane protein YD857.14c; probable membrane protein YD972
NyAlternate names: probable membrane protein YD877.14c; probable membrane protein YD972
C;Specias Saccharomyces cerevisiae
C;Date: 23-Reb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S51256; S52671
Submitted to the EMBL Data Library, January 1995
A;Reference number: S51243
A;Accession: S51243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C; Accasion. H55900
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Fitler: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable L-fuculose phosphate aldolase protein [imported] - Sinorhizobium meliloti (stra
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A;Residues: 1-473 <MUR>
A;Residues: 1-473 <MUR>
A;Residues: U-473 <MUR>
A;Cross-references: UNIPROT:Q12116; EMBL:Z47746; NID:g633627; PID:g633641; MIPS:YDR105c
R;Murphy, L.; Shore, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A;Reference number: S52671
A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                         0; Indels
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1; Mismatches
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                                                                                                                                                                                                            Score 39;
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Pred. No.
                                                                                                                                                                                                          76.5%;
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Best Local Similarity 66.77
Conservative
                                                                                                                                                                                                       Query Match 76.5
Best Local Similarity 87.5
Matches 7; Conservative
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81 YSVYGTTL 88
                                                                                                                                                                                                                                                                                                      2 YSLYGTTL 9
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82450
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Makalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
Kyseidues: 1-1013 -KHEI>
A;Cross-references: UNIPROT:Q9KW67; GB:AE004382; GB:AE003853; NID:g9657917; PIDN:AAF964.
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ca2+-transporting ATPase (BC 3.6.3.8), plasma membrane - Paramecium tetraurelia C; Species: Paramecium tetraurelia C; Species: Paramecium tetraurelia C; Species: Paramecium tetraurelia C; Species: O2-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004 C; Accession: T31688 R; Elwess, N.L.; van Houten, J.L. 7. 1997 A; Elwaryot Microbiol. 44, 250-257, 1997 A; Title: Cloning and molecular analysis of the plasma membrane Ca(2+)-ATPase gene in Paramece rumber: Z21062; MUID: 97326901; PMID: 9183714 A; Accession: T31688
                                                                                                                                                                                                                                                                                                                                                  probable exonuclease SbcC VCA0521 [imported] - Vibrio cholerae (etrain N16961 serogroup
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       Gaps
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Indels
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1; Mismatches
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hypothetical protein CP0597 [imported] - Chlamydophila pneumoniae (strains CML029 and A C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Accession: D72109; D81558
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389; 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606; PMID:10192388
A; Residues: D72109
A; Residues: D72109
A; Residues: D72109
A; Residues: L94RN
A; Residues: L94RN
A; Residues: L94RN
A; Residues: L94RN
A; Cross-references: UNIPROT:Q92911; GB:AE001604; GB:AE001363; NID:94376438; PIDN:AAD183
A; Experimental source: strain CWL029
A; Experimental source: strain CWL029
A; Experimental source: strain CWL029
C; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Accession: D91558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 - REA>-
A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38414.1; PID:g71895
A;Experimental source: strain AR39, HL cells
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B6 protein - human papillomavirus type 52

C;Species: human papillomavirus type 52

C;Species: human papillomavirus type 52

C;Accession: A61237

R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, Int. J. Cancer 48, 516-522, 1991

A;Title: Cloning and characterization of human papillomavirus type 52 from cervical car A;Reference number: A61237; MUID:91258022; PMID:1646174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                836573 -- human papillomavirus type 52 c;pspecies: human papillomavirus type 52 c;pspecies: human papillomavirus type 52 c;pspecies: human papillomavirus type 52 c;psecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 c;Accession: 836573 R;Delius, H.; Hofmann, B. aubmitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of human papillomavirus types. A;Reference number: 836469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 16;
0; Mismatches
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C, Superfamily: papillomavirus E6 protein
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Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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51 CFSVYGTS 58
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A;Gene: CPn0173; CP0597
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A;Molecule type: DNA
A;Residues: 1-148 <TAM
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R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Rxishirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Axitle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q22396; EMBL:Z74042; PIDN:CAA98528.1; GSPDB:GN00023; CESP:TI
A;Experimental source: clone T11F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 -STO>
A;Cross-references: UNIPROT:Q92911; GB:BA000008; NID:g8978546; PIDN:BAA98383.1; GSPDB:GN
A;Experimental source: strain J138
A;Cross-references: UNIPROT:Q27829; EMBL:U05880; NID:g505622; PID:g505623; PIDN:AAB81284
                                                        A;Genetic code: SGC5
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein CPj0173 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T11F9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24836
R;Lennard, N
submitted to the EMBL Data Library, June 1996
A;Reference number: 219941
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                    Indels
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A;Molecule type: DNA
A;Residues: 1-323 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.5%; Score 37; DB 2;
100.0%; Pred. No. 21;
ive 0; Mismatches
                                                                                                                                                                         Score 38; DB 2
Pred. No. 46;
1; Mismatches
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                                                                                                                                                                           74.5%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                            1085 CYSYYGLTI 1093
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CFSVYGTS 58
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A; Introns: 115/2; 229/3
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A,Molecule type: DNA
A,Residues: 1-1068 -HBB>
A,Residues: 1-1068 -HBB>
A,Experimental source: strain $288C
A,Experimental source: strain $288C
S,Chen, W.; Balal, E.; Capieaux, E.; Choder, M.; Goffeau, A.
Yeast 7, 287-299, 1991
A,Title: The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1 lo
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A;Reaidues: 1-262 <WIL>
A;Cross-references: UNIPROT:022149; EMBL:268299; PIDN:CAA92612.1; GSPDB:GN00022; CESP:Toss-references: Clone T0482
C;Genetics:
A;Gene: CESP:T04B2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;MOlecule type: DNA
A;Residues: 1-410,'K',412-529,'R',531-819,'A',821-920,'I',922-980,'S',982-1009,1015-106
                                                                                                                                              pleiotropic drug resistance control protein PDR1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G3722; protein YGL013c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-410,'K',412-819,'A',821-920,'I',922-980,'S',982-1009,1015-1068 <BAL>
A;Cross-references: EMBL:J03487; NID:g172111; PIDN:AAA34849.1; PID:g172112
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24439
                                                                                                                                                                                            C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 16-Aug-2004
C;Accession: S64015; S31560; A28466
R;Hebling, U; Hofmann, B.; Delius, H.
Bubmitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:558126
R;Balzi, E.; Chen, W.; Ulaszewski, S.; Capieaux, E.; Goffeau, A.
J. Biol. Chem. 262, 16871-16879, 1987
A;Title: The multidrug resistance gene PDR1 from Saccharomyces cerevisiae.
A;Reference number: A28466; MUID:88059084; PMID:3316228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ntrolling pleiotropic drug resistance.
A;Reference number: $15040; MUID:91353083; PMID:1882553
A;Accession: $31560
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F;11-77/Domain: GAL4 zinc binuclear cluster homology <G
F;754-770/Domain: transmembrane #status predicted <TMl>
F;812-828/Domain: transmembrane #status predicted <TM2>
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A;Accession: T24439
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Map position: 7L
C;Superfamily: GAL4 zinc binuclear cluster homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2;
Pred. No. 1e+02;
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66.7%;
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Best Local Similarity 66.،
احد 6; Conservative
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YLLYGTTL
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A Molecule type: DNA
A Moseidues: 1-149 eXIR>
A Moseidues: 1-149 eXIR>
A Cross-references: UNIPROT: P26555; GB:D90400; NID:g222386; PIDN:BAA31845.1; PID:g333709
C; Superfamily: papillomavirus E6 protein
C; Superfamily: papillomavirus E7 protein
E;30-66/Region: zinc finger CCCC motif
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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S;Wuperfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
A,Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148 < DEL>
A;Residues: 1-184 < DEL>
A;Cross-trences: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAA52585.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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                                                                                                                                                                             Length 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: E36779
R; Kitil, Y; I mamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Stechsion: E36779
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
16;
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Pred. No. 16;
0; Mismatches
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Pred. No. 26;
0; Mismatches
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Pred. No. 16;
                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein - human papillomavirus type 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: human papillomavirus type 58 A; Note: host Homo sapiens (man)
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87.5%;
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87.5%;
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Best Local Similarity 87.5.
Loca 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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81 YSLYGDTL 88
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Best Local Similarity
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Gaps

A,Map position: 4 A;Introns: 43/3; 124/3; 221/3; 243/1 C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 68.6%; Score 35; DB 2; Length 262; Best Local Similarity 75.0%; Pred. No. 42; Matches 6; Conservative 0; Mismatches 2; Indels

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Search completed: June 29, 2005, 01:38:48 Job time: 12.2747 secs

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Q80886
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Q80887
Q919b8
Q919b0
Q919c0
                                                                                                                                                                                                                                                                                                                                                      2; Length 90;
                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
STRAIN=HPV16; TISSUB=Cervical tissue;
STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -..
EMBL; U14512; AAB60566.1; -..
EMBL; C.Host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (PEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513; AAB60567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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Q80884;
Q80884;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 25, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; dgNNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
                                                                                                                                                                                                                    RNA stage; Papillomaviridae;
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                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 2; 100.0%; Pred. No. 0.06;
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        Q9QDH5
Q9QDH7
Q9QDH9
Q919B1
Q919C6
Q80886
Q80882
Q80882
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01,
25,
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Human papillomavirus.
Viruses; dsDNA viruses, no
Papillomavirus.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 "Sequence visal cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404703; AAL01363.1; -.
EMBL; AF404703; AAL01363.1; -.
GO; GO:0001807; F:DNA binding; IEA.
Ffam; PR00518; E6; 1.

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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AR040692; AL01142.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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Viruses; dsphillomaviruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                              99 AA; 12005 MW; C2B96025EC370E38 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
                                                                                 100.0%; Score 51; DB 2; 100.0%; Pred. No. 0.066;
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01-OCT-2003 (TrEMBLrel. 25, Last ann
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9, Conservative
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Pfam; PF00518; E6; 1.
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NCBI_TaxID=10581;
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MEDLINE=21846229; PubMed=11857370;
MEDLINE=21846229; PubMed=11857370;
MALES K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL, AR404704; AAL01365.1; ---
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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STRAIN=HPV16; TISSUB=Cervical tissue;
STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DBDJ databases.
RMBL; U14514; AAB60568.2; ---
GO; GO:0003672; F:DMA binding; IEA.
InterPro; IPR001334; E6.
F Fam; PF00518; E6; 1.
NON TER 90
                                                                                                                  100.0%; Score 51; DB 2; Length 90; 100.0%; Pred. No. 0.06; ive 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; debnix viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                   SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0003677; F:DNA binding; IEA.
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         InterPro; IPR011334; E6.
Pfam; PF00518; E6; 1.
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NCBI_TaxID=10581;
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MEDLINE=20112892; PubMed=10644829;
Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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  Query Match 100.0%; Score 51; DB 2; Length 151; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels
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05-701-2004 (TrENBLrel. 27, Created)
05-JUL-2004 (TrENBLrel. 27, Last sequence update)
05-JUL-2004 (TrENBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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Human papillomavirus.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TAXID=10566;
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SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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05-JUL-2004 (TrEWBLrel. 27, Created)
05-JUL-2004 (TrEWBLrel. 27, Last sequence update)
05-JUL-2004 (TrEWBLrel. 27, Last annotation update)
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
Int. J. Cancer 97:868-874(2002).
Int. J. Ap404695; AhLol1347.1;
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNA binding; IEA.
FPfam; PPF00318; BG; 1.
SEQÜENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:199-2208 (1997).
Gen. Virol. 78:199-2208 (1997).
GO, GO:0042025; C:host cell nucleus; IEA.
GO, GO:0042025; C:host cell nucleus; IEA.
GO, GO:003677; P:DNA binding; IEA.
InterPro; IPR001347; E6.
InterPro; IPR001347; E6.
Fram: PP00518; E6; 1.
SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
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100.0%; Pred. No. 0.086;
tive 0; Mismatches 0; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-0CT-2003 (TrEMBLrel.
E6 protein (Fragment).
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MEDINE=20112892; PubMed=10644829;
van Duin M., Sniders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verhetjen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.,
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genocypes in cervical carcinogenesis.";
EMBL, AR469197; AA015691.1; -.
EMBL, AA469197; AA015691.1; -.
GQ; GG:0042025; C:host cell nucleus; IEA.
GG; GG:0003677; F:DNA binding; IEA.
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Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 oroprotein (TremBlrel. 27, Last annotation update)
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBL_TaxID=10581;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
            EMBL; AJ388061; CAB45114.1; -.
EMBL; AJ388066; CAB45124.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Interpro; IFR00134; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
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SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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EMBL; AJ388056; CAB45104.1; -.
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
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"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L12, and L1 coding segments.",
J. Virol. 69:7743-7753(1995).
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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PONGLIKITHONGKOL M., Vaeteewoottacharn K.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; U34129, AAA91676.1; -.

EMBL; A7469198; AAA916621; -.

EMBL; U34115, AAA91667.1; -.

EMBL; U34124; AAA91667.1; -.

EMBL; U34124; AAA91677.1; -.
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
Human papillomavirus.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.
Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
J. Virol. 69:7743-7753 (1995).
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Farmer A.D.;

Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.

EMBL; U34117; AAA91675.1; -.

EMBL; U34117; AAA91664.1; -.

EMBL; U34118; AAA91665.1; -.
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Human papillomavirus.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPRO01334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; FERON BEGO:
FETPRO; PRO01334; EG.
Pfam; PF00518; EG; 1.
SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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SEQUENCE FROM N.A.
MEDLINE=96079021; PubMed=7494284;
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                Papillomavirus.
NCBI_TaxID=10566;
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Q89708
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Q89755
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           Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments";
J. Virol. 69:7743-7753(1995).
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
                                                                                                                                                                                                                                                                                                             ö
                                                                                                      100.0%; Score 51; DB 2; Length 151; 100.0%; Pred. No. 0.1; 0; Indels tive 0; Mismatches 0; Indels
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Best Local Similarity 100.00
Best Local Similarity 100.00
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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  44358, A
9554, Ap
10, Appl
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                                                                                                                                                         June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 278,
Sequence 166,
Sequence 10, A
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Sequence 4, Al
Sequence 12,
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/laa/pCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/laa/pCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-117-083-14
US-09-485-885-21
US-09-485-885-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                    513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                         US-08-170-344-73
56
1 RFHNIRGRW 9
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Match Length
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Perfect score:
Sequence:
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                                                                                                                                                                 Run on:
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Sequence 10, Application US/09980523A

Sequence 10, Application US/09980523A

Fatent No. 6783763

GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: GUNGAULT VILLADA, ISABELLE

APPLICANT: GUNGAULT VILLADA, ISABELLE

APPLICANT: GUNCAN-GENANGERARD

APPLICANT: GUNCAN-GENANGERARD

TITLE OF INVENTION: PROTEBITOPIC PROTEIN FRAGMENTS OF THE B6 AND B7

TITLE OF INVENTION: PROTEBINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PRATICULARLY IN VACCINATION

FILLE REFERENCE: NOB1 AO INS

CURRENT APPLICATION NUMBER: PC1/FR00/01513

FRIOR PILING DATE: 2002-04-29

FRIOR PILING DATE: 2000-05-31

FRIOR PILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PARCHIN VOY: 2.1

SOFTWARE: PARCHIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 56; DB 2; Length 21; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 9; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFFCATION: 435
PRIOR APPLICATION NUMBER: 07/949,836
FILING DATE:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 166:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Human Papillomavirus
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-934-915-166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||||
14 RFHNIRGRW 22
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ORGANISM:
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APPLICANT: THIAM, KADER
APPLICANT: AURIAULT, CLAUDE
APPLICANT: GRAS-MASEE, HELENE
APPLICANT: GRAS-MASEE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: LOING, ESTELLE
APPLICANT: USRWAREDE, CLAUDIE
APPLICANT: USRWAREDE, CLAUDIE
APPLICANT: USRWAREDE, CLAUDIE
APPLICANT: USRWAREDE, CLAUDIE
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: USC/09/601,729
CURRENT APPLICATION NUMBER: PCT/FR99/00259
FRIOR APPLICATION NUMBER: 98 01439
FRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE: PALENTIN VET: 2.1
SSOTTWARE: PALENTIN VET: 2.1
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-278
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100.0%; Score 56; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                          100.0%; Score 56; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DILLARR, JOAKIM
APPLICANT: DILLARR, LENA
APPLICANT: DILLARR, LENA
APPLICANT: DILLARR, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: DAPLILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                        Sequence 278, Application US/09601729
Patent No. 6683052
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 166, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                              Query Match
Best Local Similarity 100.v.
Best Acanservative
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          US-08-159-339A-245
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US-08-934-915-166
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Sequence 4, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES:
ACCRESPONDENCE ADDRESS:
ADDRESSEE: Jagitani & Associates
STREET: Glize Rocky Way Court
CITY: Centreville
                                                                                                                                                                         Query Match 100.0%; Score 56; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 56; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 0.012; Matches 9; Conservative 0; Mismatches 0; Indels .
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                  TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
LENGTH: 162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: (703) 803-9387 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 162 amino acids
                                                                            HYPOTHETICAL: NO US-08-316-239B-3
                                                                                                                                                                                                                                                                                                           131 RFHNIRGRW 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08116239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                     APPLICANT: CHOPPIN,
APPLICANT: CHOPPIN,
APPLICANT: CHOPPIN,
APPLICANT: CHOPPIN,
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: PROTEING OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOBL AO INS
CURRENT APPLICATION NUMBER: PCT/FR00/01513
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
             Sequence 2, Application US/09980523A
Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION UNDHER: 35,205
REFERENCE/DOCKET UNMER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human Papillomavirus
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Best Local Similarity 100.
Matches 9; Conservative
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131 RFHNIRGRW 139
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                                                            GENERAL INFORMATION:
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US-08-117-083-10
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i Sequence 12, Application US/09359382

i Patent No. 6306397

i GENERAL INPORMATION:

APPLICANT EDWARDS, Stirling John

APPLICANT: COX, John Cooper

i APPLICANT: COX, John Cooper

i APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian

i TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

i TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

i FILE REFERENCE: 017227/0148

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER FILING DATE: 1995-10-22

i EARLIER FILING DATE: 1995-12-20

i EARLIER FILING DATE: 1994-12-20

i SEQ ID NO 12

i LENGTH: 172

i TUDENCE IN OFF. 2.0

i SEQ ID NO 12

i TUDENCE IN OFF. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-12
               GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: PRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 56; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 9; Conservative 0; Mismatches 0; Indels
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j ORGANISM: Human papillomavirus type 16
US-09-359-382-12
Sequence 12, Application US/08860165A
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US-08-117-083-10
; Sequence 10, Application US/08117083
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LENGTH: 172
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Gaps

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Query Match
100.0%; Score 56; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                         100.0%; Score 56; DB 4; Length 266; 100.0%; Pred. No. 0.02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             US-US-485-885-4

J Sequence 4, Application US/09485885

Retent No. 634224

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Delise, Anne-Marie Eva Fernande

APPLICANT: Delise, Anne-Marie Ghislaine

APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45.07

CURRENT APPLICATION: Vaccine

FILE REPERENCE: B45.07

CURRENT APPLICATION NUMBER: US/09/485,885

FRIOR APPLICATION NUMBER: B77/EP98/05285

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 273
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Patent No. 634224
GERERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: BCT/EP98/05285
FRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                          ; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapien
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LENGTH: 292
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US-09-485-885-4
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                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-359-382-10
; Sequence 10. Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: WARLANTS OF HUMAN PAPLILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 01727/0148
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER PILING DATE: 1995-12-20
; EARLIER FILING DATE: 1995-12-20
; RARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 2.0
; SEOTHARE: PALENTIN VEY: 2.0
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APPLICANT: MACFARLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT PILING DATE: 1999-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 6

SOPTWARE: PATCHIN VOS: 6
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US-09-359-382-10
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US-09-367-309A-1
'S Gquence 1, Application US/09367309A
'Patent No. 6428807
                                                                                                    ORGANISM: Artificial Sequence FEATURE:
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                          131 RFHNIRGRW 139
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131 RFHNIRGRW 139
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LENGTH: 266
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Query Match 100.0%; Score 56; DB 3; Length 292; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 256 RFHNIRGRW 264
Search completed: June 29, 2005, 01:44:28
Job time: 17.9126 secs

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34, Appl
12, Appl
66, Appl
55, Appl
126, Appl
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16, Appl
2, Appli
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                                                                                                                        June 29, 2005, 05:18:25; Search time 53.8517 Seconds (without alignments) 64.268 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-476-570-34
US-10-476-570-12
US-10-476-570-12
US-10-751-845-65
US-10-751-845-126
US-10-751-845-126
US-10-751-845-126
US-10-353-384-2
US-10-353-384-2
US-10-353-384-2
US-10-357-057-16
US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                      1717557 segs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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51
1 CYSLYGTTL 9
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100.0
100.0
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Perfect score:
                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
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                                                                                     OM protein
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Maximum I
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No.
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sequence 10, Appl
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 19, Appl
Sequence 79, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 31, Appl
Sequence 103, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 24, Appl
Sequence 25, Appl
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Fublication No. US20050100928A1

FUBLICATION NO. US20050100928A1

FUBLICAMT: Hedley, Mary Lynne

FAPPLICAMT: Hedley, Mary Lynne

FAPPLICAMT: Chicz, Roman M.

FILER REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

FILER REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/20/664,225

FRIOR PILING DATE: 2000-08-18

FRIOR PELLONION NUMBER: US 60/169,846

FRIOR FILING DATE: 1999-12-09

FRIOR APPLICATION NUMBER: US 60/154,665

FRIOR FILING DATE: 1999-10-09-16

FRIOR PERSON NUMBER: FARENCE FARE
Sequence 160,
Sequence 1, App
Sequence 4, Ap
Sequence 10, A
Sequence 10, A
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                                                                    3 US-10-000-903-4
3 US-10-000-903-4
3 US-10-009-903-10
3 US-10-009-903-10
3 US-10-009-903-6
3 US-10-009-903-6
3 US-10-009-903-14
4 US-10-009-903-14
4 US-10-175-1845-79
5 US-10-175-1845-88
6 US-10-75-1845-91
7 US-10-75-1845-91
8 US-10-75-185-31
8 US-10-75-185-31
8 US-10-75-185-34
8 US-10-282-122A-77615
8 US-10-282-122A-77615
8 US-10-966-732-103
8 US-10-966-732-103
8 US-10-966-732-103
8 US-10-966-732-103
8 US-10-966-732-103
8 US-10-966-732-103
8 US-10-425-115-319864
8 US-10-425-115-316746
8 US-10-425-115-316746
8 US-10-425-115-316746
8 US-10-289-762-1162
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Similarity 100.0%; Pred. No. 1.6e+06;
9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-149-310-292
US-09-742-153-4
US-09-742-153-2
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                                     US-09-367-309A-1
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CYSLYGITL 12
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LENGTH: 20
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US-10-476-570-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95 US-10-476-570-33
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Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MAILLERE, Bernard

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: BOURGAULT-VILLADA, Sandra

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION WIMBER: US 10/476,570

CURRENT APPLICATION NUMBER: PCT/FR02/01533

PRIOR FILING DATE: 2003-05-03

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATCHT IN OF 34

LENGTH: 15

LENGTH: 15
                                                                                                                               APPLICANT: COMMISSARIAT A L'ENERGIE ATONIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATONIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BETNART
APPLICANT: BOUGGAUIT-VILLADA, Isabelle
APPLICANT: POUVELLB-MORATILLE, Sandra
APPLICANT: QUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: MARIER: US/10/476,570
CURRENT FILING DATE: 2003-11-05
PRIOR FILING DATE: 2003-11-05
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 63
SEOTT NO. 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 51; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 9; Conservative 0; Mismatches 0; Indels
                        US-10-476-570-33; Application US/10476570; Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
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Gaps

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95 US-10-476-570-12
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                                                            APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MALLERER, BETTAT
APPLICANT: BOUNGALLT-VILLADA, Isabelle
APPLICANT: BOUNGALLE-WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 4563-5971-US
CURRENT APPLICATION NUMBER: US/10/476,570
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Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 17; Length 23; 100.0%; Pred. No. 0.023;
                                                                                                                                                                                                                                            CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN Ver. 2.1
US-10-476-570-12
Sequence 12, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 CYSLYGTTL 20
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Best Local Similarity
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APPLICANT: Holdey, Mary Lynne
APPLICANT: Holdey, Mary Lynne
APPLICANT: Holdey, Mary Lynne
APPLICANT: Holdey, Mary Lynne
APPLICANT: Chicz, Roman M.
TITLE OP INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-10-16
PRIOR PILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                       100.0%; Score 51; DB 17; Length 29; 100.0%; Pred. No. 0.029;
                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-126
                                                                                                                        Mismatches
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; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
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ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
....nes 9; Conservative
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 2
LENGTH: 158
                                                                                                                     Conservative
                                                                                                                                                                                                              B CYSLYGTTL 16
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                                                          Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                            1 CYSLYGTTL
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SOFTWARE: Fast
SEQ ID NO 126
   US-10-858-384-8
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1 OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55
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OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
OTHER INFORMATION: for E6 of HPV
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                                                                                                                                                                                                                                                                                              | GENERAL INFORMATION NO. USZU040170644A1 |
| GENERAL INFORMATION NO. USZU040170644A1 |
| GENERAL INFORMATION |
| APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE |
| APPLICANT: MAILLERE, GENTRAIG |
| APPLICANT: MAILLERE, SANTE ET DE LA RECHERCHE MEDICALE |
| APPLICANT: MAILLERE, Sandra |
| APPLICANT: POUVELLE-MORATILLE, Sandra |
| APPLICANT: POUVELLE-MORATILLE, Sandra |
| APPLICANT: GUILLET, Jean-Gerard |
| TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7 |
| TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7 |
| TITLE OF INVENTION: MIXTURE OF PEPTICATION NUMBER: US/10/476,570 |
| CURRENT PILING DATE: 2003-11-04 |
| PRIOR FILING DATE: 2003-11-04 |
| PRIOR FILING DATE: 2001-05-04 |
| NUMBER OF SEQ ID NOS: 63 |
| SEQ ID NO SS |
| LENGTH: 29 |
| LENGTH: 2001-05-04 |
| LENGTH: 29 |
| LENGTH: 2001-05-04 |
| LENGTH: 29 |
| LENGTH: 29 |
| LENGTH: 2001-05-04 |
| LENGTH: 2001-05-05 |
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Sequence 8, Application US/10858384

Sequence 8, Application US/10858384

BOURDALL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOUNGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

TITLE OF INVENTION: POLYEPTIOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN

TITLE OF INVENTION: PARTICILARLY IN VACCINATION

CURRENT FILING DATE: 1030-10

CURRENT FILING DATE: 1099-06-03

PRIOR PRIOR PLICATION NUMBER: 1999-06-03
   Gaps
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   Indels
   ..
0
Mismatches
                                                                                                                                                                                                                                                         Sequence 55, Application US/10476570 Publication No. US20040170644A1
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ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
LENGTH: 29
9; Conservative
                                                                                         9 CYSLYGTTL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CYSLYGTTL 16
                                                       1 CYSLYGTTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CYSLYGTTL 9
Matches
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Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
    APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
; FILE REFERENCE: 08191-01301
; CURRENT APPLICATION NUMBER: US/10/751,845
; FILE REFERENCE: 08191-01301
; CURRENT APPLICATION NUMBER: US/09/664,225
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR PELLING DATE: 2000-08-18
; PRIOR PELLING DATE: 1999-12-09
; PRIOR PELLING DATE: 1999-12-09
; PRIOR PELLING DATE: 1999-12-06
; RINGN APPLICATION NUMBER: US/00/164,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FABCEQ for Windows Version 4.0
; TENCRE ABCECT OF 183
                                                                                                                                                                                               APPLICANT: Heddey, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
FILE REFREENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
FRIOR APPLICATION NUMBER: US/09/664,225
PRIOR PILING DATE: 2000-08-18
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-0-12-09
PRIOR FILING DATE: 1999-0-12-09
SOFTWARE: PRECE for Windows Version 4.0
SEQ ID NO 157
LENGTH: 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 237;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Artificial fusion sequence
                                                                                                                            ; Sequence 157, Application US/10751845; Publication No. US20050100928A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 9; Conservative
92 CYSLYGTTL 100
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53 CYSLYGTTL 61
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US-10-751-845-158
                                                                                                      US-10-751-845-157
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Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Publication No. US20040171806A1

SEQUENCE 1. APPLICATION:

APPLICANT: Cid-Arregui, Angel

APPLICANT: Cid-Arregui, Angel

TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination

TITLE OF INVENTION: Word it is and E7 genes and proteins useful for vaccination

TITLE OF INVENTION NUMBER: US 10/10/472,724

CURRENT APPLICATION NUMBER: DE7/EP02/03271

PRIOR PILING DATE: 2003-09-17

PRIOR FILING DATE: 2001-03-22

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NOS: 27

SEQ ID NOS: 27

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                     100.0%; Score 51; DB 17; Length 158; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        ### Sequence 16, Application US/10367057

### Sequence 16, Application US/10367057

### Publication No. US20050100554A1

### GENERAL INFORMATION:

### APPLICANT: Cuthill, Scott;

### APPLICANT: Jackson, Amanda;

### APPLICANT: Lewin, David A.;

### APPLICANT: Lewin, David A.;

### APPLICANT: Ooi, Chean Eng

### TITLE OF INVENTION: Complexes and Methods of Using Same

### PIER REPERENCE: 21402-559

### CURRENT APPLICATION NUMBER: 06/256,911

### PRIOR PILING DATE: 2003-02-14

### PRIOR PILING DATE: 2003-02-14

### NUMBER OF SEQ ID NOS: 198

### SOFTWARE: CuraSeqList version 0.1

### SOFTWARE: CuraSeqList version 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 100...
Post Jone 9, Conservative
                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-367-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 CYSLYGTTL 95
                                                                                                                               1 CYSLYGTTL 9
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Job time : 54.8517 secs
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                                                                                         Sequence 160, Application US/10751845

Sequence 160, Application US/10751845

Publication No. US20050100928A1

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Chicz, Roman M.

TITLE OF INVERTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES

FILE REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

CURRENT FILING DATE: 2004-01-05

PRIOR PILING DATE: 2000-08-18

PRIOR PILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: US 60/169,846

PRIOR APPLICATION NUMBER: US 60/154,665

PRIOR PILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 163

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 160

LENGTH: 261
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100.0%; Score 51; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 51; DB 9; Length 266; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
54 CYSLYGTTL 62
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                                                                                       US-10-751-845-160
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US-09-367-309A-1
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27, Appli 1, Appli 1, Appli 1, Appli 6191, Ap

12868, A

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Run on:

Sequence:

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Sequence 8,
Sequence 23
Sequence 21
Sequence 21,
Sequence 46,
Sequence 46,
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       Sequence
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Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Rubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cells, Esteban
ITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CIIY: San Francisco
US-08-462-467B-2
US-08-159-339E-8
US-08-134-000C-4230
US-09-134-000C-4275
US-08-191-866D-21
US-09-21-866D-21
US-09-764-100-27
US-09-764-100-27
US-09-107-532A-6191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALL
STATE: CALL
STATE: CALL
COUNTRY: USA
ZIP: 94111-384
ZIP: 9411-384
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEM DOS
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Blen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPERENCE/DOCKET NUMBER: 32,762
REPERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
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                                                       364
441
441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
   RESULT 1
US-08-159-339A-563
     4, Appli
4, Appli
244, App
Appli
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Sequence 175, App
Sequence 4, Appli
Sequence 4, Appli
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Sequence 1171, Ap
Sequence 44, Appl
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                                                                                                                           June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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Sequence 6
Sequence 1
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-934-915-44

US-08-934-915-44

US-08-980-523A-8

US-09-980-523A-8

US-08-980-15-163

US-08-980-165-12

US-08-860-165-12

US-08-860-165-14

US-09-359-382-12

US-09-359-382-12

US-09-359-382-10

US-09-359-382-10

US-09-359-382-10

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US-09-438-185A-175
US-08-462-467B-4
US-08-936-135-4
US-08-936-135-2
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-044-359-4
                                                                                                                                                                                                                                                                                                                                              513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seg length: 200000000
                                                                                                                                                                                                         US-08-170-344-72
51
1 CYSLYGTTL 9
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.Match Length
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Perfect score:
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Minimum DB Maximum DB

Database

Result No.

Searched:

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US-08-934-915-44
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                                   100.0%; Score 51; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                             RESULT 2
US-08-159-339A-1171
; Sequence 1171, Application US/08159339A
; Patent No. 607135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: Has Binding peptides and Their
TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESC for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: Blan Lauver
NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                  Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CYSLYGTTL 11
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                                                                                                                     1 CYSLYGITL 9
                                                                                                                                          TOPOLOGY: linear
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US-08-159-339A-563
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Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESSS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DILLINER, JOAKIM
APPLICANT: DILLINER, LENA
APPLICANTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: DAPLILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 13, 13 AND 56,
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
ADDRESSEE: MASON & ASSOCIATES, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUCH:
NAME: LOUISE A. FOUCH:
REFERENCE/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44:
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-934-915-44
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; Sequence 2, Application US/09980523A; Patent No. 6783763
       CYSLYGITL 16
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Patent No. 6783763

GENERAL INFORMATION:
APPLICANT: CHORPIN, JEANNINE
APPLICANT: CHORPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: PCT/FROO/01513
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
SEQ ID NOS: 24
SOFTWARE PATENTIN VOIL STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                              COUNTRY: 10.3.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,13.
REPERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 163:
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US-09-980-523A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: peptide US-08-934-915-163
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11 CYSLYGTTL 19
CLEARWATER
FLORIDA
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1 CYSLYGTTL 9

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PREMIURATION NOT STATES.

PREMIULARY: GORGANITY TULLADAY. EARELLE

**PAPLICANY: GORGANITY TULLADAY. EARLINE

**PAPLICANY: GORGANITY TULLADAY. EARLINE

**PAPLICANY: GORGANITY TULLADAY. EARLINE

**PAPLICANY: GORGANITY TULLADAY. EARLINE

**PAPLICANY: GORGANITY STRANCINE

**PAPLICA
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RESULT 11
US-09-359-382-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: ERAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08860165A
Sequence 14, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COW, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT APPLICATION NUMBER: PCT/AU95/0086B
SARLIER FILING DATE: 1995-12-20
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100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 51; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.073; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 807-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: procein
HYPOTHETICAL: NO
US-08-316-239B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 CYSLYGTTL 95
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                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: EDWARDS, Stirling John;
APPLICANT: EDWARDS, Stirling John;
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 14, Application US/09359382
| Sequence 14, Application US/09359382
| Patent No. 6306397
| GENERAL INFORMATION:
| APPLICANT: EDWARNS, Stirling John
| APPLICANT: EMBER, Elizabeth Ann
| APPLICANT: FRAZER, Ian
| TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
| FILE REFERENCE: 017227/0148
| CURRENT APPLICATION NUMBER: US/09/359,382
| CURRENT FILING DATE: 1999-07-23
| EARLIER FILING DATE: 1997-09-23
| EARLIER FILING DATE: 1997-09-23
| EARLIER FILING NUMBER: PCT/AU95/00868
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                                                                                                                                                                                                                                                                                                             Length 172;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 51; DB 3; Best Local Similarity 100.0%; Pred. No. 0.073; Matches 9; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Human papillomavirus type 16
EARLIER APPLICATION NUMBER: AU PN0157
BARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-359-382-12; Sequence 12, Application US/09359382; Patent No. 6306397; GENERAL INFORMATION:
                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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| GENERAL INFORMATION: |
| APPLICANT: EDWARDS, Stirling John |
| APPLICANT: EDWARDS, Stirling John |
| APPLICANT: WEBB. Elizabeth Ann |
| TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS |
| FILE REFERENCE: 1722/130 |
| CURRENT APPLICATION NUMBER: US/08/660,165A |
| CURRENT FILING DATE: 1997-09-22 |
| EARLIER FILING DATE: 1997-09-12 |
| EARLIER FILING DATE: 1997-09-12 |
| EARLIER FILING DATE: 1994-12-20 |
| NUMBER OF SEQ ID NOS: 15 |
| SEQ ID NO 10 |
| LENTH: 266 |
| LENTH
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| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: WEBB. Elizabeth Ann
| APPLICANT: WEBB. Elizabeth Ann
| APPLICANT: WEBB. Elizabeth Ann
| TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
| FILE REFERENCE: 071227/0148
| CURRENT APPLICATION NUMBER: US/09/359,382
| CURRENT FILING DATE: 1999-07-23
| EARLIER FYLING DATE: 1999-07-23
| EARLIER FYLING DATE: 1999-07-24
| EARLIER RPPLICATION NUMBER: PCT/AU95/00868
| EARLIER RPPLICATION NUMBER: AU PNO157/94
| EARLIER FILING DATE: 1994-112-20
| EARLIER PLILING DATE: 1994-112-20
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 10
| LENGTH: 266
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US-08-866-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
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; Patent No. 6306397
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ORGANISM: Artificial Sequence
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; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
    APPLICANT: Boursnell, Michael E.
    APPLICANT: Inglis, Stephen C.
    APPLICANT: Munro, Alban J.
    TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
    TITLE OF SEQUENCES: 7
    CORRESPONDENCE ADDRESS: 7
    CORRESPONDENCE ADDRESS: 7
    STREET: 4 Embarcadero Center, Suite 3400
    CITY: San Francisco
    STATE: CA
    COUNTRY: USA
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the open reading frame."
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SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,083

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-58783

TELEPHONE: 415-781-1989

TELEPHONE: 415-398-3249

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHRACTERISTICS:

LENGTH: 182 amino acids

TYPE: ATTORNEY AND ACIDS

TYPE
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14
                                                           PN0157/94
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MEDIUM TYPE: Floppy of
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-117-083-10
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RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACLARRON, JIM
; TITLE OF INVENTION:
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR FILING DATE: 1998-02-13
; PRIOR PRILICATION NUMBER: AU PO 5178
; RIOR FILING DATE: 1998-02-13
; PRIOR PRILICATION NUMBER: AU PO 5178
; ROSTWARE: PATENTING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PATENTING DATE: 26
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; CORGANISM: Human papillomavirus type 16
; ORGANISM: Human papillomavirus type 16
; CORGANISM: Human papillomavirus type 16
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Search completed: June 29, 2005, 01:44:27 Job time: 16.9126 secs

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STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -..
GO; GO:0004267; C.Host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513, AB860567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                       Q80883;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; deNMA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
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          Q919C0
Q919C2
Q919D2
Q919D2
Q919D4
Q177JC7
Q77JC7
Q77JC7
Q80963
Q89852
Q8BB10
Q8BB10
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 37 HYCYSLYGT 45
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Papillomavirus
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Best Local S
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Watte K.J., Thompson C.H., Cossar Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-974(2002).

EMBL; AF404695; AALO1347.1; Cost Coll nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

Péan; PF00518; B6; 1.
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                                                                               100.0%; Score 57; DB 2; Length 103; 100.0%; Pred. No. 0.045;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 procein (Fragment).
Human papillomavirus type 16.
Viruses; despin viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                 NON TER 1 1 SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
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GO; GO:0003677; F:DNA binding; IEA. Pfam; PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404692; AAL01342.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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MEDLINE=21846229; PubMed=11857370;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Tremgment).
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
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EMBL, AF404704, AAL01365.1; -...

GO; GO:0002677; F: DNA binding; IEA.

Pfam; PF00518; E6; 1 1 1

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SEQUENCE 99 AA; 12005 MW; C2B96025EC3
   GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
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NCBI_TaxID=10581;
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MEDINE-20112892; PubMed=10644829;
W MEDLINE-20112892; PubMed=10644829;
A van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
A van Duin M., Snijders P.J., Weijer C.J., Walboomers J.M.;
M Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
T. "Analysis of human papillomavirus type 16 E6 variants in relation to page 35 codon 72 polymorphism genotypes in cervical carcinogenesis.";
T. Gen. Virol. 81:317-325(2000).
T. EMBL; AJ388065, CAB4514.1;
T. REMBL; AJ388066; CAB4514.1;
T. RO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0043077; F:DNA binding; IEA.
T. GO; GO:0043077; F:DNA binding; IEA.
T. C. GO: GO:003677; F:DNA binding; IEA.
T. C. GO: GO:0042025; C:host cell nucleus; IEA.
T. G. GO: GO:0042025; C:host cell nucleus; IEA.
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
Li., and Ll coding segments";
J. Virol. 69:7743-7753(1995).
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      100.0%; Score 57; DB 2; Length 151; 100.0%; Pred. No. 0.064; ive 0; Mismatches 0; Indels
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
[3]
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Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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SEQUENCE FROM N.A.
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NCBI_TaxID=10566;
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MEDLINE=97437474; PubMed=9292007;
MATOMERELIO M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"T type 16 in penile carcinomas from Ugandan patients.";
"J. Gen. Virol. 78:2199-2208 (1997).

MEMBL, AF003016; AAB70733.1;

MEMBL, AF003016; AAB70733.1;

GO, GO:000367; P:DNA binding; IEA.

MR TOCKPRO, IPR001334; EG.

MR THEEPRO, IPR001334; EG.

MR Pfam; PF00518; E6; 1.
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MEDLINE=21046229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868=874 (2002).
GO; GO:0044702; AAL01361.1;
EMBL, AF404702; Chost cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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Human papillomavirus type 16.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
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SEQÜENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                  143 AA
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                           Query Match
Best Local Similarity 100...
9; Conservative
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Best Local Similarity
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
SEQUENCE
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WEDLINE-20112892; PubMed=10644829;
WEDLINE-20112892; PubMed=10644829;
WEDLINE-20112892; PubMed=10644829;
A van Duin M., Snijdere P.J., Vossen M.T., Klaassen E., Voorhorst F.,
A van Duin M., Snijdere P.J., Vossen M.T., Walboomers J.M.;
A varheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Thalysis of human papillomavirus type 16 E6 variants in relation to XT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
The EMBL, AJ388058; CAB45110.1; -.
DR GO, GO:0003679; F.DNA binding; IEA.
DR GO, GO:0003679; F.DNA binding; IEA.
DR GO, GO:0003679; F.DNA binding; IEA.
DR Ffam; PF00518; E6; 1.
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF546023; AA016239.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PP00518; E6; 1.
SEQUENCE 151 AA; 18348 MW; FE3F2DSFCD7A69B2 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                               Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Matches 9; Conservative
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                                                                                                                                                                                                Papillomavirus.
NCBI_TaxID=10566;
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Q9W931
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BIDLINE=96679021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                     Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; 034129; AAA91676.1; -.
EMBL; 034129; AAA91653.1; -.
EMBL; 034120; AAA91667.1; -.
EMBL; 034120; AAA9167.1; -.
EMBL; 034120; AAA9167.1; -.
EMBL; 034120; AAA9167.1; -.
EMBL; 034120; AAA9167.1; -.
EMBL; 034124; AAA9167.1; -.
GO; GO:0004025; C:host cell nucleus; IEA.
GO; GO:001331; EO.
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Human papillomavirus.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10566;
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34126; AAA91673.1; -.
EMBL; U34111; AAA91658.1; -.
EMBL; U34123; AAA91658.1; -.
EMBL; U34123; AAA91670.1; -.
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SEQUENCE 151 AA; 18334 MW; PF8P2A2FCEBA6C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Q8B564
ID Q8B564 PRELIMINARY; PRT; 151 AA.
AC Q8B564;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Best Local Similarity 100...
9, Conservative
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78 HYCYSLYGT
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Best Local Similarity
Matches 9; Conserv
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Q89755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20112892; PubMed=10644829;
MEDLINE-20112892; PubMed=10644829;
Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R. H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
EMBL, AJ388060; CAB45112.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 31-50 FROM N.A.
MEDLINE=90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
"Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 57; DB 2; Length 151; 100.0%; Pred. No. 0.064; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-85246220; PubMed=2990099;
Sedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18387 MW; E2244784BEBA6C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
EE protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HYCYSLYGT 9
                         NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10581;
Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA
Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VE6_HPV16
P03126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-71 57

1 HYCYSLYGT 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•		de 			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
-	57	100.0	158	-	W6WLHS	protein E6 - human
7	40	70.2	148	~	A61237	ein -
m	40	70.2	148	~	S36573	protein - 1
4	40	70.2	149	٦	W6WL58	protein -]
S	40	70.2	153	~	S36503	protein -
9		68.4	646	~	837165	e mol
7	38	66.7	216	7	JX0265	platelet aggregati
œ	38	66.7		~	D64343	hypothetical prote
σ	38	66.7	2573	0	D71614	hypothetical prote
10	37	64.9	97	7	S59427	
11		64.9	109	~	PH1668	
12	37	64.9	149	-	W6WL33	E6 protein - human
13	37	64.9	152	П	VGBEY9	early glycoprotein
14	37	64.9	323	7	T24836	hypothetical prote
15	37	64.9	383	7	D88633	protein F56B3.2 [i
16	37	64.9	419	~	S41607	atrolysin A (EC 3.
17	37	64.9	571	~	S24789	jararĥagin C precu
18	37	64.9	759	0	876989	sensory transducti
19	37	64.9	944	~	AC2073	two-component sens
20	37	64.9	1716	7	T14103	probable DNA-direc
21	37	64.9	1717	~	T13961	DNA-directed RNA p
22	36.5	64.0	307	~	D75143	udp-glucose 4-epim
23	36	63.2	209	~	JX0266	platelet aggregati
24	36	63.2	350	~	B39364	GDF-1 embryonic gr
	36	63.2	406	~	F70632	probable met prot
56		63.2	419	~	A59414	metalloproteinase
27	36	ë	421	~	S40819	probable transport
28	36	63.2	421	0	C86075	
53	36	63.2	421	~	D91228	probable resistanc

hypothetical prote	X-Pro dipeptidase	X-Pro dipeptidase	dipeptide transpor	catrocollastatin p	probable potassium	anaerobic ribonucl	3',5'-cyclic-nucle	3',5'-cyclic-nucle	AAA protein L4171.	hypothetical prote	hypothetical prote	Ig kappa chain V r	hypothetical prote	probable membrane	hypothetical prote
876768	A32454	S72196	T44635	S55270	T28852	D82452	A40981	JC2486	T02831	E86512	D72109	S20810	F86669	832968	T28166
~	N	~	N	~	N	~	-	-	N	~	~	~	~	~	7
489	493	493	551	609	664	206	921	928	1541	91	91	101	108	187	246
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63	63	63	63	63.	63.	63.	63.2	63	63.	61.	61.4	61.4	61.4	61.	61.
36	36	36	36	36	36	36	36	36	36				35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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protein B6 - human papillomavirus type 16
C; Species: human papillomavirus type 16
C; Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C; Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C; Accession: A03682; T10427
R; Sedeofr K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A; Title: Human papillomavirus type 16 DNA sequence.
A; Reference number: A22355; MUID:85246220; PMID:2990099
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J, Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the leval of the properties of the paper: 217014; MUID:91162763; PMID:1848319
A; Reference number: 217014; MUID:91162763; PMID:1848319
A; Accession: T10427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
G;Genetics:
A;Gene: E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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Best Local S
Matches 9
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HYCYSLYGT 93 1 HYCYSLYGT 9 ઠે 셤

RESULT 2

Actors

Modelian

Be protein - human papillomavirus type 52

Be protein - human papillomavirus type 52

Cipecies: human papillomavirus type 52

Cipecies: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996

C;Accession: A61237

A;Tatkani, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, Int. J. Cancer 48, 516-522, 1991

A;Title: Cloning and characterization of human papillomavirus type 52 from cervical car A;Accession: A61237

A;Accession: A61237

A;Actus: preliminary

A;Molecule type: DNA

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A;Accession: S36503
A;Molecule type: DNA
A;Residues: 1-153 < DBL>
A;Residues: 1-153 < DBL>
A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: S37165
A,Aolcoule type: mRNA
A,Residues: 1-646 LAU>
A,Cross-references: UNIPROT:Q24768; EMBL:Z26134; NID:g401828; PIDN:CAA81135.1; PID:g401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: involved in protein folding and assembling/disassembling of protein comp C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JX0265

JACOBA STATE AND ADDITIONAL OF The diamond rattlesnake (fragment)

NyAlternate names: disintegrin
C;Species: Crotalus ruber ruber (red diamond rattlesnake)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: JX0265
R;Takeya, H; Nishida, S; Nishino, N; Makinose, Y; Omori-Satoh, T.; Nikai, T.; Sugih A;Title: Primary structures of platelet aggregation inhibitors (disintegrins) autoprote hese enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related
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NyAlternate names: heat shock protein
NyAlternate names: heat shock protein
Cispeciaes: Eimeria acervulina
Cispeciaes: Eimeria acervulina
Cipute: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
CiAccession: S37165
Rilaurent, F.; Bourdieu, C.; Yvor, P.; Pry, P.
submitted to the EMBL Data Library, September 1993
A; Description: Cloning of a 70 kDa protein of E.acervulina sporozoite which is:
A; Reference number: S37165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                    R.Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
A.Description: Primer-directed sequencing of human papillomavirus types.
A.Reference number: S36469
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Pred. No. 52;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: JX0265; MUID: 93293798; PMID: 8514736
                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                           / Match 70.2%; Score 40; DB Local Similarity 87.5%; Pred. No. 11; nes 7; Conservative 0; Mismatches
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A,Residues: 1-216 <TAK>
A,Cross-references: UNIPROT: Q9PSN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.4%;
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Best Local Similarity 66.7
Matches 6; Conservative
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546 NYCYSMRGT 554
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81 HYNYSLYG 88
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C; Accession: S36503
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-149 eKIFN
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAA31845.1; PID:g333709
C;Superfamily: papillomavirus E6 protein
C;Stwyords: DNA binding; aarly protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;MOJECCUIE type: DNA
A;Residues: 1-148 <DEL>
A;Residues: 1-148 <DEL>
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAA52585.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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836503
85 603
85 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
R;Kiril, Y; Iwamoto, S.; Matsukura, T.
R;Kiril, Y; Iwamoto, S.; Matsukura, T.
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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                                                                              Length 148;
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                                                                                                                                       1; Indels
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Pred. No. 10;
0; Mismatches
                                                                              Score 40; DB
Pred. No. 10;
                                                                                                                                    0; Mismatches
                          C; Superfamily: papillomavirus E6 protein
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Best Local Similarity 87.5%;
Matches 7; Conservative C
                                                                           Query Match
70.2%;
Best Local Similarity 87.5%;
Matches 7; Conservative (
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A; Residues: 1-148 <TAK>
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Rimithly, L.; Harris, D.

Submitted to the EMBL Data Library, March 1995

A; Reference number: S59423

A; Accession: S59427

A; Molecule type: DNA

A; Residuae: 1-97 < MUR>
A; Residuae: 1-97 < MUR>
A; Residuae: 1-97 < MUR>
A; Cross-references: UNIPROT: Q04923; EMBL: Z48612; NID: 9728671; PID: 9728676; GSPDB: GN0000

A; Experimental source: strain AB972

A; Genetics:
A; Genetics: A; MS: YDR220c

A; Cross-references: SGD: S0002628

A; Cross-references: SGD: S0002628

A; Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (clone 3G5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1668
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl A;Reference number: PH1642; MUID:93301610; PMID:8315388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-149 <COL>
A,COSS-references: UNIPROT:P06427, GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g46317
C,Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein - human papillomavirus type 33
C; Species: human papillomavirus type 33
C; Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C; Accession: A03683
R; Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A; Title: Genome organization and nucleotide sequence of human papillomavirus type 33, A; Accession: A03683
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A;Molecule type: mRNA
A;Residues: 1-109 <HILD
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>
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Pred. No. 25;
1; Mismatches
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Best Local Similarity 75.04
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Best Local Similarity 75.0
Matches 6; Conservative
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86 YYCASLYG 93
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C; Accession: S59427
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PH1668
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E6 prot
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-2573 <GAR>
A;Cross-references: UNIPROT:096185; GB:AE001396; GB:AE001362; NID:g3845188; PIDN:AAC7188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
(S.Species: Plasmodium falciparum
(S.Species: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
(S.Accession: D71614
(R.Gardner, M.J.; Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A,Reference number: A71600; MUID:99021743; PMID:9804551
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N;Alternate names: hypothetical protein YD9934.05c
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
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A,Start codon: GTG
C,Superfamily: Methanococcus jannaschii hypothetical protein MJ0348
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Pred. No. 2.5e+02;
1; Mismatches 1; Indels
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Pred. No. 92;
2; Mismatches
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ilarity 71.4%;
Conservative 1
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Best Local Similarity 62.5°
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115 HQCYALFGS 123
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695 YCYRIYGS 702
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                  HYCYSLYGT
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Best Local Similarity
Matches 5; Conserv
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Search completed: June 29, 2005, 01:38:47 Job time: 12.2747 secs
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hes 6; Conserv
                                                                                                                                                                                                                                                                                             1-383 <STO>
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Matches
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                                                                                                                                                                early glycoprotein gp48 precursor - human cytomegalovirus (strain AD169)
N.Alternate names: early glycoprotein ULA
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S09767
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus A;Reference number: S09767
A;Accession: S09767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A) Gross-references: UNIPROT: P17146; EMBL:X17403; NID: 959591; PIDN: CAA35437.1; PID: 959609
A;Note: possible protein-coding frames are given
A;Note: the DNA sequence was submitted to the EMBL Data Library, December 1989, in compu C;Superfamily: cytomegalovirus early glycoprotein gp48
C;Keywords: early protein; glycoprotein predicted <a href="Mailto:Assistance">Mailto:Assistance</a>, E;125/Pomain: slgnal sequence #status predicted <a href="Mailto:Assistance">Mailto:Assistance</a>, 125,152/Product: early glycoprotein gp48 #status predicted <a href="Mailto:Assistance">Mailto:Assistance</a>, 108,112,122,139,148/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Cross-references: UNIPROT:022396; EMBL:274042; PIDN:CAA98528.1; GSPDB:GN00023; CESP:T1
A,Experimental source: clone T11F9
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24836
R;Lennard, N.
Submitted to the EMBL Data Library, June 1996
A;Reference number: Z19941
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A;Molecule type: DNA
A;Residues: 1-152 <CHE>
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Pred. No. 34;
2; Mismatches 1; Indels
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C;Species: Caenorhabditis elegans
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A;Molecule type: DDA
A;Residues: 1.-123 <MILA
A;Cross-references: UNIPROT:Q22396; EMBL:Z74042; PI
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Similarity 62.5%;
5; Conservative 2
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19 YCYCVFGT 26
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HYNYSVYG 85
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HYCYSLYG
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Gene: CESP:T11F9.3
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C;Accession: D88633
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID: 99069613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:chr_IV; PIDN:AAC02613.1; PID:g2854199; GSPDB:GN00022; CESP:F56B3 A;Note: contains similarity to tenascins C;Genetics: A;Gene: F56B3.2
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Score 57; DB 17;
llarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Papilloma virus
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33, Appl
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                                                                                                                                                                                             (without alignments)
64.268 Million cell updates/sec
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                                                                                                                                                           June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-751-845-91

US-10-476-570-33

US-10-476-570-34

US-10-476-570-12

US-10-751-845-66

US-10-858-384-8

US-10-858-384-8

US-10-858-384-8

US-10-858-384-8

US-10-858-384-8

US-10-858-384-126

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Length 9; Indels

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114, Appl
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32, Appl
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86, Appl
86, Appl
106, Appl
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                                                      sequence 4, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 31, Appli
Sequence 11, Appli
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Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Hedley, Mary Lynne
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT PLING DATE: 2004-01-05
CURRENT APPLICATION NUMBER: US/99/664,225
RIOR APPLICATION NUMBER: US 60/163,846
PRIOR PLICATION NUMBER: US 60/163,846
PRIOR PELING DATE: 1999-12-09
PRIOR PLING DATE: 1999-12-09
PRIOR PLING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SSEQ ID NOS: 163
                                                                                                                                                                                                                                                                                                                                                    Sequence 1
Sequence 1
Sequence 1
                                                    US-10-000-903-4
US-10-000-903-10
US-10-899-771-10
US-10-899-771-10
US-10-899-771-16
US-10-899-771-16
US-10-899-771-14
US-10-899-771-14
US-10-899-771-14
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US-10-751-845-93
US-10-751-845-85
US-10-751-845-80
US-10-476-770-31
US-10-476-1845-80
US-10-476-1845-80
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US-10-476-1948-90
US-10-476-1948-90
US-10-437-965-193431
                                                                                                                                                                                                                                                                                                                                                  US-10-343-710-110
US-10-343-710-112
US-10-437-963-129996
US-10-359-012-6
                                            US-09-367-309A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BERNARGIE
APPLICANT: MAILLERE, BERNARGIE
APPLICANT: MOURGAULT-VILLADA, ISAbelle
APPLICANT: BOUNGALE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Papillomavirus proteins and uses thereof
TITLE OF INVENTION: Papillomavirus proteins and uses thereof
TITLE OF INVENTION: WUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/PR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOUTHWERE OF SEQ ID NOS: 63
                                 Sequence 91, Application US/10751845
Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
FILE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
FRIOR FILING DATE: 2000-08-18
FRIOR FILING DATE: 1999-12-09
FRIOR PRIOR APPLICATION NUMBER: US 60/169,846
FRIOR FILING DATE: 1999-12-09
FRIOR PRIOR APPLICATION NUMBER: US 60/164,665
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR PRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION NUMBER: US 60/154,665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: artificial seguence
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Matches 9; Conservative
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US-10-751-845-91
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5 HYCYSLYGT 13

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| UB-10-76-570-34
| UB-10-76-5
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TYPE: PRT ORGANISM: Artificial Sequence
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                          9; Conservative
                                                                                                   HYCYSLYGT 14
                                                                        1 HYCYSLYGT 9
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-858-384-8
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55
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Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: DELLA SANTE E7

FILE REFERENCE: 45636-5071-US

CURRENT APPLICATION UNBER: US/10/476,570
                                                                                                                                                                                                                                             ## CENTREAL INFORMATION:
## APPLICANT: Hedley, Mary Lynne
## APPLICANT: Hedley, Mary Lynne
## APPLICANT: Hedley, Mary Lynne
## APPLICANT: Chica, Roman M
## TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
## TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
## TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
## TITLE OF INVENTION: NUMBER: US/10/751,845
## PRIOR FILING DATE: 2000-08-18
## PRIOR PLING DATE: 1999-12-09
## PRIOR FILING DATE: 1999-12-09
## PRIOR FILING DATE: 1999-09-16
## NUMBER OF SEQ ID NOS: 163
## NUMBER OF SEQ ID NOS: 163
## NUMBER OF SEQ ID NOS: 163
## NUMBER PASTERED WATCH WINDOWS VERSION 4.0
    Gaps
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    0; Indels
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR PLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ 1D NOS: 63
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                   US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human Papilloma virus US-10-751-845-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial sequence
  9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                             10 HYCYSLYGT 18
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LENGTH: 23
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LENGTH: 29
  Matches
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100.0%; Score 57; DB 16; Length 29;

Query Match

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Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0; Charles 9; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Connervative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches ```

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Sequence 2, Application US/10472724

Publication No. US20040171806A1

Publication No. US20040171806A1

APPLICANT: Cid-Arregui, Angel
APPLICANTON: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: PG7/EP02/03271
PRIOR FILING DATE: 2003-09-17
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin version 3.2

SEQ ID NO 2

LENGTH: 171
 Sequence 157, Application US/10751845

| Sequence 157, Application US/10751845
| Publication No. US20060100928A1
| GENERAL INFORMATION:
| APPLICANT: Heddey, Mary Lynne
| APPLICANT: Chicz, Roman M.
| TITE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITORE POLYPEPTIDES
| TITE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITORS
| TILE REFERENCE: 08191-013001
| CURRENT APPLICATION NUMBER: US/10/751,845
| CURRENT FILING DATE: 2004-01-05
| PRIOR FILING DATE: 2000-08-18
| PRIOR FILING DATE: 1999-12-09
| PRIOR APPLICATION NUMBER: US 60/169,846
| PRIOR APPLICATION NUMBER: US 60/154,665
| PRIOR APPLICATION NUMBER: US 60/154,665
| PRIOR FILING DATE: 1999-09-16
| NUMBER OF SEQ ID NOS: 163
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 157
 Gaps
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 Query Match 100.0%; Score 57; DB 17; Length 236; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels 0
 Query Match
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels (
 ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-157
) OTHER INFORMATION: Synthetic Construct US-10-472-724-2
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 90 HYCYSLYGT 98
HYCYSLYGT 93
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 1 HYCYSLYGT 9
 1 HYCYSLYGT
 51 HYCYSLYGT
 RESULT 12
US-10-472-724-2
 85
 FEATURE:
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 Gaps
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 APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GONNAN, FRANCINE
APPLICANT: GONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT PILING DATE: 2004-06-02
PRIOR FILING DATE: 1999-06-03
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 100.0%; Score 57; DB 17; Length 117; 100.0%; Pred. No. 0.08; cive 0; Mismatches 0; Indels 0
 Query Match
100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels (
 Query Match 100.0%; Score 57; DB 17; Length 158; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels (
 US-10-367-057-16

Sequence 16, Application US/10367057

Publication No. US20050100554A1

GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Looi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same;
FILE REFERENCE: 12402-2514

CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SEQ ID NO 16

LENGTH: 158
 Sequence 2, Application US/10858384
Publication No. US20050033025A1
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
 LENGTH: 158
TYPE: PRT
ORGANISM: Human Papillomavirus
US-10-858-384-2
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 2
 Query Match
Best Local Similarity 100...
9, Conservative
 51 HYCYSLYGT 59
) ORGANISM: Homo sapiens
US-10-367-057-16
 85 HYCYSLYGT 93
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
 US-10-858-384-2
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 Sequence 158, Application US/10751845
Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Or USATION:
TITLE OF INVENTION NUCLEIC ACIDS ENCODING POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/09/664,225
FILMS PAPLICATION NUMBER: US/09/664,225
FRIOR FILING DATE: 2004-01-05
FRIOR PELICATION NUMBER: US/09/664,225
FRIOR PELICATION UMBER: US/09/664,225
FR
 US-10-751-845-160

Sequence 160, Application US/10751845

Publication No. US20050100928A1

Sequence 160, Application US/10751845

Publication No. US20050100928A1

APPLICANT: Hedley, Mary Lynne

APPLICANT: Chicz, Roman M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES

TITLE OF INVENTION: UNCHER: 2004-01-05

CURRENT RILING DATE: 2004-01-05

PRIOR APPLICATION NUMBER: US/09/664,225

PRIOR APPLICATION NUMBER: US/09/664,225

PRIOR PILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 163

NUMBER OF SEQ ID NOS: 163

SOFTWARE: FastESEQ for Windows Version 4.0
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 Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels
 Query Match
100.0%; Score 57; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels (
 ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-158
 ; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 TYPE: PRT
ORGANISM: Artificial Sequence
 52 HYCYSLYGT 60
 1 HYCYSLYGT 9
US-10-751-845-158
 SEQ ID NO 160
LENGTH: 261
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1 HYCYSLYGT 9

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76 HYCYSLYGT 84
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Search completed: June 29, 2005, 05:48:14 Job time: 53.8517 secs

Ivis bade glauk (nsbto)

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GENERAL INFORMATION:

APPLICANT: Grey, Howard M.
APPLICANT: Greis, Beteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
ZIP: 94111-3834
COMPUTER: BEADABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: OS-NOV-1993
CLASSIFTCATION NUMBER: US 08/027, 746
FILING DATE: 07-NUC-1992
APPLICATION NUMBER: US 08/027, 746
FILING DATE: 06-AUG-1993
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
 US-08-159-339A-1171
Sequence 1171, Applequence 163, Applequence 163, Applemence 2, Applipaguence 2, Applipaguence 12, Applipaguence 12, Applemence 12, Applemence 14, Applemence 10, Applemence 10, Applemence 10, Applemence 11, Applemence 12, Applemence 14, Applemence
 Sequence 14, Appl
Sequence 251, Appl
Sequence 235, App
Sequence 263, App
Sequence 2132, App
Sequence 6191, App
Sequence 6191, App
Sequence 24718, A
 2, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
 Description
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Sequence 1
Sequence 1
Sequence 1
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-08-159-339A-1171

US-08-934-915-14

US-09-980-523A-8

US-09-980-523A-8

US-09-980-523A-8

US-08-116-23B-3

US-08-116-23B-3

US-08-116-23B-3

US-08-116-12

US-08-116-12

US-08-116-12

US-09-1359-382-12

US-09-1359-382-10

US-09-1359-382-10

US-09-1359-382-10

US-09-1359-382-10

US-09-105-106-10

US-09-105-106-10

US-09-105-106-10

US-09-106-106-10

US-09-106-106-10

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US-09-106-106-10

US-09-106-106-10

US-09-106-106-10

US-09-106-106-10

US-09-106-106-10

US-09-107-532A-6191

US-09-107-532A-6191

US-09-107-532A-6191

US-09-228-796A-24718
 Total number of hits satisfying chosen parameters:
 513545 seqs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-08-170-344-71
57
 1 HYCYSLYGT 9
 Query
Match Length
 Scoring table:
 Perfect score:
 Score
 Seguence:
 Searched:
 Run on:
 Result
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324, App
13, Appl
11688, A
 12, Appl
7922, Ap
4, Appli
2, Appli
39, Appl
39, Appl
 Sequence 39, 7
Sequence 39, 7
Sequence 39, 7
 Sequence 1
Sequence 1
Sequence 5
Sequence 7
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 Sequence
US-08-936-135-4
US-08-936-135-2
US-09-9460-295B-13
US-09-949-016-11688
US-09-949-016-5911
US-09-949-016-7911
US-09-949-016-7922
US-09-949-016-7922
US-09-949-016-7922
US-09-754-250-2
US-09-754-250-2
US-09-754-250-2
US-08-297-510-39
US-08-297-510-39
US-08-455-526-39
US-08-455-526-39
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ALIGNMENTS

Sequence 1171, Application US/08159339A Patent No. 6037135

CHENG, HWEE-MING FENTION: SYNTHETIC PEPTIDES OF HUMAN

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 100.0%; Score 57; DB 3; Length 11; 100.0%; Pred. No. 0.0023; Live 0; Mismatches 0; Indels
 100.0%; Score 57; DB 2; Length 20; 100.0%; Pred. No. 0.0043; trive 0; Mismatches 0; Indels
 Sequence 44, Application US/08934915
Fatent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEPTLIA NI IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Flory disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Mindows 3.0
SOFTWARE: Mindows 3.0
SOFTWARE: Mindows 3.0
SOFTWARE: 18M PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: 18M PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: 18M PC compatible
OFFICIATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/949,836
FILING DATE: ATTORNEY: 37,133
REGISTRATION NUMBER: 37,133
REGISTRATION NUMBER: 1946.6
TELECHONINI CATION INPORMATION:
TELECHONINI CATION INPORMATION:
TELECHONE: 313-538-3800
 INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 TELEPHONE: 813-538-380
TELEFAX: 813-538-3820
 TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-934-915-44
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
US-08-159-339A-1171
 US-08-934-915-44
 RESULT 2
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US-08-934-915-163 ; Sequence 163, Application US/08934915 ; Patent No. 5932412 ; GENERAL INPORMATION:

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GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, BETELLE
APPLICANT: FERRIES, BETELLE
APPLICANT: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TILLE REPERRANCE: WOBL OO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: PS/09/980,523A
PRIOR APPLICATION NUMBER: PS/09/980,523A
PRIOR PLILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
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 100.0%; Score 57; DB 2; Length 20; 100.0%; Pred. No. 0.0043; tive 0; Mismatches 0; Indels
APPLICANT: DILLINER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 SCETWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REFERENCE/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
 Sequence 8, Application US/09980523A Patent No. 6783763
 STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
 INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 TELEFAX: 813-538-3820
 TOPOLOGY: linear
MOLECULE TYPE: peptide
 9 HYCYSLYGT 17
 1 HYCYSLYGT 9
 TELEPHONE:
 US-08-934-915-163
 US-09-980-523A-8
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
 Sequence 12, Application US/08860165A
Sequence 12, Application US/08860165A
Sequence 12, Application US/08860165A
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: RABER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA
FILE REFERENCE: 1722/130
CURRENT APPLICATION VUMBER: US/08/860,165A
CURRENT APPLICATION NUMBER: PCT/AUS/00668
EARLIER PILING DATE: 1997-09-22
EARLIER PLING DATE: 1995-12-20
EARLIER PLING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER PLING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
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 100.0%; Score 57; DB 1; Length 162; 100.0%; Pred. No. 0.037; tive 0; Mismatches 0; Indels
 100.0%; Score 57; DB 3; Length 172; 100.0%; Pred. No. 0.039; tive 0; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagitani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: 10MB-0001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
TYPE: amino acide
TYPE: amino acide
TYPE: Amino acide
TYPE: Amino acide
 ; Sequence 14, Application US/08860165A
 STRANDEDNESS: not relevant TOPOLOGY: not relevant
 TYPE: PRT ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
 Query Match
Best Local Similarity 100.
 85 HYCYSLYGT 93
 23 HYCYSLYGT 31
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
 HYPOTHETICAL: NO
 MOLECULE TYPE:
 US-08-316-239B-3
 US-08-860-165-12
 RESULT 8
US-08-860-165-14
 SEQ ID NO 12
LENGTH: 172
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 d
 Sequence 3, Application US/08316239B

Patent No. 5679509

Patent No. 5679509

GENERAL INFORMATION:
APPLICANT: Wheeler, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES:
ADDRESSE: Jagtiani & Associates
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 APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT FILING DATE: 2002-04-29
PRIOR PLILING DATE: 2002-06-23
PRIOR PLILING DATE: 2002-06-31
PRIOR PLILING DATE: 1000-05-31
PRIOR PLILING DATE: 1000-05-31
PRIOR PLILING DATE: 1000-05-31
PRIOR PLILING DATE: 1000-05-31
SHOR PILING DATE: 1000-05-31
SHOR PLILING DATE: 1000-05-31
SHOR PLILING DATE: 1000-05-31
FRIOR PLILING DATE: 1000-05-31
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 100.0%; Score 57; DB 4; Length 158; 100.0%; Pred. No. 0.036;
 Query Match 100.0%; Score 57; DB 4; Length 29; Best Local Similarity 100.0%; Pred. No. 0.0063; Matches 9; Conservative 0; Mismatches 0; Indels
 0; Indels
 0; Mismatches
 ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
 Sequence 2, Application US/09980523A Patent No. 6783763
 ; ORGANISM: Human Papillomavirus
US-09-980-523A-8
 ORGANISM: Human Papillomavirus
 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 8 LENGTH: 29 TYPE: PRT
 ZIP: 20120-3400
COMPUTER READABLE FORM:
 6 HYCYSLYGT 14
 85 HYCYSLYGT 93
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
 GENERAL INFORMATION:
 USA
 -09-980-523A-2
 US-08-316-239B-3
 US-09-980-523A-2
 COUNTRY:
 STATE:
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 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-14
 USCOULED 12. Application US/09359382

| Sequence 12, Application US/09359382
| Patent No. 6306397
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: FRAZER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANT: PRAZER, Ian
| CURRENT FILE OF THORMATION: VARIANTS OF HUMAN PAPLILCOMA VIRUS ANTIGENS
| FILE REFERENCE: 01722/0148
| CURRENT APPLICATION NUMBER: US/09/359,382
| CURRENT APPLICATION NUMBER: US/09/359,382
| EARLIER PILING DATE: 1997-09-22
| EARLIER PILING DATE: 1997-09-22
| EARLIER PILING DATE: 1995-12-20
| SEALIER PILING DATE: 1994-12-20
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NO S: 27
| SEQ ID NO S: 27
GENERAL INFORMATION:
APPLICANT: BOWARDS, Stirling John
APPLICANT: BOWARDS, Stirling John
APPLICANT: WOM COOPER
APPLICANT: WOM, John COOPER
APPLICANT: WEAZER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: PRAZER, Ian
FILLE OF TOVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILLE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-11-20
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 100.0%; Score 57; DB 3; Length 172; 100.0%; Pred. No. 0.039; tive 0; Mismatches 0; Indels
 Query Match
100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels
 ORGANISM: Human papillomavirus type 16
 Sequence 14, Application US/09359382
Patent No. 6306397
 ORGANISM: Artificial Sequence
 Best Local Similarity 100.
Matches 9; Conservative
 154 HYCYSLYGT 162
 23 HYCYSLYGT 31
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
 RESULT 10
US-09-359-382-14
 US-09-359-382-12
 Query Match
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PREDICANT: EMBRISS: SILIING John
APPLICANT: COX, John Cooper A
PRILICANT: MRBB, Elizabeth Ann
APPLICANT: MRBB, Elizabeth Ann
```

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GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lonbardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT FILING DATE: 2000-2-18
FRIOR APPLICATION NUMBER: CGP 9717953.5
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
 ; Sequence 4, Application US/09485885; Patent No. 6342224
 SOFTWARE: Patentin Ver. 2.0
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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85 HYCYSLYGT 93
 85 HYCYSLYGT 93
 1 HYCYSLYGT 9
 1 HYCYSLYGT 9
 TYPE: PRT
ORGANISM: Homo sapien
 RESULT 14
US-09-367-309A-1
 SEQ ID NO 10
LENGTH: 266
 LENGTH: 266
 RESULT 15
US-09-485-885-4
 US-09-485-885-4
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 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
 APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00668
EARLIER APPLICATION NUMBER: PCT/AU95/00668
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
 US-09-359-382-10

Sequence 10, Application US/09359382

Sequence 10, Application US/09359382

Sequence 10, Application US/09359382

Sequence 10, Application US/09359382

SERVERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPERENCE: 07727/0148

CURRENT FILING DATE: 1999-07-23

SEALIER FILING DATE: 1999-07-23

EARLIER FILING DATE: 1997-09-22

EARLIER FILING DATE: 1995-07-23

SARLIER PLING DATE: 1995-07-3

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 27
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 100.0%; Score 57; DB 1; Length 182; 100.0%; Pred. No. 0.042;
 100.0%; Score 57; DB 3; Length 266; 100.0%; Pred. No. 0.062;
 LOCATION: 1..182
OTHER INFORMATION: /note= "Xaa refers to stop codon in
OTHER INFORMATION: the open reading frame."
 0; Indels
 0; Indels
 0; Mismatches
 0; Mismatches
 RESULT 12
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Eatent No. 6004557
; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
MOLECULE TYPE: protein
 66 HYCYSLYGT 74
 85 HYCYSLYGT 93
 NAME/KEY: Protein
 1 HYCYSLYGT
 1 HYCYSLYGT
 US-08-117-083-10
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 GENERAL INFORMATION:

APPLICANT: MACKPARLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 011227/0149

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: US/09/367,309A

PRIOR APPLICATION NUMBER: DSTAU98/00080

PRIOR APPLICATION NUMBER: AD PO 5178

PRIOR APPLICATION NUMBER: AU PO 5178

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN VOS: 6

SOFTWARE: PATENTIN VOY: 2.1
 100.0%; Score 57; DB 4; Length 266; 100.0%; Pred. No. 0.062; ive 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0: Indela
TYPE: PRT; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
 TYPE: PRT , ORGANISM: Human papillomavirus type 16 US-09-367-309A-1
 ; Sequence 1, Application US/09367309A; Patent No. 6428807
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Query Match
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Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 HYCYSLYGT 9 |||||||| 191 HYCYSLYGT 199

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Search completed: June 29, 2005, 01:44:27 Job time : 17.9126 secs

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001334
017jc7
077jc7
0077zj5
080963
089852
080bb19
 100.0%; Score 56; DB 2; Length 90; 100.0%; Pred. No. 0.18;
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STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.C., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -.
 SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513, AB860567.2; --
GO; GO:0042025; C:host cell nucleus; IEA.
 E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 080884 PRELIMINARY; PRT; 90 AA.
080884; PRELIMINARY; PRT; 90 AA.
01-NOV-1996 (TEMBLE) 01, Last sequence update)
01-OCT-2003 (TEMBLE) 25, Last annotation update)
61-OCT-2003 (TEMBLE).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Last sequence update)
Last annotation update)
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InterPro: PR001334; E6.
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0919D2
091335
0777C7
077Z75
080963
08852
088819
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01-OCT-2003 (TrEMBLrel.
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 6
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Best Local Similarity
9; Conserv
 EYRHYCYSL
 Papillomavirus.
NCBI_TaxID=10566;
 Papillomavirus.
NCBI_TaxID=10566;
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NON TER
SEQUENCE
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 RESULT 2
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 Description
 June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
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08gre1
09gdh3
09gdh5
09gdh7
09gdh9
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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 1612378 seqs, 512079187 residues
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Q89755
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 Score
 Minimum DB
Maximum DB
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 Database
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Gaps

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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002)
EMBL; AF404695; AAL01347.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Mequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404703; AAL01363.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Pfam; PF00518; E6; 1.
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 54 EYRHYCYSL 62
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 1 EYRHYCYSL 9
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 Papillomavirus.
NCBI_TaxID=10581;
 Papillomavirus.
NCBI_TaxID=10581;
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 Q919D0
 0919B4
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 SEQUENCE FROM N.A.

MEDLINE=21846229; PubMed=11857370;

MALLS K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868=874(2002).

EMBL, AF404704, AAL01365-1; ---
GO, GO:00042025; C:host cell nucleus; IEA.

GO, GO:000577; F:DNA binding; IEA.

NON TER 99 99
 Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404692; AAL01342.1; -.
GO: GO:0042025; C:host cell nucleus; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Pfam, PF00518; E6; 1.
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 34 EYRHYCYSL 42
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Q919D6;
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MEDLINE=20112892; PubMed=10644829;
Nambuly Manale Solution M., Shijdere P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Nanalysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
BENEL; AJ388061; CAB45104.1;
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BENEL; AJ388065; CAB45124.1;
CO:0042025; CAB45114.1;
RENEL; AJ388061; CAB45114
 Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments";
J. virol. 69:7743-7753(1995).
 NEDLINE FROM N.A.
MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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 2; Length 151;
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ive 0; Mismatches 0; Indels
 0; Indels
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Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
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NCBI_TaxID=10581;
 Farmer A.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
 Early transforming protein E6.
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 05-JUL-2004 (TrEMBLrel. 27, Created)
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NCBI_TaxID=10566;
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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, AF040702; AL01361.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0043027; F:DNA binding; IEA.
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Tornesello M.L.; Buonaguro F.M.; Meglio A.; Buonaguro L.,
Tornesello M.L.; Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
U. Gen. Virol. 78:2199-2208(1997).
EMBL; AF003016; AAB70733.1; -..
GO; GO:0042025; C:Nost cell nucleus; IEA.
InterPro; IPR001334; E6.
 Gaps
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Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
 Human papillomavirus type 16.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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 151 AA
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54 EYRHYCYSL 62
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 Query Match
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 Papillomavirus
SEQUENCE
 Query Match
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MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).

EMBL; AJ388059; CAB45110.1; -. GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

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Ponglikitmongkol M., Vaeteewoottacharn K.;
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003877; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PP00518; E6; 1.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 Humer papillomavirus.
Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
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 MEDLINE=96079021; PubMed=7494284; MEDLINE=96079021; PubMed=7494284; Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.; Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments "; J. Virol. 69:7743-7753(1995).
 °;
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EMBL; 034129; AAA91676.1; -.
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EMBL; 034120; AAA91667.1; -.
EMBL; 034120; AAA9167.1; -.
EMBL; 034124; AAA9167.1; -.
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EMBL; 034124; PAA9167.1; -.
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GO; GO:0003677; F:DNA binding; IEA.
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 Farmer A.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34111; AAA91673.1; -.
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 RESULT 11
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Du M., Fan X., Hong B., Chen J.J.;

"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.",

"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.",

Biochem Biochem B. Commun. 296:962-969(2002).

-I- FUNCTION: This protein has transforming activity in vitro.

-I- FUNCTION: Exhibits a strong, but non specific affinity for double stranded DNA (in vitro).
 -!- SUBUNIT: Interacts with FBLNI.
-!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
-!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.
 [3] INTERACTION WITH FBLAI, AND INHIBITION OF E6-MEDIATED TRANSFORMATION. MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
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MEDLINE=90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
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ive 0; Mismatches 0; Indels
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Sedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
 Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Sequence 158, App
Sequence 160, App
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US-10-239-313A-313

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Sequence 313, Application US/10239313A

Publication No. US20030175285A1

GENERAL INFORMATION:

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: GOFFICH, Lilian

APPLICANT: GOFFICH, Lilian

APPLICANT: GOFFICH, Lilian

TITLE OF INVENTION: NO-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM

TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID

TITLE OF INVENTION NUMBER: US/10/239,313A

CURRENT APPLICATION NUMBER: PR 00/03711

PRIOR APPLICATION NUMBER: PT 01/70772

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2001-03-23

PRIOR FILING DATE: 2001-03-23

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 Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-10-239-313A-313
US-10-751-845-86
US-10-751-845-93
US-10-751-845-93
US-10-476-570-31
US-10-476-570-32
US-10-476-570-12
US-10-476-570-12
US-10-751-845-66
US-10-751-845-66
US-10-476-570-55
US-10-476-570-55
 Total number of hits satisfying chosen parameters:
 1717557 seqs, 384547976 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 US-08-170-344-70
56
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110
110
110
110
 ВВ
 1 EYRHYCYSL 9
 Query
Match Length
 100.0
100.0
100.0
100.0
100.0
100.0
 Scoring table:
 Title:
Perfect score:
 Score
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 US-10-/31-843-80

Sequence 80, Application US/10751845

Publication No. US20050100928A1

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Chira, Robert G.

CURRENT APPLICATION NUMBER: US/09/664,225

PRIOR APPLICATION NUMBER: US 60/169,846

PRIOR PILING DATE: 1999-12-09

PRIOR PILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: US 60/164,665

PRIOR APPLICATION NUMBER: US 60/154,665

NUMBER OF SEQ ID NOS: 163

SOFTWARE: FaatSEQ for Windows Version 4.0

LENGTH. 10
 APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
TITLE OF INTENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE FRAESEQ for Windows Version 4.0
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 ö
 Query Match 100.0%; Score 56; DB 17; Length 10; Best Local Similarity 100.0%; Pred. No. 0.019; Matches 9; Conservative 0; Mismatches 0; Indels
 Length 9;
 0; Indels
 Query Match
100.0%; Score 56; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
 Sequence 86, Application US/10751845 Publication No. US20050100928A1 GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-86
 ; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-80
 EYRHYCYSL 10
 1 EYRHYCYSL 9
 EYRHYCYSL 9
 1 EYRHYCYSL 9
 RESULT 3
US-10-751-845-80
US-10-751-845-86
 SEQ ID NO 86
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RESULT

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, OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-90 US-10-476-570-31
 ö
 ö
 GENERAL INCOMMISSABLAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSABLAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BERTRAT
APPLICANT: MAILLERE, BERTRAT
APPLICANT: BOUNGAULE-VILLADA, ISADelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: MIXTURE DES 1004-10.6
FILE REFERENCE: 45636-501-08
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR PLING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 31
LENGTH: 15
Sequence 93, Application US/10751845

Publication No. US2005010092841

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Hedley, Mary Lynne

APPLICANT: Other, Robert G.

APPLICANT: Other, Roman M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES

FILE REPRENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

FRIOR APPLICATION NUMBER: US 60/169,846

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 163

SOFTWARE: PRIORS WINDOWS Version 4.0

SEQ ID NOS: 103

SOFTWARE: PRIORS PR
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 100.0%; Score 56; DB 17; Length 10; 100.0%; Pred. No. 0.019; tive 0; Mismatches 0; Indels
 Query Match 100.0%; Score 56; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 9; Conservative 0; Mismatches 0; Indels
 Sequence 31, Application US/10476570 Publication No. US20040170644A1
 ORGANISM: Human Papilloma virus
 TYPE: PRT ORGANISM: artificial sequence
 Best Local Similarity 100.
Matches 9; Conservative
 7 EYRHYCYSL 15
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 US-10-476-570-31
 US-10-751-845-93
 Query Match
 g
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; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66
 TYPE: PRT
ORGANISM: artificial sequence
 2 EYRHYCYSL 10
 7 EYRHYCYSL 15
1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 SOFINATE SEQ ID NO 66
 FEATURE:
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 FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95
US-10-476-570-33
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 78-92 US-10-476-570-32
 ö
 ö
 US-10-476-570-33

US-10-476-570-33

Sequence 33, Application US/10476570

Publication No. US200401706441

GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Dapillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT FILING DATE: 2003-11-04
PRIOR PELICATION NUMBER: PCT/FR02/01533
PRIOR PELICATION NUMBER: FR 01 05980
PRIOR PELING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 1.5
 Sequence 32, Application US/10476570

Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MAILLER, BETANT

APPLICANT: MAILLER, BETANT

APPLICANT: BOURGAUIT-VILLADA, Isabelle

APPLICANT: BOURGAUIT-VILLADA, Isabelle

APPLICANT: POUVELLE-WORATILLE, Sandra

APPLICANT: POUVELLE-WORATILLE, Sandra

APPLICANT: POUVELLE, Jean-Gerard

ITILE OF INVENTION: MIXTURE of peptides derived from E6 and/or E7

ITILE OF INVENTION: MARIER: US/10/476,570

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT APPLICATION NUMBER: PCT/FR02/01533

PRIOR PRING DATE: 2002-05-03

PRIOR PRING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 32

LENGTH: 15
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 Query Match 100.0%; Score 56; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 9; Conservative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 56; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 9; Conservative 0; Mismatches 0; Indels
 TYPE: PRT ORGANISM: artificial sequence
 ORGANISM: artificial sequence
 EYRHYCYSL 13
 1 EYRHYCYSL 9
 TYPE: PRT
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95 US-10-476-570-12
 ö
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WESTON 12

SEQUENCE 12, Application US/10476570

SEQUENCE 12, Application US/10476570

SEQUENCE 12, Application No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLERE, Bernard

APPLICANT: MAILLERE, Bernard

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: POUNEMILE-MORATILLE, Sandra

APPLICANT: POUNEMILE-MORATILLE, Sandra

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

FILE REFERENCE: 45536-5071-05

CURRENT FILING DATE: 2003-11-04

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 12

LENGTH: 20

LENGTH: 20

LENGTH: 20
 Sequence 66, Application US/10751845
; Publication No. US205010928A1
; Publication No. US2050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT PAPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; RIOR APPLICATION NUMBER: US 60/169,846
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR APPLICATION NUMBER: US 60/159,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE FEASESEQ for Windows Version 4.0
 Gaps
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0
 Query Match 100.0%; Score 56; DB 17; Length 23; Best Local Similarity 100.0%; Pred. No. 0.039; Matches 9; Conservative 0; Mismatches 0; Indels
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Query Match
Best Local Similarity 100...
 1 EYRHYCYSL 9
 RESULT 12
US-10-751-845-126
 US-10-858-384-2
 Query Match
 FEATURE:
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 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108 US-10-476-570-55
 ; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment; OTHER INFORMATION: for E6 of HPV US-10-858-384-8
 ö
 APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: CONMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BETTANT
APPLICANT: MAILLERE, BETTANT
APPLICANT: POUNGAULT-VILLADA, 18abelle
APPLICANT: POUNGAULT-VILLADA, 18abelle
TITLE OF INVENTION: MAXLUTE OÉ PEDLIGES derived from BG and/or E7
TITLE OF INVENTION: MAXLUTE OÉ PEDLIGES derived from BG and/or E7
TITLE OF INVENTION: MAXLUTE OF PEDLIGES
TITLE OF INVENTION: MAXLUTE OF 1000 APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR PRILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 63
SUCTION NUMBER: PCT/FR02/01538
NUMBER OF SEQ ID NOS: 63
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 APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: R 9907012
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 Query Match 100.0%; Score 56; DB 16; Length 29; Best Local Similarity 100.0%; Pred. No. 0.049; Matches 9; Conservative 0; Mismatches 0; Indels
 US-10-476-570-55
; Sequence S5, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
 Sequence 8, Application US/10858384 Publication No. US20050033025A1 GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
 ORGANISM: artificial sequence
 NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 8
LENGTH: 29
 EYRHYCYSL 12
 3 EYRHYCYSL 11
 1 EYRHYCYSL 9
 EYRHYCYSL 9
 US-10-858-384-8
 FEATURE:
 RESULT 11
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 100.0%; Score 56; DB 17; Length 117; 100.0%; Pred. No. 0.17;
100.0%; Score 56; DB 17; Length 29; 100.0%; Pred. No. 0.049; ive 0; Mismatches 0; Indels
 0; Indels
 ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-126
 0; Mismatches
 ; Sequence 126, Application US/10751845; Publication No. US20050100928A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Human Papillomavirus
 TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity 100.
Matches 9; Conservative
 3 EYRHYCYSL 11
 48 EYRHYCYSL 56
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Search completed: June 29, 2005, 05:48:14
Job time : 53.8517 secs
 DEFLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cur Hausen, Harald
TITLE OF INVENTION: Wodified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 412-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR PILING DATE: 2002-03-22
PRIOR FILING DATE: 2001-03-23
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
LENGTH: 171
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Query Match 100.0%; Score 56; DB 17; Length 158; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 56; DB 16; Length 171; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels (
 Sequence 16, Application US/10367057

Publication No. US20050100554A1

GENERAL INFORMATION:
APPLICANT: Cutili, Scott;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: O., Chean Eng
TITLE OF INVENTION: Complexes and Methode of Using Same;
TITLE OF INVENTION: Complexes and Methode of Using Same;
TITLE OF INVENTION: Complexes and Methode of Using Same;
CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CutaSeqList version 0.1

SEQ ID NO 16

LENGTH: 158

TYPE: PRT
 ', OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
 ; Sequence 2, Application US/10472724; Publication No. US20040171806A1; GENERAL INFORMATION:
 ORGANISM: Artificial Sequence FEATURE:
 82 EYRHYCYSL 90
 ; ORGANISM: Homo sapiens
US-10-367-057-16
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82 EYRHYCYSL 90
 87 EYRHYCYSL 95
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 RESULT 14
US-10-367-057-16
 US-10-472-724-2
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Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq

Sequence Sequence Sequence

Sequence

Sequence 1 Sequence 6

Sequence

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Length 20;
 US-UB-934-915-44

| Sequence 44, Application US/08934915 |
| Patent No. 592412 |
| GENERAL INFORMATION: |
| APPLICANT: DILLAIER, JOAKIM |
| APPLICANT: DILLAIER, LENA |
| APPLICANT: DILLAIER, LENA |
| APPLICANT: CHENG, HWEE-MING |
| TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8 |
| TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8 |
| TITLE OF INVENTION: DIAGNOSTIC PURPOSES |
| TITLE OF INVENTION: HAY. 19 NORTH, SUITE 500 |
| TITLE OF INVENTION: AND ADDITION: WINDOWS 3.0 |
| COUNTRY: U.S.A. |
| COMPUTER READABLE FORM: WINDOWS 3.0 |
| SOFTWARE: MICROSOFT WORD 6.0 |
| CURRENT APPLICATION NUMBER: US/08/934,915 |
| FILING DATE: 22-SEP-1997 |
| TILING DATE: 22-SEP-1997 |
| TELESPHONE APPLICATION NUMBER: 07/949,836 |
| FILING DATE: APPOCKET NUMBER: 37,133 |
| REGISTRATION NUMBER: 37,133 |
| REGISTRATION NUMBER: 37,133 |
| REBERNICE/OFFICE OFFICE
US-08-709-662-6
US-09-489-019A-13995
US-09-949-016-5911
US-09-248-796A-22612
US-09-248-796A-21392
US-09-248-796A-18861
US-09-248-796A-18861
US-08-158-735A-2
US-09-382-256-6
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US-09-395-115-6
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US-08-436-265-6
 Score 56; DB 2;
Pred. No. 0.017;
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 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TOPOLOGY: linear
MOLECULE TYPE: peptide
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 US-08-934-915-44
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 Sequence 6, Appli
Sequence 134, App
Sequence 1171, Ap
Sequence 6, Appli
 24718, A
4132, Ap
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 4132
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 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 US-08-934-915-44
US-08-934-915-163
US-09-980-523A-8
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US-08-316-23B-3
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US-08-359-382-14
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US-09-485-885-4
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US-09-107-523A-4132
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US-08-159-339A-1171
US-08-159-339A-1171
 Total number of hits satisfying chosen parameters:
 513545 segs, 74649064 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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 seq length: 0
seq length: 200000000
 US-08-170-344-70
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 DB
 1 EYRHYCYSL 9
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 Scoring table:
 Perfect score:
 Score
 Minimum DB
Maximum DB
 Sequence:
 Searched:
 Run on:
 Result
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RESULT 2

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE B6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE REFERENCE: WOBL AO INS
TITLE OF INVENTION OF PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE REFERENCE: WOBL AO INS
CURRENT FILING DATE: 2002-04-29
PRIOR PALLING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: FCT/FRO0/01513
PRIOR APPLICATION NUMBER: FC 99/07012
PRIOR APPLICATION NUMBER: FC 99/07012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEO ID NOS: 24
SOFTWARE: PATENTIN VOR: 2.1
SEQ ID NO 2
LENGTH: 158
 TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT PILLING DATE: 2002-04-29
FRICH REPT FILLING DATE: 2002-04-29
PRIOR FILLING DATE: 2000-05-31
PRIOR FILLING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE PARENTING DATE: 1999-06-03
SOFTWARE PARENTING DATE: 1999-06-03
SOFTWARE PARENTING DATE: 1999-06-03
SOFTWARE PARENTING DATE: 2000-05-31
SOFTWARE PARENTING DATE: 2000-05-31
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 100.0%; Score 56; DB 4; Length 29; 100.0%; Pred. No. 0.024; tive 0; Mismatches 0; Indels
 Sequence 3, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
 US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
 TYPE: PRT
ORGANISM: Human Papillomavirus
 : Human Papillomavirus
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 3 EYRHYCYSL 11
 82 EYRHYCYSL 90
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 , ORGANISM: Hur
US-09-980-523A-2
 US-08-316-239B-3
 US-09-980-523A-8
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 Query Match
100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels
 Indels
 APPLICANT: DILLARE, JOAKIM
APPLICANT: DILLARE, LENA
APPLICANT: DILLARE, LENA
APPLICANT: CRENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARMATER
STATE: FLORIDA
COMUNTY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Mismatches
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
 Sequence 8, Application US/09980523A
Batent No. 6783763
GENERAL INCRATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BUNGANLT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-CERARD
APPLICANT: CONNAM, FRANCINE
 US-08-934-915-163
; Sequence 163. Application US/08934915
Patent No. 5932412
; GENERAL INFORMATION:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUCCh
REGISTRATION NUMBER: 37,133
REPERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
 37,133
 ö
 163:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
 9; Conservative
 TELEFAX: 813-538-3820
 , MOLECULE TYPE: peptide US-08-934-915-163
 EYRHYCYSL 14
 EYRHYCYSL 14
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 1 EYRHYCYSL 9
 RESULT 3
US-09-980-523A-8
 Matches
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US-08-860-165-14
 US-09-359-382-12
 US-08-860-165-14
 US-09-359-382-12
 Query Match
 Query Match
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 Distinguishing a Subset of HPV that is Associated with an Increased Risk of Developing Cervical Dysplasia and Cervical Cancer
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 Gaps
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-12
 US-08-860-165-12

Sequence 12, Application US/08860165A

Patent No. 6004557;
GRNERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
FILE RFERENCE: 17227/130
CURRENT APPLICATION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/660,165A
CURRENT APPLICATION NUMBER: PCT/AU55/00868
EARLIER APPLICATION NUMBER: PCT/AU55/00868
BARLIER FILING DATE: 1995-12-20
EARLIER PILING DATE: 1994-11-20

NUMBER OF SEQ ID NOS: 12.0
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 DB 1; Length 162;
 Query Match 100.0%; Score 56; DB 1; Length 16
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels
 CUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISA COMPATION

COMPUTER: Floppy disk

COMPUTER: ISA COMPATION

COMPUTER: ISA COMPATION

COMPUTER: ISA COMPATION

COMPUTER: ISA COMPATION

COMPATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATE: 30-SEP-1994

FLING DATE: 30-SEP-1994

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: Jaggiani, Ajay A.

REFERENCE/DOCKET NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION SEQ ID NO: 3:

SEQUIENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 3:

SEQUIENCE CHARACTERISTICS:
TITLE OF INVENTION: Distinguishing a TITLE OF INVENTION: Increased Risk of ITLE OF INVENTION: Cervical Cancer NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSE: STREET: ADJESSE: STREET: G126 Rocky Way Court CITY: Centreville
 not relevant
 ORGANISM: Artificial Sequence
 LENGTH: 162 amino acids TYPE: amino acid
 not relevant
 TOPOLOGY: not relevan
MOLECULE TYPE: protein
HYPOTHETICAL: NO
 FYRHYCYSL 90
 1 EYRHYCYSL 9
 STRANDEDNESS:
 US-08-316-239B-3
 82
 TYPE: PRT
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 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
 Sequence 14, Application US/08860165A

Sequence 14, Application US/08860165A

Patent No. 600457.

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: EDWARDS, Stirling John

APPLICANT: EDWARDS, Stirling John

APPLICANT: ERAZER, Ian

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 1722/130

CURRENT APPLICATION NUMBER: US/08/860,165A

CURRENT FILING DATE: 1995-12-20

EARLIER APPLICATION NUMBER: AD PNOS7

EARLIER APPLICATION NUMBER: AD PNOS7

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 14

LENGTH: 172
 Sequence 12, Application US/09159382

Sequence 12, Application US/09159382

Sequence 12, Application US/09159382

Sequence 12, Application US/09159382

Sequence 12, Application US/08159382

APPLICANT: EDWARDS, Stirling John

APPLICANT: WEBB. Elizabeth Ann

APPLICANT: WEBB. Elizabeth Ann

APPLICANT: PRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 077227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER APPLICATION NUMBER: AU PNO157/94

EARLIER PILING DATE: 1994-112-20

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 12

LENGTH: 172
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100.0%; Score 56; DB 3; Length 172; 100.0%; Pred. No. 0.13; ive 0; Mismatches 0; Indels
 100.0%; Score 56; DB 3; Length 172; 100.0%; Pred. No. 0.13; tive 0; Mismatches 0; Indels
 DB 3; Length 172;
 100.0%; Score 56;
 TYPE: PRT ORGANISM: Human papillomavirus type 16
 TYPE: PRT
ORGANISM: Artificial Sequence
 9; Conservative
 Best Local Similarity 100.
Matches 9; Conservative
 151 EYRHYCYSL 159
 20 EYRHYCYSL 28
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 Best Local Similarity
Matches 9; Conserv
 Query Match
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REFERENCE/DOCKET NUMBER: A-58783
TELECOMUNICATION INCORMATION:
TELEPHONE: 415-781-1989
TELERA: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
 US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
 REGISTRATION NUMBER: 24,190
 ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100.0
....hes 9; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
 STRANDEDNESS: single
 NAME/KEY: Protein
LOCATION: 1..182
OTHER INFORMATION:
OTHER INFORMATION:
 63 EYRHYCYSL 71
 82 EYRHYCYSL 90
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 RESULT 12
US-09-359-382-10
 US-08-860-165-10
 US-08-117-083-10
 FEATURE:
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 US-09-359-382-14

Sequence 14, Application US/09359382

Sequence 14, Application US/09359382

Patent No. 3036397

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: ECX, John Cooper

APPLICANT: FRZER, Ian

APPLICANT: FRZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER APPLICATION NUMBER: AU PNO157/94

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 14

IENEGTH: 172
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 Sequence 10, Application US/08117083
Patent No. 5719054
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boursenl, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
 Query Match 100.0%; Score 56; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.13; Matches 9; Conservative 0; Mismatches 0; Indels
 0; Indels
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PLICATION NOTE: US/08/117,083
FILING DATE: 10-SEP-1993
 Pred. No. 0.13;
Best Local Similarity 100.0%; Pred. No. 0.1 Matches 9; Conservative 0; Mismatches
 ORGANISM: Human papillomavirus type 16
 ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 151 EYRHYCYSL 159
 San Francisco
 20 EYRHYCYSL 28
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 USA
 CITY: Sar
STATE: CA
COUNTRY:
 US-08-117-083-10
 US-09-359-382-14
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 OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
 | FACEURAL NO. 000455)
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: COX, John Cooper
| APPLICANT: FRAZER, Is |
| APPLICANT: FRAZER, Is |
| TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
| FILE REFERENCE: 12227/130
| CURRENT APPLICATION NUMBER: US/08/860,165A
| CURRENT PILING DATE: 1997-09-22
| EARLIER PILING DATE: 1997-09-22
| EARLIER PILING DATE: 1998-12-20
| FARLIER PILING DATE: 1998-12-20
| FARLIER PILING DATE: 1994-12-20
| SARLIER PILING DATE: 1994-12-20
| SARLIER PILING DATE: 1996-12-20
| SOFTWARE: PATENTIN VUMBER: AU POOLS
| SARLIER PILING DATE: 1996-12-20
| SARLIER PILING DATE: 1997-03-20
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 Query Match
100.0%; Score 56; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels
 100.0%; Score 56; DB 3; Length 266; 100.0%; Pred. No. 0.19; Live 0; Mismatches 0; Indels
/note= "Xaa refers to stop codon in the open reading frame."
 Sequence 10, Application US/09359382; Patent No. 6306397; GENERAL INFORMATION: APPLICANT: EDWARDS, Stirling John APPLICANT: COX, John Cooper, APPLICANT: WEBB, Elizabeth Ann
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PRIOR APPLICATION NUMBER: PCT/EP98/05285; PRIOR PLUING DATE: 1998-08-17; PRIOR FILING DATE: 1998-08-17; PRIOR FILING DATE: 1997-08-22; NUMBER OF SEQ ID NOS: 23; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 4; LENGTH: 273; LENGTH: 273
 SEQ ID NOS: 23
FastSEQ for Windows Version 3.0
 Search completed: June 29, 2005, 01:44:26
Job time : 16.9126 secs
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Best Local Similarity 100.0
 Query Match
Best Local Similarity 100.'
 188 EYRHYCYSL 196
 207 EYRHYCYSL 215
 TYPE: PRT
ORGANISM: Homo sapien
 TYPE: PRT
ORGANISM: Homo sapien
 1 EYRHYCYSL 9
 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10
LENGTH: 292
 1 EYRHYCYSL
 US-09-485-885-10
 US-09-485-885-10
 US-09-485-885-4
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 Ian
1: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
 Sequence 1, Application US/09367309A

Sequence 1, Application US/09367309A

Patent No. 642807

GENERAL INFORMATION:

APPLICANT: MACIFALAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: AU PO 5178

PRIOR FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 6

SEQ ID NOS: 6

LENGTH: 266
 100.0%; Score 56; DB 3; Length 266; 100.0%; Pred. No. 0.19; tive 0; Mismatches 0; Indels
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100.0%; Score 56; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
 Sequence 4, Application US/09485885
Patent No. 634224
GENERAL INFORMATION
APPLICANT: Brick, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
 APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLIO)
FILE REPERENCE: 01727/0148
FILE REPERENCE: 01727/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT PILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/660,165
EARLIER PILING DATE: 1997-09-22
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHIN Ver. 2.0
 ORGANISM: Human papillomavirus type 16
 ORGANISM: Human papillomavirus type 16
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 82 EYRHYCYSL 90
 1 EYRHYCYSL 9
 1 EYRHYCYSL 9
 US-09-359-382-10
 US-09-367-309A-1
 SEQ ID NO 10
LENGTH: 266
 US-09-367-309A-1
 US-09-485-885-4
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100.0%; Score 56; DB 3; Length 273; 100.0%; Pred. No. 0.19; ive 0; Mismatches 0; Indels
 100.0%; Score 56; DB 3; Length 292; 100.0%; Pred. No. 0.2; ive 0; Mismatches 0; Indels
 Sequence 10, Application US/09485885
Fatent No. 634224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Bruck, Claudine
APPLICANT: Bruck, Claudine
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
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 SEQUENCE FROM N.A.

MEDLINE=21046229; PubMed=11857370;

MEDLINE=21046229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874 (2002).

EMBL; AF404700; AAL01357.1;
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 Q9wh13
Q919c6
Q919d4
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Q8qrd9
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Q9qdh3
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071bi7
 100.0%; Score 49; DB 2; Length 26; 100.0%; Pred. No. 0.016;
 Shippy R., Siwkowski A., Hampel A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59900; AAB03505.1; -.
GO; GO:0004277; C.host cell nucleus; IEA.
GO; GO:0003777; F:DNA binding; IEA.
 0; Indels
 Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
 0919C0 PRELIMINARY, PRT; 130 AA.
0919C0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TremBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 segs, 512079187 residues
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 Post-processing: Minimum Match 0%
Maximum Match 100%
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 protein search, using sw model
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0777E16
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 MEDLINE=21846229; PubWed=11857370;
MEDLINE=21846229; PubWed=11857370;
MALTE K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868 =874 [2002].
EMBL; AF404659; AAL01355.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; E:DNA binding; IEA.
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MEDLINE=21046229; PubMed=11857370;

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"Sequence variation and physical state of human papillomavirus type 16

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"Sequence isolates from Australia and New Caledonia.";

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GO; GO:000577; F.DNA binding; IEA.
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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 MEDLINE=21846229; PubMed=1185/370;
Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Wattal cancer valuation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
GO, GO:0042025; AbLolis 11.
GO, GO:0003677; P.DNA binding; IEA.
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Fram; PRO0318; E6; 1.
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Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Matts K.J., Thompson C.H., Cossart title and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002)
Int. J. Cancer 97:868-874 (2002)
EMBL, AP404694; AAL01345-1;
EMBL, AP404694; AAL01345-1;
GO; GO:0003677; F:DNA binding; IEA.
Fram, PP00518; E6; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI TaxID=10581;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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 NON TER 1 1 SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
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NCBI_TaxID=10581;
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Bequence variations and viral genomic state of human papillomavirus
'Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 [1997].
Gen. Virol. 78:2199-2208 [1997].
GO, GO:0003677; F:DNA binding; IEA.
InterPro; IPR00134; E6.
Ffam; PF00318; E6; 1.
SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, Li2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34114; AAA916611; -.
EMBL; U34125; AAA91672.1; -.
EMBL; U34131; AAA91677.1; -.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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 MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AR404698; AAL01353.1; -..
GO; GO:00023677; F:DNA binding; IEA.
PFo0518; E6; 1.
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 MEDLINE=97437474; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
T. Gen. Virol. 78:2199-2208(1997).
EMBL; AF003015; AAB70732.1; -..
GO; GO:0042025; C:Nost cell nucleus; IEA.
GO; GO:004207; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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BEMBL, AJ388066; CAB45104.1; ---

EMBL, AJ38066; CAB45124.1; ---

GO; GO:0042025; C:Nest cell nucleus; IEA.

GO; GO:0042025; C:Nest cell nucleus; IEA.

InterPro; IPR001334; E6.
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Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
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MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y; DeFilippis V.R., Ayala F.J., Villarreal L.P.; "Evidence of diversifying selection in human papillomavirus type 16 E6
 STEAIN-Xinjiang;
Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
"cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang.";
Biopsies wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
 Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
"Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).

EMBL, AF463197; AA015691.; -.
EMBL, AJ388063; CAB45118.1; -.
G0; G0:0042025; C:host cell nucleus; IEA.
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Early transforming protein E6 variant (Transforming protein E6).
Human papillomavirus type 16.
Viruses; dsDNa viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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CTUZ M.R., Martins C.R.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A7327851; AAG45940.1; -.
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Pfam; PF00518; E6; 1.
 0; Indels
 Martins C.R.F.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
 Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
 100.0%; Score 49; DB 2
100.0%; Pred. No. 0.1;
 151 AA.
 0; Mismatches
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 SEQUENCE FROM N.A.

MEDLINES-91437474; PubMed-9292007;
MEDLINES-91437474; PubMed-9292007;
A method of control
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 "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments"; J. virol. 69:7743-7753(1955).
 SEQUENCE FROM N.A.
MRDILNE-96079021; PubMed=7494284;
Yamad T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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 100.0%; Score 49; DB 2; Length 151; 100.0%; Pred. No. 0.1; vative 0; Mismatches 0; Indels
 Query Match 100.0%; Score 49; DB 2; Length 151; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses debNA viruses, no RNA stage; Papillomaviridae;
 Q80963 PRELIMINARY; PRT; 151 AA.
Q80963;
Q800963;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Early transforming protein E6.
Human papillomavirus.
Viruses; dsNNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
 Farmer A.D.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;
 151 AA
 PRT;
 Ouery Match
Best Local Similarity 100...
 PRELIMINARY;
 22 TIHDIILEC 30
 22 TIHDIILEC 30
 1 TIHDIILEC 9
 1 TIHDIILEC 9
 Papillomavirus.
NCBI_TaxID=10581;
 SEQUENCE FROM N.A.
SEQUENCE
 Q772J5
Q772J5;
 RESULT 14
Q77ZJS
 RESULT 15
 080963
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DR EMBL; U34122; AAA91669.1; -.

DR GO; 020.0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:nDNA binding; IEA.

DR InterPro; IPR00134; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match

Best Local Similarity 100.0%; Score 49; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 TIMDILLEC 9

| | | | | | | | | | | | |

Db 22 TIMDILLEC 30

Search completed: June 28, 2005, 19:19:21

Job time: 55.3 secs
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 18:23:48; Search time 11.2 Seconds Run on:

(without alignments)
77.317 Million cell updates/sec

.US-08-170-344-7 Title: Perfect score:

1 TIMDIILEC 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STRMMADIES

|           | Description    | protein E6 - human | small heat shock p | transferrin precur | hypothetical prote | E6 protein - human | gag-related protei |        | tumor suppressor p | ATP adenylyltransf | protein F15D4.7 [i | hypothetical prote | hypothetical prote | F      | II protei | ŭ      |        | E6 protein - rhesu | hypothetical prote | molybdopterin bios | hypothetical prote | hypothetical prote | transcription regu | conserved hypothet | chromosome 6 open | dnaK-type molecula | protein-tyrosine k | 4      | hypothetical prote |        |
|-----------|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|-----------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------|--------------------|--------|
| SUMMARIES | ID             | WEWLHS             | H83709             | A36500             | AI3163             | W6WLPR             | S54361             | T24772 | T03814             | XXBYP1             | F88349             | T20984             | T19833             | S19906 | S19909    | S23825 | W6WL33 | W6WLR1             | B97948             | B32352             | T16004             | C70903             | D82485             | D86979             | JC7837            | T07620             | S24550             | T10000 | T04742             | JC1269 |
|           | DB             | -                  | 7                  | -                  | ~                  | -                  | 7                  | ~      | ~                  | ٦                  | ~                  | ~                  | ~                  | ~      | ~         | ~      | 7      | П                  | ~                  | ~                  | ~                  | 7                  | 7                  | ~                  | ~                 | ~                  | ч                  | ~      | ~                  | н      |
|           | Length         | 158                | 145                | 681                | 75                 | 158                | 324                | 519    | 1164               | 321                | 1140               | 1140               | 1496               | 32     | 35        | 47     | 149    | 191                | 217                | 249                | 303                | 342                | 358                | 359                | 437               | 465                | 505                | 216    | 523                | 924    |
| d         | Query<br>Match | 100.0              | 75.5               | 75.5               | 73.5               | 73.5               | 73.5               | 73.5   |                    | 71.4               | 71.4               | 71.4               | 71.4               | 69.4   | 69.4      | 69.4   | 69.4   | 69.4               | 69.4               | 69.4               | 69.4               | 69.4               | 69.4               | 69.4               | 69.4              | 69.4               | 69.4               | 69.4   | 69.4               | 68.4   |
|           | Score          | 49                 | 37                 | 37                 | 36                 | 36                 | 36                 | 36     | 36                 | 32                 | 35                 | 35                 | 32                 | 34     | 34        | 34     | 34     | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                 | 34                | 34                 | 34                 | 34     | 34                 | 33.5   |
|           | Result<br>No.  | п                  | 8                  | m                  | 4                  | D.                 | 9                  | 7      | œ                  | σ                  | 10                 | 11                 | 12                 | 13     | 14        | 15     | 16     | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                | 25                 | 56                 | 27     | 28                 | 29     |

| RNA polymerase sig | hydrolase, haloaci | hypothetical prote | hypothetical prote | probable phospholi | probable glycosylt | ADAM 4 protein pre | protein-tyrosine k | long-chain-fatty-a | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | YMF46 protein - Ac | hypothetical prote | dnak-type molecula |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| AI2215             | A87284             | T45586             | B85344             | T00421             | E96008             | 149283             | 833569             | 823052             | T27859             | T39287             | S62419             | T34469             | S46445             | B83815             | S48023             |
| 8                  | N                  | N                  | ~                  | ď                  | N                  | N                  | ~                  | ~                  | N                  | 7                  | ~                  | ~                  | N                  | N                  | 0                  |
| 218                | 221                | 306                | 326                | 326                | 447                | 473                | 536                | 700                | 1276               | 1297               | 1428               | 1208               | 142                | 171                | 210                |
| 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 67.3               | 66.3               | 65.3               | 65.3               | 65.3               |
| 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 32.5               | 32                 | 32                 | 32                 |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

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procein B6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Sededorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A2235; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:9333031; PIDN:AAA46939.1; PID:933303
B;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J, Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: Z17014; MUID:91162763; PMID:1848319
 ö
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rosidues: 1-158 <KEN>
A;Cross-references: EMBL:KO2718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
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 'Match 100.0%; Score 49; DB 1; Length 158; Local Similarity 100.0%; Pred. No. 0.032; les 9; Conservative 0; Mismatches 0; Indels
 C;Superfamily: papillomavirus E6 protein
K,Keywords: DNA binding; early protein; zinc finger
E;37-73Kegion: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
 29 TIHDIILEC 37
 1 TIHDIILEC 9
 Query Match
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mail heat shock protein BH0480 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004
C;Accession: H83709
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res 28, 4317-4317, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: H83709
A;Accession: H83709
A;Accession: H83709
A;Avacession: H83709
A;Avacesion: Bacilminary
A;Molecule type: DNA

RESULT 2

22 HDLLLEC 28

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Ef protein - human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Accession: C40509
K;Reuter, 3. Dellus, H; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, B.
J virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A;Reference number: A40509; MUID:91374616; PMID:1716694
 gag-related protein - Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Species: Trypanosoma cruzi
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54361
R;Martin, F.; Maranon, C.; Olivares, M.; Alonso, C.; Lopez, M.C.
A;Title: Characterization of a non-long terminal repeat retrotransposon cDNA (L1Tc) from A;Reference number: S54359; MUID:95205412; PMID:7534829
 hypothetical protein T10B10.7 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T24772 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 R; Sims, M.
 Gaps
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 73.5%; Score 36; DB 1; Length 158; 44.4%; Pred. No. 11;
 Length 324;
 1; Indels
 1; Indels
 submitted to the EMBL Data Library, May 1996
A;Reference number: 219934
A;Accession: T24772
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A;Residues: 1-519 <WIL>
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A,Residues: 1-158 «REU>
A,Cross-references: UNIPROT:P27962; GB:M73258
C,Superfamily: papillomavirus E6 protein
C,Superfamily: papillomavirus E6 protein;
C,Reywords: DNA binding: early protein; zinc finger
E,732-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
 DB 2;
 Score 36; DB 2
Pred. No. 23;
3; Mismatches
 4; Mismatches
 A;Cross-references: UNIPROT:Q9Y028; EMBL:X83098
C;Genetics:
 73.5%;
55.6%;
 44.48;
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A;Status: translation not shown
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Matches 4; Conservative
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Matches 5; Conservative
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TLHHLLLEC 276
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24 TLHDVTIDC 32
 1 TIMDIILEC 9
 1 TIMDIILEC
 1-324 <MAR>
 A;Accession: S54361
A;Status: preliminary
A;Molecule type: mRNA
 A;Start codon: GTG
 Query Match
 A; Residues:
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 C;Species: Manduca sexta (tobacco hornworm)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A36500
R;Bartfeld, N.S.; Law, J.H.
J. Biol. Chem. 256, 21684-21691, 1990
A;Title: Isolation and molecular cloning of transferrin from the tobacco hornworm, Mandu A;Title: Isolation and molecular cloning of transferrin from the tobacco hornworm, Mandu A;Reference number: A36500, MUID:91072368; PMID:2254322
A;Accession: A36500
A;Accession: A36500
A;Residues: preliminary
A;Residues: 1-681 -68AR
A;Residues: 1-681 -68AR
C;Resicues: UNIPROT:P22297; GB:M62802; GB:M36296; NID:g159543; PIDN:AAA29338.1;
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication
A;Cross-references: UNIPROT:Q9KFJ9; GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BAB041
A;Experimental source: strain C-125
C;Genetics:
 A,Cross-references: UNIPROT:QBUKR5; GB:AE008687; PIDN:AAL45727.1; PID:g17743458; GSPDB:G
A,Experimental source: strain C58 (Dupont)
 hypothetical protein Atu5034 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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 Species: Agrobacterium tumefaciens
.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 Gaps
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 A;Gene: BH0480
C;Superfamily: alpha-crystallin-related small heat shock protein
 Score 37; DB 2; Length 145;
Pred. No. 6.6;
2; Mismatches 1; Indels
 Length 681;
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 Indels
 DB 1;
 Score 37; DB 1
Pred. No. 32;
1; Mismatches
 transferrin precursor - tobacco hornworm
 75.5%;
 75.5%;
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Best Local Similarity 66.77
Matches 6; Conservative
 6; Conservative
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670 TIHDVISSC 678
 54
 1 TIHDIILEC 9
 1 TIHDIILEC 9
 Best Local Similarity
Matches 5; Conserv
 | |::||||
46 TDHEVILEC
 Query Match
Best Local Similarity
 3 HDIILEC 9
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <KUR>
 A; Accession: AI3163
 A; Genome: plasmid
 Query Match
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Matches

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A; Gene: F15D4.7
 Query Match
 C;Genetics:
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 ATP adenylytransferase (EC 2.7.7.53) I - yeast (Saccharomyces cerevisiae)

N'Alternate names: diadenosinetetraphosphate alpha-beta-phosphorylase I; protein YCL050G
N'COntains: sulfate adenylytransferase (ADP) (EC 2.7.7.5)
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence revision 30-Jun-1993 #text change 09-Jul-2004
C;Date: 31-Mar-1991 #sequence revision 30-Jun-1993 #text change 09-Jul-2004
C;Date: 31-Mar-1991 #sequence revision 30-Jun-1993 #text change 09-Jul-2004
A;Raushal, V.; Avila, D.M.; Hardies, S.C.; Barnes, L.D.
Gene 95, 79-84, 1990
A;Title: Sequencing and enhanced expression of the gene encoding diadenosine 5',5'''-P(1 A;Reference number: JQ0793; MUID:91071609; PMID:2174812
A;Reference number: JQ0793; MUID:91071609; PMID:2174812
A;Molecule type: DNA
A;Molecule type: DNA
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A;Cross-references: UNIPROT:P16550; GB:M35204; NID:g171425; PIDN:AAA34581.1; PID:g171426
A;Accession: S17970
A;Cross-references: UNIPROT:Q22374; EMBL:Z72514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:T1
A;Experimental source: clone T10B10
C;Genetics:
 R;van Slegrenhorst, M.; de Hoogt, R.; Hermans, C.; Nellist, M.; Janssen, B.; Verhoef, S.; Fox, M.; Ekong, R.; Osborne, J.; Wolfe, J.; Povey, S.; Snell, R.G.; Cheadle, J.P.; Jd Science 277, 805-808, 1997
 A;Molecule type: DNA
A;Residues: 1-321 <FUL>
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42394.1; PID:g5311; GSPDB:GN00003
 A; Authors: Richardson, D.; Wilmer, F.; Munro, C.; Hawkins, T.L.; Sepp, T.; Ali, J.B.M.; latkowski, D.J.
A; Title: Identification of the tuberous sclerosis gene TSC1 on chromosome 9q34.
A; Reference number: Z15098; MUID:97390505; PMID:9242607
 Cross-references: UNIPROT: Q92574; EMBL: AF013168; NID: g2331280; PIDN: AAC51674.1; PID: g2
 ö
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 C;Species: Homo sapiens (man)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03814
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 Length 1164;
 Length 519;
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 A;Molecule type: protein **RAND>**Residues: 49-78, "W',80-84;281-321 <KAU2>**R.**Fuller, L.J.; Kelly, A.; Lewis, C.; McKee, R.A.; Pearson, submitted to the Protein Sequence Database, March 1992
 A;Gene: CESP:T10B10.7
A;Map position: X
A;Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3
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 DB '
 3; Mismatches
 Score 36;
Pred. No.
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57.1%;
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335 IYDLILEC 342
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253 HDVVIEC 259
 2 INDIILEC 9
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Best Local Similarity
Matches 6; Conserv
 3 HDIILEC 9
 A;Cross-references: Un
C;Genetics:
A;Gene: TSC1
A;Map position: 9q34
 A; Accession: S19380
 Genetics:
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo Kreference number: A75000; MUID:99066613; PMID:9851916 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
 submitted to the EMBL Data Library, September 1996
A;Reference number: 219354
A;Accession: T20984
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Rediues: 1-1140 (*ML>
A;Cross-references: UNIPROT:Q93515; EMBL:Z80344; PIDN:CAB02490.1; GSPDB:GN00020; CESP:F
 A, Cross-references: UNIPROT: 093515; GB: chr_II; PIDN: CAB02490.1; PID: 93875970; GSPDB: GNO
R.Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.
J. Bacteriol. 171, 6437-6445, 1989
A; Title: Isolation, characterization, and inactivation of the APA1 gene encoding yeast A; Reference number: S07847; MUID:90078083; PMID:2556364
 A/Accession: S07847
A/Molecule type: DNA
A/Rossidues: 1-99, 'E',101-321 < PLA>
A/Accession: A37535
A/Accession: A37535
A/Accession: A37535
A/Accession: A37535
A/Accession: A37535
A/Accession: A37536
A/Accession: A37536
A/Accession: A37536
A/Accession: A37539-99, 'E',101-260,263-321 < PLA2>
C/Genetics: DP1A, MPS:YCL050C
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A/Access references: SGD:S0000555; MPS:YCL050C
A/Access references: Access references: SGD:S0000555; MPS:YCL050C
A/Access references: SGD:S0000555; MPS:YCL050C
A/Accession: 3L
C/SUperfamily: ATP ademylyltransferase
C/Keywords: acetylated amino end; blocked amino end; mature form) #status predicted
F;2-321/Product: ATP ademylyltransferase I #status predicted
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 protein F15D4.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Daccies: D-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20984
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 Score 35; DB 1; Length 321;
Pred. No. 36;
2; Mismatches 0; Indels
 1; Indels
 2; Mismatches
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75.0%;
 6; Conservative
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nes 5; Conservative
 299 INDILLEC 306
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551 IHDMVAEC 558
 2 IHDIILEC 9
 2 INDIILEC 9
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Best Local Similarity
 A;Status: preliminary
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 A; Accession: F88349
 A; Map position: 2
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Gaps

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Length 35; 1; Indels

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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S19909
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; M: submitted to the EMBL Data Library, January 1992
A;Pescription: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via A;Pescription: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via A;Pecession: S19909
A;Molecule type: mRNA
A;Residues: 1-35 < SNI>
A;Cross-references: UNIPROT:Q81887; EMBL:X64087; NID:g60286; PIDN:CAA45438.1; PID:g6028
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
 BG-I protein - human papillomavirus type 33 (fragment)
C;Species: human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 20-Peb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: 823825, 823829
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Misubmitteed to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via A;Reference number: 819906
 A;Accession: S23825
A;Molecule type: mRNA
A;Residues: 1-47 <SNI>
A;Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; EMBL:X64084; NID:g60273; PIDN:CAA45
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C;Keywords: DNA binding; early protein; zinc finger
 69.4%; Score 34; DB 2; Length 47; 66.7%; Pred. No. 8.1; 2ive 2; Mismatches 1; Indels
 69.4%; Score 34; DB 2;
66.7%; Pred. No. 6;
iive 2; Mismatches
 Search completed: June 28, 2005, 19:23:21
Job time : 13.2 secs
 Best Local Similarity 66.7
Matches 6; Conservative
 10 TIHNIELQC 18
 10 TIHNIELOC 18
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 1 TIHDIILEC 9
 1 TIHDIILEC
 Query Match
 RESULT 15
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 E6-II protein - human papillomavirus type 33 (fragment)
C;Species: human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Unn-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: 819906
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me submitted to the EMBL Data Library, January 1992
A;Reference number: 819906
A;Accession: 819906
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
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A;Residues: 1-1496 <WIL>
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A;Experimental source: clone C38D9
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A; Residues: 1-32 <SNI>
A; Cross-references: UNIPROT:Q81885; EMBL:X64086; NID:g60282; PIDN:CAA45435.1; PID:g60283
C; Superfamily: papillomavirus E6 protein
C; Keywords: early protein
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 ispecies: Caenorhabditis elegans
;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004;Ancession: T1983
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 Score 35; DB 2; Length 1140;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
 71.4%; Score 35; DB 2; Length 1496; 62.5%; Pred. No. 1.7e+02; Ative 2; Mismatches 1; Indels
 Score 34; DB 2; Length 32;
Pred. No. 5.5;
 1; Indels
 819909
E6-III protein - human papillomavirus type 33 (fragment)
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 submitted to the EMBL Data Library, November 1996 A;Reference number: Z19184 A;Accession: T19833
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Best Local Similarity 66.7%;
Matches 6; Conservative
 Query Match
Best Local Similarity 62...
5, Conservative
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 551 İHDMVAEC 558
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 2 INDIILEC 9
 Query Match
Best Local Similarity
Matches 5; Conserv
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 C,Genetics:
A,Gene: CESP:F15D4.7
A,Map position: 2
A,Introns: 747/3
 A;Gene: CESP:C38D9.3
A;Map position: 5
A;Introns: 786/3
 RESULT 14
 RESULT 12
 RESULT 13
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Gaps

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Sequence 1, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 6, Appli Sequence 11, Appli Sequence 11, Appli Sequence 10, Appli Sequence 24, Appli Sequence 24, Appli Sequence 11, Appli

Sequence:

Run on:

Searched:

Database

Sequence 2, Appli

Sequence

Sequence 21847, A Sequence 10846, A Sequence 33593, A Sequence 205547, Sequence 194068,

Sequence Sequence Sequence

Sequence 358720,

Sequence Sequence Sequence

275411,

Sequence

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Gaps

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2643978611

Result

Length 9; Indels

us-08-170-344-7.rapb

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APPLICANT: Sinard, John J. L.
APPLICANT: Sinard, John J. L.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Diamond, David C.
APPLICANT: Lei, Xiang-Dong
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.02221
CURRENT APPLICATION NUMBER: US/10/777,053
CURRENT PLING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 60/336,968
PRIOR PLING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 979
SOFTWARE: FastSEQ for Windows Version 4.0
7 US-10-484-063-20

7 US-10-488-063-27

7 US-10-6858-324-2

7 US-10-6858-324-2

8 US-10-367-3054-1

9 US-10-307-303-1

10S-10-303-303-1

10S-10-309-771-4

10S-10-309-771-4

10S-10-309-771-1

10S-10-37-963-1

10S-10-37-963-1

10S-10-37-963-1

10S-10-476-570-1

10S-10-476-570-1

10S-10-476-570-1

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 US-10-425-115-236213
US-10-947-979-10
 100.0%; Score 49; DB 16; 100.0%; Pred. No. 1.6e+06;
 Mismatches
 ALIGNMENTS
 ; Sequence 547, Application US/10777053; Publication No. US20040132088A1; GENERAL INFORMATION:
 Human Papillomavirus 16
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 Conservative
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 Query Match
Best Local Similarity
Matches 9; Conserv
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 ; ORGANISM: Hum
US-10-777-053-547
 LENGTH:
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 June 29, 2005, 01:35:30 ; Search time 57.55 Seconds (without alignments) 60.138 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 US-10-777-053-547
US-10-837-217-547
US-10-128-711-72
US-10-133-210-280
US-10-476-570-22
US-10-476-570-23
US-10-858-384-4
US-10-858-384-4
US-10-476-570-9
US-10-476-570-9
US-10-476-570-19
US-10-177-390-6
 Total number of hits satisfying chosen parameters:
 1717557 seqs, 384547976 residues
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 Published_Applications_AA:*
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Minimum DB seq length: 0
Maximum DB seq length: 200000000
 US-08-170-344-7
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 1 TIMDIILEC 9
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 Query
Match Length
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 Scoring table:
 Perfect score:
 Score
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 1 TIHDIILEC 9
 US-10-128-711-72
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 APPLICANT: Simard, John J. L.
APPLICANT: Diamond, David C.
TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
FILE REFERENCE: MANNK.022C2
CURRENT APPLICATION NUMBER: US/10/837,217
CURRENT APPLICATION NUMBER: 10/292,413
PRIOR PILING DATE: 2004-01-07
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-11-07
SOFTWARE FREE FREE FOR WINDOWS VERSION 4.0
SEQ ID NOS: 979
LINGS DATE: DOIL NOS: 979
LINGS DATE: DOIL NOS: 979
SEQ ID NO 547
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 RESULT 3

RESULT 3

RESULT 3

Sequence 72, Application US/10128711

Publication No. US2030099654A1

GENERAL INFORMATION:

GENERAL INFORMATION:

CHESTNOT. WITHELLO, Maria A.

CHESTNOT. Robert W.

SETTE. Alessandro D.

CRLIS, Esteban

CRLIS, Esteban

CRLIS, MAN MAREN COMPOSITIONS AND METHODS FOR ELICITING

CRLIS, Esteban

CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STREET: Steuart Street Tower, One Market Plaza

CITY: San Francisco

STREET: Seleuart Street Tower, One Market Plaza

CONTRY: US

STREET: Seleuart Street Tower, One Market Plaza

CONTRY: US

STREET: Seleuart Street Tower, One Market Plaza

CONTRY: 184 PC -0.192

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MD-DS

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MD-DS

COMPUTER: IBM PC compatible

OPERATING SYSTEM: COMPATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 22-Apr-2002

APPLICATION NUMBER: US 07/935,811

FILING DATE: 27-ARR-1992

APPLICATION NUMBER: US 07/827,682
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 Length 9;
 Indels
 100.0%; Score 49; DB 16;
100.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 0;
US-10-837-217-547
; Sequence 547, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
 ORGANISM: Human Papillomavirus 16
US-10-837-217-547
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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 RESULT 5
US-10-476-570-22
US-10-476-570-22
Sequence 22, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: BOURGAULT-VILLADA, Isabelle
 Sequence 280, Application US/10133210
Publication No. US20030103964A1
GENERAL INFORMATION:
APPLICANT: Delisi, Charles
APPLICANT: Berzofesty, Jay
APPLICANT: Gulwota, Kamalakar
APPLICANT: Waccaro, Dennis
APPLICANT: Wang, Zhiping
APPLICANT: Yaccaro, Dennis
APPLICANT: Zhang, Chao
TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
TITLE OF INVENTION: COMPOSITIONS THEREOF
FILE REPREMENCE: BU-035AX
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-280
 ;
 ö
 100.0%; Score 49; DB 14; Length 10; 100.0%; Pred. No. 0.0098; tive 0; Mismatches 0; Indels
 Length 10;
 0; Indels
 Query Match
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0;
 NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPAR: (206) 467-9600
TELEPAR: (206) 623-6793
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
 CURRENT APPLICATION NUMBER: US/10/133,210
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 280
LENGTH: 10
 MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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; Sequence 4, Application US/10858384; Publication No. US20050033025A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: artificial sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match
Best Local Similarity 100..
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15 TIHDIILEC 23
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15 TIHDIILEC 23
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 US-10-858-384-4
 US-10-858-384-4
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 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
US-10-476-570-22
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 THER INFORMATION: Description of the artificial sequence: peptide E6 28-42
 Sequence 23, Application US/10476570

Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: GUILLET, Jean-Gerard

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived hereof

FILE REFERENCE: 45636-5071-US

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT FILING DATE: 2003-11-03

PRIOR FILING DATE: 2003-11-04

PRIOR FILING DATE: 2005-05-03

PRIOR FILING DATE: 2005-05-04

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 23

LENGTH: 15

LENGTH: 15
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APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver: 2.1
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 Query Match 100.0%; Score 49; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 9; Conservative 0; Mismatches 0; Indels
 RESULT 7
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
 ORGANISM: artificial sequence
 TYPE: PRT ORGANISM: artificial sequence
 1 TIMDIILEC 9
 1 TIHDIILEC 9
 US-10-476-570-23
 US-10-476-570-23
 SEQ ID NO 22
LENGTH: 15
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44 US-10-476-570-53
 ö
 OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment OTHER INFORMATION: for E6 of HPV
 ö
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, BERTARIA
APPLICANT: MAILLERE, BERTARIA
APPLICANT: MAILLERE, GERTARIA
APPLICANT: MAILLER, GERTARIA
APPLICANT: GUILLET, JOHN 'GARATILLE, Sandra
APPLICANT: GUILLET, JOHN GERTARIA
TITLE OF INVENTION: Mixture proteins and uses thereof
TITLE OF INVENTION: MAILLER, US/10/476,570
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR FILING DATE: 2003-11-04
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VONSER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 53
LENGTH: 30
THENTH: 30
THENTH: MAILLERE CHARLES AND THE CHARLES AN
 APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOUGGAULT VILLADA, ISABELLE
APPLICANT: BOUGGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: DARTICULARLY IN VACCINATION
FILE REPERENCE: 2004-06-02
PRIOR PELICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE PARENCE: 2004-06-03
SEQ ID NO 4
LENGTH: 30
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 100.0%; Score 49; DB 16; Length 30; 100.0%; Pred. No. 0.032; tive 0; Mismatches 0; Indels
 Query Match 100.0%; Score 49; DB 17; Length 30; Best Local Similarity 100.0%; Pred. No. 0.032; Matches 9; Conservative 0; Mismatches 0; Indels
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 Best Local Similarity
Matches 9; Conserv
 RESULT 13
US-10-484-063-27
 US-10-484-063-20
 US-10-177-390-6
 TYPE: PRT
 Query Match
 Query Match
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) OTHER INFORMATION: Description of the artificial sequence: peptide B6 14-46 US-10-476-570-19
 ; OTHER INFORMATION: Description of the artificial sequence: peptide B6 14-45 US-10-476-570-9
 ö
 Sequence 9, Application US/10476570

| Sequence 9, Application US/10476570
| Publication No. US20040170644A1
| GENERAL INFORMATION:
| APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
| APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
| APPLICANT: BOURGAULT-VILLADA, Isabelle
| APPLICANT: BOURGAULT-VILLADA, Isabelle
| APPLICANT: BOURGAULT-VILLADA, Isabelle
| APPLICANT: GUILLET, Jean-Gerard
| APPLICANT: GUILLET, Jean-Gerard
| TITLE OF INVENTION: Mixture of peptides derived from B6 and/or B7
| TITLE OF INVENTION: Mixture of peptides derived from B6 and/or B7
| TITLE OF INVENTION: Papillomavirus proteins and uses thereof
| TITLE OF INVENTION NUMBER: US/10/476,570
| CURRENT APPLICATION NUMBER: PC7/FR02/01533
| PRIOR FILING DATE: 2002-05-03
| PRIOR FILING DATE: 2001-05-04
| NUMBER OF SEQ ID NOS: 63
| SOFFWARE: Patentin Ver. 2.1
 GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUTU NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MOSTITUTU NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GILLEL, Jean-Gerard
TITLE OF INVENTION: MAXTILLE, Sandra
TITLE OF INVENTION: MAXTURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXTURE OF 1004/476,570
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR FILING DATE: 2003-11-04
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET. 2.1
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 100.0%; Score 49; DB 16; Length 32; 100.0%; Pred. No. 0.035; tive 0; Mismatches 0; Indels
 Sequence 19, Application US/10476570 Publication No. US20040170644A1
 TYPE: PRT
ORGANISM: artificial sequence
 ORGANISM: artificial sequence
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 16 TIHDIILEC 24
 1 TIHDIILEC 9
 US-10-476-570-9
 SEQ ID NO 9
LENGTH: 32
 SEQ ID NO 19
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 Sequence 6, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Polynuclectides by Electroporation
TITLE OF INVENTION: Polynuclectides by Electroporation
TITLE OF INVENTION: Polynuclectides by Electroporation
TITLE OF INVENTION UNMBER: US/10/177,390
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT PILING DATE: 2002-06-20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
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 100.0%; Score 49; DB 14; Length 151; larity 100.0%; Pred. No. 0.19; Conservative 0; Mismatches 0; Indels C
 100.0%; Score 49; DB 17; Length 151; 100.0%; Pred. No. 0.19;
 Indels
 0; Mismatches
 , ORGANISM: Human papillomavirus type 16
US-10-177-390-6
 ; Sequence 27, Application US/10484063; Publication No. US20050048467A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Human papillomavirus
 Best Local Similarity 100.
Matches 9; Conservative
 22 TIHDIILEC 30
 22 TIHDIILEC 30
16 TIHDIILEC 24
 1 TIMDIILEC 9
 1 TIHDIILEC 9
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HEV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REPREMENCE: UTSC:560U8
CURRENT APPLICATION NUMBER: US/10/484,063
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR PLILING DATE: 2004-01-16
PRIOR PLILING DATE: 2004-07-19
PRIOR PLILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VOF: 2.1
SOFTWARE: PATENTIN VOF: 2.1
 Sequence 2, Application US/10858384

Publication No. US20050033025A1

GENERAL INFORMATION:
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEAN-GERARD
APPLICANT: GHOPPIN, PRANCINE
APPLICANT: GHOPPIN, PRANCINE
APPLICANT: GHOPPIN, PRANCINE
APPLICANT: GHOPPIN, PRANCINE
APPLICANT: GONNAN, FRANCINE
APPLICANT: GONNAN, PRANCINE
APPLICANT: GONNENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
ITILE OF INVENTION: PARTICULARLY IN VACCINATION
ITILE OF INVENTION: DARTICULARLY IN VACCINATION
CURRENT PAPLICATION NUMBER: US/10/858,384
CURRENT PILING DATE: 2004-06-02
PRIOR PLING DATE: 199-06-03
NUMBER OF SEQ ID NOS: 24

SOSTWARE: PATENTIN VAC: 3.2
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 100.0%; Score 49; DB 17; Length 151; 100.0%; Pred. No. 0.19; tive 0; Mismatches 0; Indels (
 100.0%; Score 49; DB 17; Length 158; 100.0%; Pred. No. 0.2; ive 0; Mismatches 0; Indels
 TYPE: PRT
ORGANISM: Human papillomavirus type 16
 Sequence 16, Application US/10367057; Publication No. US20050100554A1; GENERAL INFORMATION:
APPLICANT: Cuthill, Scott; APPLICANT: Lacken, Amanda; APPLICANT: Lewin, David A.; APPLICANT: Ooi, Chean Eng
 TYPE: PRT
ORGANISM: Human Papillomavirus
US-10-858-384-2
 Best Local Similarity 100.0
Matches 9; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 22 TIHDIILEC 30
 29 TIHDIILEC 37
 1 TIMDIILEC 9
 1 TIHDIILEC 9
 RESULT 15
US-10-367-057-16
 J OKGANISH: 114
 RESULT 14
US-10-858-384-2
 LENGTH: 158
 Query Match
 SEQ ID NO 2
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TITLE OF INVENTION: Complexes and Methods of Using Same
| FILE REPERENCE: 21402-559
| CURRENT APPLICATION NUMBER: US/10/367,057
| CURRENT FILING DATE: 2003-02-14
| PRIOR FILING DATE: 2003-02-14
| NUMBER OF SEQ ID NOS: 198
| SOFTWARE: CURASeqList version 0.1
| SEQ ID NO 16
| LENGTH: 158
| TYPE: PRT
| ORGANISM: Homo sapiens
| Ouery Match
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| Cuery Match
| Cuery Match
| Cuery Match
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-64 54 1 VCPICSQKP 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
1: pir3:\*
1: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|           | Description    | E7 protein - human | E7 protein - human | ᅩ      | hypothetical prote |        | 18.2K protein - ph | in     | formate dehydrogen | protein F1504.19 [ | transcription regu | probable anti-sigm | unknown protein F1 | drought-induced pr | zinc-finger-like p | hypothetical prote | probable RING zinc | hypothetical prote | probable membrane | transcription fact | mitosis initiation | mitosis initiation | hypothetical prote | agrin precursor - | E7 protein - human | recombination prot | drought-induced pr | formamidopyrimidin | TIF1 protein - mou | hypothetical prote |
|-----------|----------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMAKIES | ID             | W7WLHS             | W7WL11             | CGHU2V | C71127             | D75036 | A40783             | S60179 | C70390             | H86477             | C69038             | C71349             | E96604             | S51478             | T45654             | AF1939             | F85016             | T01716             | S63176            | 839356             | T13648             | A38436             | T16169             | AGCH              | M7WL6              | E70428             | T01522             | 839200             | B40951             | T30114             |
|           | н ов           | 1                  |                    | ب<br>و |                    |        |                    | ώ<br>6 |                    |                    |                    |                    |                    |                    |                    |                    |                    | 9                  | -                 |                    |                    |                    |                    |                   |                    |                    | 4 2                |                    |                    | ın.                |
|           | Length         | 6                  | o                  | 1496   | 7                  | o,     | 166                | 1295   | 58                 |                    |                    |                    |                    |                    |                    | 56                 | 50                 | 206                | 28                | 644                | 695                | 708                | 1042               | 195               | σ                  | 211                | 214                | 27                 | 331                | 43                 |
| æ         | Query<br>Match | 100.0              | 83.3               | 79.6   | 75.9               | 75.9   | 75.9               | 75.9   | 74.1               | 74.1               | 74.1               | 72.2               | 72.2               |                    | 72.2               | 72.2               | 72.2               | 72.2               | 72.2              | 72.2               | 72.2               | 72.2               | 72.2               | 72.2              | 70.4               | 70.4               | 70.4               | 70.4               | 70.4               | 70.4               |
|           | Score          | 5.4                | 45                 | 43     | 41                 | 41     | 41                 | 41     | 40                 | 40                 | 40                 | 39                 | 39                 | 39                 | 39                 | 39                 | 39                 | 39                 | 39                | 39                 | 39                 | 39                 | 39                 | 39                | 38                 |                    | 38                 |                    |                    | 38                 |
|           | Result<br>No.  |                    | 8                  | е      | 4                  | S      |                    | 7      | 80                 | σ                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                | 19                 | 20                 | 21                 | 22                 | 23                | 24                 | 25                 | 26                 | 27                 | 28                 | 29                 |

B7 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Species: human papillomavirus type 11
C;pate: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 09-Jul-2004
C;Accession: A03690

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RESULT 2 W7WL11

| hypothetical prote<br>52K autoantigen Ro | glutamyl tRNA-Gln<br>hypothetical prote | NA helica<br>ligase (N | DNA ligase - Helic<br>transcription init | TIF1 protein - mou<br>hypothetical prote | hypothetical prote<br>conserved hypothet | hypothetical prote | probable cytochrom<br>small T antioen - | T anti |
|------------------------------------------|-----------------------------------------|------------------------|------------------------------------------|------------------------------------------|------------------------------------------|--------------------|-----------------------------------------|--------|
| T17306<br>A37241                         | H72274<br>T32661                        | JC5517<br>G64596       | A71916<br>F64397                         | S55259<br>B97870                         | AE0684<br>C69310                         | 890155             | T03033<br>TVVPAB                        | TVVPSS |
| 2 4                                      | 00                                      | 7 7                    | 2 4                                      | 0 0                                      | 0 0                                      | ~                  | ~ -                                     | -      |
| 468<br>475                               | 482<br>560                              | 645<br>656             | 656<br>673                               | 1051<br>54                               | 64                                       | 118                | 169                                     | 172    |
| 70.4                                     | 70.4                                    | 70.4<br>70.4           | 70.4                                     | 70.4                                     | 68.5                                     | 68.5               | 68.5<br>68.5                            | 68.5   |
| 38                                       | 38                                      | 38                     | 38<br>38                                 | 38                                       | 37                                       | 37                 | 37                                      | 37     |
| 30<br>31                                 | 332                                     | 3.4<br>5.4             | 36<br>37                                 | 8 6<br>8 7                               | 40<br>41                                 | 42                 | 4 4<br>4 3                              | 45     |

## ALIGNMENTS

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C;Species: 18-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004
C;Species: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004
C;Scession: A03688; S12367; Til428
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03688
A;Molecule type: DNA
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A;Cross-references: UNIPROT: P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g33303
B;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.
R;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.
B;Aftle: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 lax
 A;Accession: S12367
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-98 cBAR>
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
A;Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: 217014; MUID:91162763; PMID:1848319
 ö
 C;Superfamily: papillomavirus E7 protein
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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type V procollagen COOH-termin

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A;Reference number: IS9025; MUID:85216505; PMID:3858826
A;Accession: IS9025
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A;Molecule type: mRNA
A;Residues: 1003-1034 <RES>
A;Cross-references: GB:M11135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A;Note: part of this sequence were determined by protein sequencing
B;Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
J. Biol. Chem. 260, 11216-11222, 1985
A;Title: Complete primary structure of the human alpha-2 type V procollag
A;Reference number: A25374; MUID:85289337; PMID:2411731
 A;Accession: A25374
A;Molecule type: mRNA
A;Residues: 1227-1417, Tr,1419-1437, 'S',1439-1496 <MYE>
A;Kestedues: 1227-1417, Tr,1418-1437, 'S',1439-1496 <MYE>
A;Cross-references: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A;Experimental source: normal fibroblasts
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 C; Function:
 A,Cross-references: GB:MI0956; NID:g180427; PIDN:AAA52007.1; PID:g180428
A;Note: part of this sequence were determined by protein sequencing
E, Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1885
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
 C;Species: Homo sapiens (mān)
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text change 09-Jul-2004
C;Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text change 09-Jul-2004
C;Accession: A31427, A54555; B43643, A25874; I55239; I59025; A25374; A30017
R;Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
A;Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the structumber: A31427; MUID:89123368; PMID:2914927
 A; Molecule type: protein
A;Residues: 288-291, P', 293-294, X', 296-297;606, X', 608-617 <MOR>
A;Residues: 288-291, P', 293-294, X', 296-297;606, X', 608-617 <MOR>
N;Weil, D.; Bernard, M.; dargano, S.; Ramirez, F.
Nucleic Pare Res. 15, 181-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill
A;Reference number: A25874; MUID:87146331; PMID:3029669
 A;Residues: 1-463 <WOO>
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S;Superfamily: papillomavirus BT protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
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 type
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A; Residues: 1-32 <GRES
A; Residues: 1-32 <GRES
A; Residues: 1-32 <GRES
A; Residues: 1-32 <GRES
B; Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Bur. J. Biochem. 221, 987-995, 1994
A; Title: Divorsairy in the processing events at the N-terminus of type-V collagen.
A; Reference number: $43642; MUID:94237164; PMID:8181482
 Gene Expr. 1, 29-39, 1991
A,Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence
A,Reference number: A54555; MUID:92314691; PMID:1820205
A,Accession: A54555
 human papilloma virus
 A; Molecule type: mRNA; DNA
A; Residues: 398-1496 <WEI>
A; Crose-references: GB: X04758; NID: g29588; PIDN: CAA28454.1; PID: g1340175
A; Crose-references: CB: X04758; NID: g29588; PIDN: CAA28454.1; PID: g1340175
A; Experimental source: rhabdomyosarcoma cell line
R; Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, S533-5541, 1985
A; Title: Partial covalent structure of the human alpha 2 type V collagen chain.
A; Reference number: I55239; MUID: 85182703; PMID: 2985598
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 Length 98;
 Indels
 Virology 151, 124-130, 1986
A;Tille: The nucleotide sequence and genome organization of
A;Reference number: A94338; MUID:86181601; PMID:3008427
A;Accession: A03609
 Schwarz, E.; Gissmann, L.; zur Hausen, H.
 S.T.; Lee, B.S.; Hoffman, G.G.
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Pred. No.
 collagen alpha 2(V) chain precursor - human
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R, Greenspan, D.S.; Lee, S.T.; Le
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 1 VCPICSOKP
 A;Accession: A03690
A;Molecule type: DNA
A;Residues: 1-98 <DAR>
 Molecule type: mRNA
 Accession: A25874
 A; Accession: I55239
 R;Dartmann, K.;
Virology 151, 12
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RiTeipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
Affittle: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located on A;Reference number: A30017; MUID:89138450; PMID:3224983
A;Accession: A30017
 A;Molecule type: DNA
A;Residues: 1449-1463, E,,1465-1495, A' <TSI>
A;Residues: 1449-1463, E,,1465-1495, Pi NID: 4779695; PIDN: AAAS1858.1; PID: 9179696
A;Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for resid
C;Comment: Prolines and lyaines at the third position of the tripeptide repeating unit
are 5-hydroxylated and subsequently O-glycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
 A; Map position: 2431-2431
A;Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 1448/
Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), a alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues
 C. Stunction: structural component of extracellular fibrous polymer associated with certification: structural component of extracellular fibrous polymer associated with certification and plan 1(1) chain, fibrillar collagen or fibrils collagen alpha 1(1) chain, fibrillar collagen arboxyl-terminal homology C. Stuperfamily: collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology C. Keywords: collagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology C. Keywords: collagen alpha 2(V) chain #status predicted cMT>
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F;40-99/Domain: von Willebrand factor type C repeat homology cWC>
F;27-108/Region: helical
F;40-99/Domain: nonhelical
F;209-1225/Region: cell attachment (R-G-D) motif
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F;1064-1066/Region: cell attachment (R-G-D) motif
F;107-1069/Region: cell attachment (R-G-D) motif
F;1134-1125/Region: cell attachment (R-G-D) motif
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F;1134-1126/Region: cell attachment (R-G-D) motif
F;1251-1496/Domain: dibrillar collagen carboxyl-terminal propeptide #status predicted
F;227/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
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F;229,1139/Binding site: shydroxylysine (Lys) (covalent) #status predicted
F;229,1139/Allodified site: slivator fil
 F:1250-1251/Cleavage site: Glu-Asp (procollagen C-endopeptidase) #status predicted F:1259,1397/Binding site: carbohydrate (Asn) (covalent) #status predicted F:1293,1299,1325/Disulfide bonds: interchain #status predicted
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 A;Gene: GDB:COL5A2
A;Cross-references: GDB:119064; OMIM:120190
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C;Accession: A40783

K;Shich, G.J.; Charng, Y.C.; Yang, B.C.; Tu, J.; Bau, H.J.; Kuo, T.T.
Virology 185, 316-322, 1991

A;Title: Identification and nucleotide sequence analysis of an open reading frame invol
A;Title: Identification and nucleotide sequence analysis of an open reading frame invol
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A; Title: The complete genome of the hyperthermophilic bacterium Aquifex acolicus.
A; Reference number: A70300; MUID:98196666; PMID:9537320
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C.Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C.Accesaion: 860179
R.Anaya, N.; Roncero, M.I.G.
Mol. Gen. Genet. 249, 637-647, 1995
A.Title: Skippy, a retrotransposon from the fungal plant pathogen Fusarium oxysporum. A;Reference number: 860179
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A;Experimental source: retrotransposon skippy
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 Length 1295;
 formate dehydrogenase formation protein FdhE - Aquifex aeolicus
 2; Length 166;
 Length 283
 1; Indels
 Indels
 Superfamily: formate dehydrogenase accessory protein FdhB
 2;
 Score 40; DB 2;
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 75.9%;
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 74.1%;
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 837 CPTCKOKP 844
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6 CPLCOEKP 13
 2 CPICSQKP 9
 Best Local Similarity
 2 CPICSOKP
 Query Match
 RESULT 7
 RESULT 8
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 A;Cross-references: UNIPROT:073989; GB:AP000003; NID:g3236130; PIDN:BAA29877.1; PID:g325 A;Experimental source: strain 0T3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank A;Genetics: A;Gene: PHS025 C;Superfamily: pyrophosphohydrolase, MazG-related, AF0820 type
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A;Experimental source: strain Orsay
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir. M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi M.; And Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
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 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-74 <KAW>
 A40783
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C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
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 Length 74;
 Indels
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1; Mismatches
 Pred. No. 45;
1; Mismatches
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Matches 6; Conservative
 75.0%;
 Conservative
 6; Conservative
 CPVCSQTP 100
 60 VCPYCGKKP 68
 90
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 2 CPICSQKP 9
Best Local Similarity
Matches 6; Conserv
 Query Match
Best Local Similarity
 VCPYCGKKP
 1 VCPICSQKP
 1 VCPICSQKP
 82
 Matches
 RESULT 6
 RESULT 5
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probable anti-sigma F factor antagonist - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
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C;Accession: C71349
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwirson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDrisy, D.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Fille: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: C71349
A;Status; preliminary; nucleic acid sequence not shown; translation not shown
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C;Species Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96604
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hudhes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hudhes, B.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: E96604
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A;Accession: E96604
A;Accession: E96604
A;Accession: E96604
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C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S51478; S43179; S43178; M.; Giraudat, J.
Mol. Gen. Genet. 246, 10-18, 1995
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1; Mismatches (
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 72.2%;
85.7%;
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 A, Map position: 1
 A; Gene: F14G9.11
 A; Gene: TP0233
 C;Genetics:
 C;Genetics:
 RESULT 12
 RESULT 13
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 transcription regulator HypF homolog - Methanobacterium thermoautotrophicum (strain Delt C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003 C; Accession: C69038 R; Smith, D. R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G. M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID: 98037514; PMID: 9371463 A; Resession: C69038 A; Reterence number: A69000; MUID: 98037514; PMID: 9371463 A; Reseidue: 1-729 < MTH>
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CiSpecies: Arabidopsis thalian (mousper)
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 Length 729;
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2;
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Pred. No.
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 74.1%;
62.5%;
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Best Local Similarity 75.0%;
Matches 6; Conservative
 Query Match
Best Local Similarity وکیت
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5; Conservative
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 CPICGPKP 152
 167 CPVCGSKP 174
 2 CPICSQKP 9
 2 CPICSOKP 9
 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <STO>
Matches
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A; Title: Abscisic acid-dependent and -independent regulation of gene expression by programmer where sold and be seen and sold an
 RiChoisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999
A;Reference number: 223010
A;Accession: T45654
 hypothetical protein all1065 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Analy Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Cross-references: UNIPROT:Q8YXZ1; GB:BA000019; PIDN:BAB73022.1; PID:g17130411; GSPDB:C
A;Experimental source: strain PCC 7120
C;Gene: all1065
A;Gene: all1065
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N;Alternate names: protein F13112.230
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45654
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Pred. No. 43;
 Score 39; DB 2; Length 206;
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 1 VCPICSOK 8
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Best Local Similarity
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Best Local Similarity
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 1 VCPICSQKP
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A;Status: preliminary
A;Molecule type: DNA
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 1717557
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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 1717557 seqs, 384547976 residues
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Maximum Match 100%
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 OM protein - protein search, using sw model
 BLOSUM62
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 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-08-170-344-64
54
1 VCPICSQKP 9
 Published |
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 Perfect score:
 Database :
 Searched:
 Sequence:
 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description                      | Sequence 52, Appl | Sequence 71, Appl |                  | Sequence 51, Appl |                  | Sequence 76, Appl | Sequence 1, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 8, Appli |
|----------------------------------|-------------------|-------------------|------------------|-------------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| ΩĮ                               | US-10-476-570-52  | US-10-306-541-71  | US-10-751-845-69 | US-10-432-465-51  | US-10-476-570-18 | US-10-890-526-76  | US-09-728-466-1   | US-09-820-765-4   | US-09-824-017-4   | US-09-986-118A-4  | US-10-267-311-8   |
| DB                               | 16                | 16                | 17               | 15                | 16               | 16                | σ                 | σ                 | σ                 | 10                | 14                |
| %<br>Query<br>Match Length DB ID | 15                | 15                | 17               | 21                | 21               | 21                | 98                | 88                | 86                | 98                | 86                |
| %<br>Query<br>Match              | 100.0             | 100.0             | 100.0            | 100.0             | 100.0            | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             |
| Score                            | 54                | 54                | 54               | 54                | 54               | 54                | 54                | 54                | 54                | 54                | 54                |
| Result<br>No.                    | 1                 | 7                 | m                | 4                 | S                | 9                 | 7                 | ω                 | 0                 | 10                | 11                |

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Ouery Match 100.0%; Score 54; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.094; Matches 9; Conservative 0; Mismatches 0; Indels

| Sequence 8, Appli<br>Sequence 19, Appl<br>Sequence 29, Appl | 19,    | ຕ່ທີ່                              | 4,           | Sequence 1, Appl1<br>Sequence 12, Appl | 7       | ທ໌          | Sequence 8, Appli | 4      | ä     | ä                | 12,              | 35,                 | Sequence 35, Appl | 1, 7     | Sequence 8, Appli | 'n    | Sequence 8, Appli | 157               | 158,              | 12,              | 12               | 16                | ٦,     | 33      | Sequence 33, Appl | 25        | 25               |
|-------------------------------------------------------------|--------|------------------------------------|--------------|----------------------------------------|---------|-------------|-------------------|--------|-------|------------------|------------------|---------------------|-------------------|----------|-------------------|-------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|--------|---------|-------------------|-----------|------------------|
| US-10-177-390-8<br>US-10-201-764-19<br>US-10-392-113-29     | 10-654 | US-10-772-988-3<br>US-10-479-541-5 | -10-042-526A | US-10-65/-399-1<br>US-10-858-384-12    | 10-484- | 10-343-448- | US-10-6/9-956-8   | 10-472 | 2     | US-10-267-311-12 | US-10-679-956-12 | -10 - 267 - 311 - 3 | -10-679-956-3     | -10-000- | US-10-000-903-8   | 7     | -10-899           | US-10-751-845-157 | US-10-751-845-158 | US-10-000-903-12 | US-10-899-771-12 | US-10-751-845-160 | 19-367 | -10-267 | -10-              | -10-267-3 | US-10-679-956-25 |
| 14<br>14                                                    | 15     | 16                                 | 17           | 17                                     | 17      | 11          | 17                | 16     | 17    | 14               | 11               | 14                  | 11                | 13       | 13                | 11    | 11                | 11                | 11                | 13               | 17               |                   | 0      | 14      | 17                | 14        | 11               |
| 8 8 8<br>8 8 8                                              | 866    | 8 6<br>6 6                         | 8 6          | 9 6<br>5 8                             | 86      | 86          | α<br>ο σ          | 111    | 117   | 121              | 121              | 198                 | 198               | 220      | 220               | 220   | 220               | 236               | 237               | 239              | 239              | 261               | 566    | 295     | 295               | 324       | 324              |
| 100.0                                                       | 100.0  | 100.0                              | 100.0        | 100.0                                  | 100.0   | 100.0       | 0.00              | 100.0  | 100.0 | 100.0            | 100.0            | 100.0               | 100.0             | 100.0    | 100.0             | 100.0 | 100.0             | 100.0             | 100.0             | 100.0            | 100.0            | 100.0             | 100.0  | 100.0   | 100.0             | 100.0     | 100.0            |
| 7 7 Y                                                       | 5,42   | 5 4<br>7                           | 54.          | 54                                     | 54      | 54          | 5 4<br>4 4        | 5, 4,  | 54    | 54               | 54               | 54                  | 54                | 24       | 54                | 54    | 54                | 54                | 54                | 54               | 54               | 54                | 54     | 54      | 54                | 54        | 54               |
| 12<br>13<br>14                                              | 15     | 17                                 | 19           | 21                                     | 22      | 23          | 4. C              | 26     | . 22  | 28               | 53               | 30                  | 31                | 32       | 33                | 34    | 35                |                   | 37                | 38               | 39               | 40                | 41     | 42      | 43                | 44        | 45               |

## ALIGNMENTS

```
US-10-476-570-52

Sequence 52, Application US/10476570

Sequence 52, Application No. US200401706441

GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: BOUYGLUE. BOUYGLUE. Sandra
APPLICANT: BOUYGRULT-VILLADA, Isabelle
APPLICANT: BOUYGRULT-NORATILLE, Sandra
APPLICANT: BOUYGRULT-NORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides current and uses thereof
TITLE OF INVENTION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: ER 01 05980
PRIOR PILING DATE: 2001-05-03
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 15
TYPE: PRT
ORGANISM: artificial sequence
FRATURE:
FRATURE:
COTHER INFORMATION: Description of the artificial sequence: peptide E7 84-98
US-10-476-570-52
```

```
1 VCPICSQKP
 US-10-476-570-18
 US-10-476-570-18
 US-10-432-465-51
 SEQ ID NO 18
LENGTH: 21
 Query Match
 RESULT 6
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 Sequence 69, Application US/10751845

| Sequence 69, Application US/10751845
| Publication No. US20050100928A1
| GENERAL INFORMATION:
| APPLICANT: Hediey, Mary Lynne
| APPLICANT: Chicz, Roman M.
| TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITORE
| FILE REFERENCE: 0819-013001
| CURRENT APPLICATION NUMBER: US/10/751,845
| CURRENT APPLICATION NUMBER: US/09/664,225
| PRIOR FILING DATE: 2000-08-18
| PRIOR FILING DATE: 1999-112-09
| PRIOR FILING DATE: 1999-112-09
| PRIOR FILING DATE: 1999-09-16
| NUMBER OF SEQ ID NOS: 163
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 69
 Gaps
 Gaps
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 ..
0
 Length 17;
 Length 15;
 Query Match 100.0%; Score 54; DB 17; Length 1 Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels
 0; Indels
 100.0%; Score 54; DB 16; 100.0%; Pred. No. 0.094;
 0; Mismatches
 Sequence 71. Application US/10306541

Publication No. US20040171081A1

GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Mittelman, Abraham
TITLE OF INVENTION: Improved Antigens
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR PILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8:0 for Windows
SEQ ID NO 71
LENGTH: 15
 RESULT 4
US-10-432-465-51
; Sequence 51, Application US/10432465
 , ORGANISM: Human Papilloma virus
US-10-751-845-69
 TYPE: PRT
CRGANISM: human papillomavirus
US-10-306-541-71
 Query Match
Best Local Similarity 100..
 7 VCPICSQKP 15
 VCPICSOKP 15
 9 VCPICSOKP 17
 σ
 1 VCPICSOKP 9
 US-10-306-541-71
 g
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GENERAL INFORMATION:

APPLICANT: Nieland, John
APPLICANT: Nieland, John
APPLICANT: Kather, Angela
APPLICANT: Kather, Angela
TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/077001
CURRENT APPLICATION NUMBER: US/10/432,465
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
 OTHER INFORMATION: Description of the artificial sequence: peptide E7 78-98
 ö
 ö
 Sequence 18 Application US/10476570

Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLERE, Bernard

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: MAXURE of peptides derived from E6 and/or E7

TITLE OF INVENTION: MAXURE of peptides derived from E6 and/or E7

TITLE OF INVENTION: MAXURE US/10/476,570

CURRENT FELING DATE: 2003-11-05

PRIOR FILING DATE: 2003-11-05

PRIOR FILING DATE: 2003-11-05

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SED TO NO. 18
 0; Gaps
 Gaps
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0
 100.0%; Score 54; DB 16; Length 21; 100.0%; Pred. No. 0.13; tive 0; Mismatches 0; Indel8
 100.0%; Score 54; DB 15; Length 21; 100.0%; Pred. No. 0.13;
 0; Indels
 NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 21
 ö
 TYPE: PRT
ORGANISM: Human papillomavirus
 TYPE: PRT
ORGANISM: artificial sequence
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 Best Local Similarity 100
Matches 9; Conservative
 13 VCPICSOKP 21
 13 VCPICSOKP 21
 1 VCPICSQKP 9
```

```
FORMULATIONS AND METHODS OF USE
 APPLICATION NUMBER: US/09/824,017
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4
 NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
 ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W
 TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
 TELECOMMUNICATION INFORMATION
 COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 DALIGATION NO. CENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
 Sequence 4, Application US/09824017
Publication No. US20020197668A1
 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
 ;
 CURRENT APPLICATION DATA:
 PRIOR APPLICATION DATA
 CITY: Washington
 INFORMATION FOR SEQ ID NO:
 Conservative
 90 VCPICSOKP 98
 Query Match
Best Local Similarity
 STATE: D.C
 US-09-824-017-4
 RESULT 9
 셤
 APPLICANT: Nieland, John
TITLE OF INVENTION: The Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE OF INVENTION: Therapy
FRIOR APPLICATION NUMBER: US/09/980,177
FRIOR APPLICATION NUMBER: US/09/980,177
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FASTESQ for Windows Version 4.0
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 100.0%; Score 54; DB 16; Length 21; 100.0%; Pred. No. 0.13;
 100.0%; Score 54; DB 9; Length 98; 100.0%; Pred. No. 0.51;
 HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 0; Indels
 APPLICANT: Fisher, Christopher
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
 0; Indels
 Mismatches
 Mismatches
 ORGANISM: Human papillomavirus type 16
 Sequence 76, Application US/10890526
Publication No. US20040258708A1
 TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
 ublication No. ...GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
 Sequence 1, Application US/09728466
Patent No. US20010029022A1
GENERAL INFORMATION:
 Sequence 4, Application US/09820765
Publication No. US20020039584A1
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 9; Conservative
 9; Conservative
 VCPICSOKP 21
 90 VCPICSOKP 98
 1 VCPICSQKP 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 Best Local Similarity
Matches 9; Conser
 GENERAL INFORMATION
 US-10-890-526-76
 US-09-728-466-1
 SEQ ID NO 1
LENGTH: 98
 13
 Query Match
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Gaps
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COUNTY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001

CLASSIFTCATION : UNANOWN>
PRIOR APPLICATION DATA:
 Length 98;
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
 Indels
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 FORMULATIONS AND METHODS OF USE
 100.0%; Score 54; DB 9; 100.0%; Pred. No. 0.51;
 NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
 APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
 Mismatches
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Indels

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Sequence 8, Application US/10267311

Sequence 8, Application US/10267311

Sequence 10. US20030050469A1

GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO

TITLE OF INVENTION INDUEST: US/09/613,303

FILE REFERENCE: 2002-10-0

CURRENT FILING DATE: 2002-10-0

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 1099-07-08

PRIOR FILING DATE: 1099-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PASTESEQ for Windows Version 4.0

LUMBER OF SEQ ID NOS: 55

 100.0%; Score 54; DB 14; Length 98; 100.0%; Pred. No. 0.51;
100.0%; Pred. No. 0.51;
tive 0; Mismatches
 0; Mismatches
 ; OTHER INFORMATION; fusion sequence US-10-267-311-8
 Query Match
Best Local Similarity 100.0%;
Marches 9; Conservative (
 TYPE: PRT
ORGANISM: Artificial Sequence
 TYPE: PRT
ORGANISM: Artificial Sequence
 Best Local Similarity 100.
Matches 9; Conservative
 Best Local Similarity 100.
Matches 9; Conservative
 90 VCPICSQKP 98
 90 VCPICSOKP 98
 1 VCPICSQKP 9
 1 VCPICSOKP 9
 1 VCPICSQKP 9
 US-10-177-390-8
 US-10-177-390-8
 Query Match
 FEATURE:
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 Gaps
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 Length 98;
 100.0%; Score 54; DB 9; Length 98; 100.0%; Pred. No. 0.51; ative 0; Mismatches 0; Indels
 Sequence 4, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
APPLICANT: HALLEK, Michael
TITLE OF INVENTION: PAPILLOWA VIRUS CAPSOWERE VACCINE
FORMULATIONS AND METHODS OF USE
 DB 10;
 FILING DATE: 1998-02-0
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 aming acids
 100.0%; Score 54;
 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4
 TOPOLOGY: linear;
MOLECULE TYPE: procein;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-986-118A-4
 STREET: 3000 K Street, N.W. CITY: Washington
 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 98 amino acids TYPE: amino acid
 INFORMATION FOR SEQ ID NO: 4:
 Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 NUMBER OF SEQUENCES:
 90 VCPICSOKP 98
 1 VCPICSOKP 9
 US-09-986-118A-4
 Query Match
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Sequence (%) Application US/10177390

Publication No. US20030143743A1

GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Autwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynuclectides by Electroporation
TITLE OF INVENTION: Polynuclectides by Electroporation
FILE REFERENCE: 02105040/JH/ml)
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 8
LENGTH: 98
 Gaps
 OTHER INFORMATION: Description of Artificial Sequence: fragment of OTHER INFORMATION: human papilloma virus type 16 B7 gene
 ó
 100.0%; Score 54; DB 14; Length 98; 100.0%; Pred. No. 0.51; tive 0; Mismatches 0; Indels
```

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US-10-654-129-4
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Sequence 19, Application US/10201764

Publication No. US20030166140A1

GENERAL INFORMATION:
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
 TITLE OF INVENTION: IMMUNE RESPONSE
 FILE REFERENCE: TBA
 CURRENT PILLING DATE: 2002-07-22
 FRIOR PILLING DATE: 2000-05-05
 FRIOR PILLING DATE: 1999-05-06
 ö
 Gaps
 Gaps
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 Sequence 29, Application US/10392113

Publication No. US20030224993A1

GENERAL INFORMATION:
APPLICANT: Land, Hartmut
APPLICANT: Land, Hartmut
APPLICANT: Deleu, Laurent
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
FILE REFERENCE: 21108.000533
CURRENT FAPLICATION NUMBER: 60/365,078
PRIOR APPLICATION NUMBER: 60/365,078
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 45

NUMBER OF SEQ ID NOS: 45
 ; OTHER INFORMATION: Description of Artificial Sequence:/Note = ; OTHER INFORMATION: Synthetic Construct US-10-392-113-29
 100.0%; Score 54; DB 15; Length 98; 100.0%; Pred. No. 0.51; ative 0; Mismatches 0; Indels
 Length 98;
 . 0.51;
-haa 0; Indels
 100.0%; Score 54; DB 14; 100.0%; Pred. No. 0.51;
 0; Mismatches
 TYPE: PRT
ORGANISM: Human papillomavirus type E7
 TYPE: PRT
ORGANISM: Artificial Sequence
 9; Conservative
 Conservative
 90 VCPICSOKP 98
 1 VCPICSOKP 9
 Best Local Similarity
Matches 9; Conserv
 Query Match
Best Local Similarity
Matches 9; Conserv
 US-10-392-113-29
 US-10-201-764-19
 SEQ ID NO 29
LENGTH: 98
 Query Match
 LENGTH:
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Gaps
 ö
 CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
 100.0%; Score 54; DB 15; Length 98; 100.0%; Pred. No. 0.51; tive 0; Mismatches 0; Indels
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCII FORMULATIONS AND METHODS OF USE
 FILING DATE: 04-Sep-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE: 03-Apr-2001
APPLICATION NUMBER: 09/026,896
FILING DATE: 03-Apr-2001
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 31,298
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 Search completed: June 29, 2005, 05:48:12
Job time: 53.8517 secs
 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
Sequence 4, Application US/10654129
Publication No. US20040081661A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
 (202) 672-5399
 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
 NUMBER OF SEQUENCES: 28
 INFORMATION FOR SEQ ID NO: 4
 Query Match
Best Local Similarity 100...
 TELEFAX:
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90 VCPICSOKP 98

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Sequence Sequence Sequence

Sequence Sequence

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Sequence Sequence Sequence Sequence

Sequence

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Sequence Sequence

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Sequence

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APPLICANT: CLEMAN, NWEE-MING
TITLE OF INVENTION: MYMEF-MING
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARMATER
STATE: FLORIDA
CONDUTRY: U.S.A.
COMPUTER: FLORIDA
COMPUTER: TIM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: MACOSOCE WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
RIGING DATE: ASCOLATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE: ATTORNEY INFORMATION:
NAME: LOUISE A. FOULCH
REGISTRATION NUMBER: 37,133
FURDER APPLICATION NUMBER: 37,133
FURD
US-09-485-885-8

US-09-485-885-12

US-08-485-885-12

US-08-889-666-20

US-08-66-20

US-08-75-776-20

US-08-776-20

US-08-117-083-9

US-08-860-165-10

US-09-359-382-10

US-09-367-311-33

US-09-511-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-33

US-09-613-303-35

US-09-613-303-25
 Score 54; DB 2;
Pred. No. 0.025;
 US-09-485-885-14
 ALIGNMENTS
 REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3820
TELEFAX: 813-538-3820
 ; Sequence 50, Application US/08934915; Patent No. 5932412; GENERAL INFORMATION: APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA APPLICANT: CHENG, HWEE-MING
 100.0%;
 : 21 amino acids
amino acid
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acide
 MOLECULE TYPE: peptide
 linear
 Query Match
Best Local Similarity
 100.0
100.0
100.0
 TOPOLOGY:
 US-08-934-915-50
 US-08-934-915-50
 $\frac{1}{4} \frac{1}{4} \frac
 Sequence 50, Appl
Sequence 157, App
Sequence 76, Appl
Sequence 5, Appli
 Appli
Appl
Appli
 Appl
 Appl
 Appli
 Sequence 6, Appli
Sequence 42, Appl
Sequence 1, Appli
 June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
 US-08-934-915-50

US-08-934-915-157

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US-08-405-54

US-08-075-5410-42

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Match Length
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Maximum DB
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US-09-486-394-5
; Sequence 5, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT HOPEI, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; TITLE OF INVENTION NUMBER: US/09/486,394
; CURRENT FILING DATE: 1998-00-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
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 0; Indels
 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES
 SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/03601
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2001-11-29
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 76
LENGTH: 21
 0; Mismatches
 0; Mismatches
 TYPE: PRT ORGANISM: Human papillomavirus type 16
 TYPE: PRT
ORGANISM: Human papillomavirus type 16
 Sequence 54, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETI
TITLE OF INVENTION: PAPILLOM
TITLE OF INVENTION: 11, 16,
TITLE OF INVENTION: DIAGNOSTITLE OF INVENTION: USEFUL I
 NAME/KEY: PEPTIDE
LOCATION: (1)..(28)
OTHER INFORMATION: E7 peptide.
US-09-486-194-5
 CHENG, HWEE-MING
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 Best Local Similarity 100.
Matches 9; Conservative
 20 VCPICSOKP 28
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 1 VCPICSQKP 9
 1 VCPICSQKP 9
 US-09-980-177A-76
 RESULT 5
US-08-934-915-54
 Query Match
 FEATURE:
 셤
 8
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 8
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jochmus, Ingrid
APPLICANT: Nieland, John
TITLE OF INVENTION: Cytocoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and
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 DB 2; Length 21;
 Query Match 100.0%; Score 54; DB 2; Length 21
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels
 Indels
 APPLICANT: DILLINER, JOAKIM
APPLICANT: DILLINER, LENA
APPLICANT: CHENG, HWEE-WING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
 ADDRESSEE:
CORRESPONDENCE AUDRESS:
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE: LOUISE A. FOULCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION NUMBER: 1946.6
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 US-09-980-177A-76; Sequence 76, Application US/09980177A; Patent No. 6838084
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Patent No. 5932412
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 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
 9; Conservative
 MOLECULE TYPE: peptide
 13 VCPICSOKP 21
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 1 VCPICSOKP 9
 1 VCPICSQKP 9
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 linear
 GENERAL INFORMATION:
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 GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FERZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
 COMPUTER: USA

ZIP: 13103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
 SSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. I: 1601 MARKET STREET, 36TH FLOOR PHILADELPHIA
 US-08-075-541D-42; Sequence 42, Application US/08075541D; Patent No. 6183745
 REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION: 215-567-2020
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Matches 9; Conservative C
 REFERENCE/DOCKET NUMBER:
 TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 aming acids
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
 single
 CITY: PHILADELPHIA STATE: PENNSYLVANIA
 90 VCPICSQKP 98
 1 VCPICSQKP 9
 Query Match
Best Local Similarity
Matches 9; Conserva
 amino acid
 linear
 STRANDEDNESS:
 COUNTRY: USA
 US-08-406-248-6
 STREET:
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 100.0%; Score 54; DB 2; Length 30; Conservative 0; Mismatch.
 ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer STREET: 200 State Street CITY: Boston
 Sequence 6, Application US/08406248

Patent No. 573618

GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusme
 ZIP: 02109
COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRAFICATION SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
 PRIOR APPLICATION 1333
PRIOR APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
 CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
 54:
 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
 TELEFAX: 813-538-3820
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 22 VCPICSOKP 30
 linear
 Query Match
Best Local Similarity
Matches 9; Conserv
 USA
 FILING DATE:
 STATE: MA
COUNTRY: US
 TOPOLOGY:
 US-08-406-248-6
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COUNTY: U.S.A.

COUNTY: U.S.A.

CONDUIER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,764

FLING DATE: 30-Mar-2001

CLASSIFICATION: CURKNOWN>
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100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
 100.0%; Score 54; DB 3; Length 98; 100.0%; Pred. No. 0.11; tive 0; Mismatches 0; Indels
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
 PRIOR APPLICATION DATA:
APPLICATION UNDBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANderCock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
 TOPOLOGY: linear MOLECTLE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-820-764-4
 NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
 RESUL: 1. C. Sequence 4, Application US/09820764
; Sequence 4, Application US/09820764
; Patent No. 6352866
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
 %Sogrand & Application US/09613303

Sequence 8, Application US/09613303

Sequence No. 6495347

SERREAL INFORMATION:

APPLICANT: Siegel, Marvin
 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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Matches 9; Conservative
 ; MOLECULE TYPE: protein US-08-944-368A-4
 90 VCPICSQKP 98
 90 VCPICSOKP 98
 1 VCPICSOKP 9
TOPOLOGY: linear
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 Query Match 100.0%; Score 54; DB 3; Length 98; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels
 APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
FRICH APPLICATION NUMBER: 09/382,616
FRICH FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
 US-08-944-368A-4

Sequence 4, Application US/08944368A

Patent No. 6228368

GENERAL INFORMATION:
TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
TITLE OF INVENTION: Formulations and Methods of Use
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
 ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSE: Borun STRET: 233 South Wacker Drive, 6300 Sears Tower CITY: Chicago STATE: 111inois COUNTRY: United States of America ZIP: 6066-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: PC-DOS/MS-DOS SOFTWARE: TBM PC COMPATIBLE COMPUTER: DATE PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING NORTH DATE: PATENT DATE:
 27013/34028
 CLASSIFICATION: 424
ATTORNEY/AGENT UNFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
 US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
 TYPE: PRT ORGANISM: Papillomavirus sylvilagi
 TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHRAACTER.STICS:
LENGTH: 98 amino acids
TYPE: amino acid
 90 VCPICSOKP 98
 90 VCPICSOKP 98
 1 VCPICSOKP 9
 GENERAL INFORMATION:
 FILING DATE:
 US-09-382-616A-1
 SEQ ID NO 1
LENGTH: 98
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 RESULT 14
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. 6641994
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: Fisher, Christopher
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
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 100.0%; Score 54; DB 4; Length 98; 100.0%; Pred. No. 0.11;
 0; Indels
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-No. 6562351-2001
CLASSIFICATION: AUNKNOWN>
 100.0%; Score 54; DB 4; 100.0%; Pred. No. 0.11;
 FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
 0; Mismatches
 0; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 TELEPHONE: (202) 672-5300
 TYPE: PRT ORGANISM: Papillomavirus sylvilagi
 (202) 672-5399
 ; Sequence 4, Application US/09824017
 TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
 NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
 Query Match
Best Local Similarity 100.º
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 Query Match
Best Local Similarity 100..
 TYPE: amino acid
 90 VCPICSOKP 98
 90 VCPICSQKP 98
 1 VCPICSQKP 9
 1 VCPICSOKP 9
 US-09-986-118A-4
 RESULT 15
US-09-824-017-4
 US-09-728-466-1
 SEQ ID NO 1
LENGTH: 98
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 Sequence 19, Application US/09566420

Patent No. 6500641

GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
ITILE OF INVENTION: IMMUNE RESPONSE
ITILE OF INVENTION: IMMUNE RESPONSE
CURRENT APPLICATION NUMBER: US/09/566,420
CURRENT PILING DATE: 2000-05-05
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 98
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR PRILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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 100.0%; Score 54; DB 4; Length 98; 100.0%; Pred. No. 0.11;
 0; Indels
 TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VA
 0; Mismatches
) ORGANISM: Human papillomavirus type E7
US-09-566-420-19
 NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSES: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
 ; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-8
 Sequence 4, Application US/09986118A Patent No. 6562351 GENERAL INFORMATION:
 APPLICANT: BURGER, Alexander HALLEK, Michael
 TYPE: PRT
ORGANISM: Artificial Sequence
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 90 VCPICSOKP 98
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 1 VCPICSQKP 9
 1 VCPICSOKP
 US-09-566-420-19
 RESULT 13
US-09-986-118A-4
 SEQ ID NO 8
LENGTH: 98
 TYPE: PRT
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GENERAL INCORMATION:
GENERAL INCORMATION:
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMILATIONS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
GITY: Washington
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTING SYSTEM: US/09/824,017
FILING DATE: 1030-00-20
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1930-00-20
ATTORNEY/AGENT INTERMATION:
MANE: SANGETORYATION:
TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE TYPE: amino acids
TYPE: amino acids
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TYPE: abscribtion iscolein
SEGUENCE TYPE: protein
 Query Match
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-09-359-382-10
US-09-359-382-10
US-09-485-885-4
US-09-485-885-6
US-09-485-885-10
US-09-485-885-10
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US-09-485-885-10
US-09-485-885-10
US-09-976-591-989
US-08-934-915-159
 Total number of hits satisfying chosen parameters:
 513545 seqs, 74649064 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 seq length: 0
seq length: 200000000
 US-08-170-344-7
49
 1 TIMDIILEC 9
 Length
 1164
1164
20
111
 Copyright
 Query
Match

 Title:
Perfect score:
 Scoring table:
 Score
 Minimum DB
Maximum DB
 Database :
 Sequence:
 Searched:
 Run on:
 Result
No.
 222
222
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| ٧.,                 | Sequence 13381, A    | Sequence 2, Appli | Sequence 12, Appl | Sequence 12, Appl | Sequence 12, Appl | Sequence 573, App  | 60201               | Sequence 29181, A    | Sequence 5486, Ap   | Sequence 112, App | Sequence 22434, A    | Sequence 44745, A   | Sequence 15186, A    |                 | Sequence 9, Appli |                  |                     |
|---------------------|----------------------|-------------------|-------------------|-------------------|-------------------|--------------------|---------------------|----------------------|---------------------|-------------------|----------------------|---------------------|----------------------|-----------------|-------------------|------------------|---------------------|
| US-09-270-767-48825 | US-09-489-039A-13381 | US-09-638-937-2   | US-08-426-509A-12 | US-08-232-545-12  | PCT-US95-05008-12 | US-08-159-339A-573 | US-09-270-767-60201 | US-09-252-991A-29181 | US-09-107-532A-5486 | US-09-266-965-112 | US-09-248-796A-22434 | US-09-270-767-44745 | US-09-248-796A-15186 | US-09-527-073-2 | US-08-448-196A-9  | US-09-785-381-11 | US-09-949-016-11498 |
| 4.                  | 4                    | 4                 | m                 | 4                 | Ŋ                 | ٣                  | 4                   | 4                    | 4                   | 4                 | 4                    | 4                   | 4                    | 4               | Н                 | 4                | 4                   |
| 111                 | 266                  | 374               | 536               | 536               | 536               | 10                 | 217                 | 227                  | 305                 | 343               | 343                  | 361                 | 512                  | 520             | 290               | 780              | 803                 |
| 69.4                | 69.4                 | 67.3              | 67.3              | 67.3              | 67.3              | 65.3               | 65.3                | 65.3                 | 65.3                | 65.3              | 65.3                 | 65.3                | 65.3                 | 65.3            | 65.3              | 65.3             | 65.3                |
| 34                  | 34                   | 33                | 33                | 33                | 33                | 32                 | 32                  | 32                   | 32                  | 32                | 32                   | 32                  | 32                   | 32              | 32                | 32               | 32                  |
| 58                  | 59                   | 30                | 31                | 32                | 33                | 34                 | 35                  | 36                   | 37                  | 38                | 39                   | 40                  | 41                   | 42              | 43                | 44               | 45                  |

## ALIGNMENTS

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US-08-197-484-72

US-GRUENEAL TO (1991)

Betent No. 641991

Betent No. 641991

CREWERAL INFORMATION:

APPLICANT: CHESTANT, ROBDERT W.

APPLICANT: CHESTANT, ROBDERT W.

APPLICANT: CHESTANT, ROBDERT W.

APPLICANT: CHESTANT, ROBDERT W.

APPLICANT: CHESTANT CTL IMMUNITY

NUMBER OF SOURNES: 133

CORRESPONDER EADRESS:

ADDRESSED: Townsend and Townsend Khourie and Crew
STREE: California

CORNERS: Townsend and Townsend Khourie and Crew
STRATE: California

CONDENTS: Elegant Street Tower, One Market Plaza

CITY: San Francisco

CITY: San Francisco

STRATE: California

CONDUTER: Internia

CARSTILICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

FILING DATE: 25-AUG-1992

RICH APPLICATION NUMBER: US 07/817,491

FILING DATE: 25-AUG-1992

FILING DATE: 25-AUG-1991

RICH APPLICATION NUMBER: US 07/817,688

FILING DATE: 25-AUG-1991

APPLICATION NUMBER: US 07/817,688

FILING DATE: 25-AUG-1991

APPLICATION NUMBER: US 07/827,682

FILING APPLICATION DATA:

APPLICATION NUMBER: US 07/817,491

FILING DATE: 25-AUG-1991

APPLICATION NUMBER: US 07/817,688

FILING DATE: 25-AUG-1991

APPLICATION NUMBER: US 07/827,689

FILING DATE: 25-AUG-1991

APPLICATION NUMBER: US 07/827,680

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RESULT 4
US-07-909-122-3
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APPLICANT: VERWAERDE, CLAUDIE
APPLICANT: USRWAERDE, CLAUDIE
TITLE OF INVENTION: LIPPOEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: US/09/601,729
CURRENT APPLICATION NUMBER: PCT/FR99/00259
FRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE PACENTIN VET: 2.1
SOFTWARE PACENTIN VET: 2.1
SEQ ID NO 273
LENGTH: 10
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                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: peptide
US-09-601-729-273
                                                                                                                                                                                                         ô
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PAPE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 49; DB 4; Length 10; 100.0%; Pred. No. 0.004; ative 0; Mismatches 0; Indels
                                                                                                                                                         Query Match 100.0%; Score 49; DB 4; Length 10 Best Local Similarity 100.0%; Pred. No. 0.004; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 72, Application PC/TUS9502121 GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273, Application US/09601729
Patent No. 6683052
PADENERAL INFORMATION:
APPLICANT: THIAM, KADER
APPLICANT: ANIRAULT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: GRAS-LAGSE, HELENE
APPLICANT: LOING, ESTELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                          TOPOLOGY: unknown ; TOPOLOGY: unknown ; MOLECULE TYPE: peptide US-08-197-484-72
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                       TYPE: amino acid
STRANDEDNESS: un
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US-09-601-729-273
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Patent No. 5415995;
GENERAL INFORMATION:
APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALESKY, JOEL M.
TITLE OF INVENTION: DIACNOSTIC PEPTIDES OF HUMAN PAPILLOMA
TITLE OF INVENTION: VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 49; DB 5; Length 10; 100.0%; Pred. No. 0.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alco
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
PILING DATE: 19920706
CURSIFICATION: STORMENT APPLICATION: STORMENT APPLICATI
PRIOR AFFLIATION NUMBER: US 08/197,484
PRIOR AFPLICATION DATA:
PRIOR AFPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR AFPLICATION DATA:
APPLICATION DATA:
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR AFPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
REGISTRATION NUMBER: 31,990
TELECOMMUNICATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REFERENCE/DOCKET NUMBER: 28600-20105.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 431-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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PCT-US95-02121-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TIMDIILEC 9
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APPLICANT: BOURGABLY VILLADA, ISABELLE
APPLICANT: BOURGABLY VILLADA,
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONIAN, FPANCINE
APPLICANT: CONIAN, FPANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 A0 INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR PLING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 30
LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-390-027-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 49; DB 4; Length 30; 100.0%; Pred. No. 0.013;
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100.0%; Score 49; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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; Sequence 6, Application US/09390027
; Patent No. 6235523
; GENERAL INFORMATION:
; APPLICANT: GALEWCZYK, Diane M.
; APPLICANT: PERSSON, Roy
; APPLICANT: TAO, Shi-xian
; APPLICANT: TARTAGLIA, James
; APPLICANT: MOINGEON, Phillipe
APPLICANT: MOINGEON, Phillipe
; APPLICANT: MOINGEON, Phillipe
; APPLICANT: MOINGEON, Phillipe
; APPLICANT: MOYINSKI, Benjamin
; TITLE OF INVENTION: TREATMENT OF CERVICAL
; FILE REFERENCE: 1038-982 MIS: ib
; CURRENT APPLICATION NUMBER: uS/09/390,027
; CURRENT FILING DATE: 1998-09-03
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO SEQ ID NOS: 2.1
; SEQ ID NO SEQ ID NOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                          Sequence 4, Application US/09980523A
Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4
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                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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100.0%; Score 49; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08363586
Patent No. 5629161
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: GISSMann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF SEQUENCES:
AUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dunner
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER: ENDY disk
COMPUTER: THOUSY disk
COMPUTER: TH
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APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-UUL-1991
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-UUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-TELECHONE: 202-408-4000
TELECHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLLGY: linear
US-07-909-122-3
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amino acid
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TIHDIILEC 14
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US-08-363-586-4
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sequence 4, Application US/08316239B; Patent No. 5679509; GENERAL INFORMATION:
                                                                                                                                   not relevant
(703) 817-9453
                                                                                     LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                           not relevant
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                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
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Matches 9; Conserv
TELEPHONE:
                                                                                                                                                        TOPOLOGY:
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US-08-316-239B-4
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Matches
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APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Jagtiani & Associates
STREET: 612 Rocky Way Court
CITY: Centreville
                                                                                                                                                                           APPLICANT: CHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FRANCINE
APPLICANT: FRANCINE
APPLICANT: FRENES, ESTELLE
ITILE OF INVENTION: PROTEINE OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PROTEINE OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PROTEINE OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION: PROTEINE OF HPV, THEIR PRODUCTION AND THEIR USE
ITILE OF INVENTION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: PO27/FR00/01513
FRIOR APPLICATION NUMBER: FR 99/07012
FRIOR APPLICATION NUMBER: FR 99/07012
FRIOR APPLICATION NUMBER: FR 99/07012
FRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE PATENT OF VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: US/08/316,239B FILING DATE: 30-SEP-1994
TORNEVALORICATION: 435
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                                                                                                        Sequence 2, Application US/09980523A Patent No. 6783763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08316239B Patent No. 5679509
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NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNM
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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50 TIHDIILEC 58
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US-08-316-239B-3
                                                                                          US-09-980-523A-2
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APPLICANT: Wheeler, Cosette M.
APPLICANT: Washington, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES:
ADDRESSEB: Jagtiani & Associates
STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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א Match 100.0%; Score 49; DB 1; Length 162;
Local Similarity 100.0%; Pred. No. 0.073;
1es 9; Conservative 0; Mismatches הדיריר.
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CUMTRY: USA

IP: 20120-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,239B

FILING DATE: 30-5EP-1994

CLASSI FLOATION: 435

ATTORNEY/AGENT INFORMATION:

NAMM: Jagitani, Ajay A.

REGISTRATION NUMBER: UNME-0001

TELECHONUNICATION INFORMATION:

TELECHONOMINICATION INFORMATION:

TELECHONOMINICATION INFORMATION:

TELECHONOMICATION INFORMATION:

TELECHONOMIC
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Sequence 10, Application US/08117083
Patent No. 5719054
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 TIHDIILEC 38
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CTHER INFORMATION:
CTHER INFORMATION:
US-08-117-083-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-08-860-165-10
US-08-117-083-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/09359382

Sequence 14, Application US/09359382

Sequence 15.06597

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: COX, John Cooper

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT PILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-12-20

EARLIER PILING DATE: 1997-12-20

SOFTWARE: PALENTIN VORSE: 20

SOFTWARE: PALENTIN VORSE: 20

SEQ ID NO 14

ILENGTH: 172
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         US-08-860-165-14

Sequence 14, Application US/08860165A

Sequence 14. Application US/08860165A

Season No. 604557

GRNERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Blizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
BARLIER APPLICATION NUMBER: PCT/AU95/00868
BERLIER FILING DATE: 1995-12-20
BARLIER PILING DATE: 1995-12-20
BARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Human papillomavirus type 16
US-09-359-382-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv...
9, Conservative
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GENERAL INFORMATION:

APPLICANT: Boursnell, Michael E.

APPLICANT: Inglis, Stephen C.

APPLICANT: Munro, Alan J.

TITLE OF INVENTION: Papilloma Virus Proteins

TITLE OF INVENTION: Papilloma Virus Proteins

NUMBER OF SEQUENCES: 70

CORRESPONDENCE ADDRESS:

ADDRESSEE: Walter H. Dreger

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STREE: CA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Parent No. 6004557
GENERAL INFORMATION:
APPLICANT: ENPARABLE, Stirling John
APPLICANT: WEBS, Blizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 49; DB 1; Length 182; 100.0%; Pred. No. 0.083;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
TELECOMMULCATION INFORMATION:
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
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US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT PILING DATE: 1999-09-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER PILING DATE: 1999-09-22
; EARLIER PILING DATE: 1999-09-22
; EARLIER PILING DATE: 1999-09-22
; EARLIER PILING DATE: 1999-10-24
; EARLIER FILING DATE: 1999-10-2
; EARLIER FILING DATE: 1999-12-20
; RARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 2.0
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
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                          PN0157
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO;
EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SEQTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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STRAIN=HPV16; TISSUE=Cervical tissue;
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14115; AAB60569.2; -..
EMBL; U142025; C.Host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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STRAIN=HPV16; TISSUE-Cervical;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14511, ABA60565.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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Q80866, Olympian (TrembLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Es protein (Fragment).
Human papillomavirus.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Last sequence update)
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Q8B564
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01-NOV-1996 (TrEMBLrel. 01, 01, 01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25, 1 EW protein (Fragment).
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NCBI_TaxID=10566;
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- 2005 Compugen Ltd.
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MEDLINE=21846229; PubMed=11857370;

MEDLINE=21846229; PubMed=11857370;

MEDLINE=21846229; PubMed=11857370;

MALES K.J., Thompson C.H., Cossart C.H., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868=874(2002).

EMBL; AR404704; AAL01365.1;

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:001877; P:DNA binding; IEA.

Pfam; PF00518; B6; 1.

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STRAIM-HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U145.6; AAB60570.1; -..
GO; GO:0004207; C:host cell nucleus; IEA.
GO; GO:000377; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Q80887;
Q0087;
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomaviruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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90 AA, 10964 MW; BC2531643ACBA76C CRC64;
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NCBI_TaxID=10581;
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NCBI_TaxID=10566;
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513; AAB60567.2; -.
GO; GO:0004777; F.NbM binding; IEA.
InterPro; IPR001334; E6.
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14514; AAB60568.2; -..
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003077; F:DNA binding; IEA.
InterPro; IRR001314; B6.
Pfam; PF00518; E6; 1.
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-NOV-1996 (TERMBLrel. 01, Created)
01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-OCT-2003 (TERMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                            84 AA; 10177 MW; SAB6B896468E1CAA CRC64;
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Last annotation update)
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
NON_TER 84 84
SEQÜENCE 84 AA; 10177 MW; SAB6B
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Best Local Similarity 100...
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Matches 9; Conservative
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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NON TER 1
NON TER 90 9
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NCBI_TaxID=10566;
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NCBI_TaxID=10566;
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RESULT 7

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Watte K.J., Thompson C.H., COSBATT Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404701; AAL01359.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:004507; F:DNA binding; IEA.
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SEQÜENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404700; AAL01357.1;
GO; GO:0002677; F:DNA binding; IEA.
PF00518; E6; 1.
                        Gaps
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBL).
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
Best Local Similarity 100.0%; Pred. No. 0.2; Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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01-OCT-2003 (
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MEDLINE=21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF4046592; AAL01342.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
Fram; PPF00518; E6; 1.
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                                     Query Match 100.0%; Score 49; DB 2; Length 99; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 0119D6 PRELIMINARY; PRT; 103 AA.
0919D6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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0919B4;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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99 AA; 12005 MW; C2B96025EC370E38 CRC64;
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
NON TER 1 1
SEQUENCE 130 AA; 15792 MW; B6C2147D22
                                                                                                                                          41 KCLKFYSKI 49
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
SEQUENCE
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404694; AAL01345.1;
GO, GO:0002057; C:host cell nucleus; IEA.

Fem., PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:86-874(2002).
EMBL; AF404695; AAL01347.1; -..
GO; GO:0042055; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
86 protein (Fragment).
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; PubMed=11857370;
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SEQUENCE
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Q919D2
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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, 5404699; AAL01355.1; -..

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0043077; F:DNA binding; IEA.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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NCBI_TaxID=10581;
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Matches
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Q919C2
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Q919C8
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DE B 03-Cot. 2003 (TrEMBLrel. 19, Last sequence update)
DE B 03-Cot. 2003 (TrEMBLrel. 19, Last sequence update)
OC Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
OC Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-69 1 KCLKFYSKI 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	E6 protein - human	•	E6 protein - human	E6 protein - rhesu	E6 protein - human		E6 protein - human	E6 protein - human		E6 protein - human	E6 protein - human	hypothetical prote	_	$\overline{}$	transcription fact	lymphocyte and mon	NADH2 dehydrogenas	E6 protein - human	E6 protein - human	protein -	protein -	E6 protein - human	probable transcrip	probable membrane	hypothetical prote		hypothetical prote		Φ
SUMMARIES	ID	W6WL35	M6WLHS	W6WL31	W6WLR1	S36584	836509	W6WL39	WGWLPR	W6WL51	W6WL18	S36561	T39200	S45872	F81293	855129	JE0177	T14244	836515	836503	836527	W6WL56	A44890	S61704	S63148	G90091	S36544	C96588	T32319	A35744
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۵	Query Match	100.0	100.0	91.8	83.7	н	σ	79.6	٠			77.6	77.6					73.5							73.5	73.5	71.4	71.4	71.4	71.4
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S t	9 P	32	35	35	35	34	34	34	34	34	34	33.5	33	33
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1
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RESULT 2

protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A03882; Just. M.; Suhai, S.; Rowekamp, W.G.
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
A;Tille: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03862
A;Molecule type: DNA

Gaps

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A;Molecule type: DNA
A;Residues: 1-154 <DEL:
A;Cross-treferences: UNIPROT:P36800; EMBL:X74463; NID:g397060; PIDN:CAA52476.1; PID:g397
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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C;Species: human papillomavirus type 32
C;Species: human papillomavirus type 32
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 836509
E;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: 83669
A;Reference number: 83669
A;Resion: 836509
A;Residues: 1-142 < DBA
A;Residues: 1-142 < DBA
A;Residues: 1-142 < DBA
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A;Re
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C;Species: human papillomavirus type 7
C;Species: human papillomavirus type 7
C;Accession: S36584
R;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Reference number: S36469
A;Reference number: S36469
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C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;60-96/Region: zinc finger CCCC motif
F;133-169/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 39; DB 2; Length 142; 75.0%; Pred. No. 3.2; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.6%; Score 40; DB 2; Length 154; 66.7%; Pred. No. 2.2;
                                                                                                                                                                                                                                                     Length 191;
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87.5%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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96 CLRFYSKI 103
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65 KCLEFYGKV 73
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67 CLEFYSKV 74
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S36509
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C; Species: human papillomavirus type 31

A;Note host Homo sapiens (man)

C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C; Accession: A3244

R; Goldsborough, M.D; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc A;Reference number: A94398; MUID:89299478; PMID:2545036

A;Reference number: A94398; MUID:89299478; PMID:2545036

A;Retais: translation not shown

A;Redidues: L-149 <GOLD

A;Redidues: L-149 <GOLD

A;Redidues: L-149 <GOLD

C;Comment: This protein may be involved in the oncogenic potential of this virus.

C;Superfamily: papillomavirus R6 protein

C;Superfamily: papillomavirus R6 protein

C;Superfamily: papillomavirus R6 protein

C;Reywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                          A;Title: A negative element in the human poapillomavirus type 16 genome acts at the leve A;Reference number: 217014; MUID:91162763; PMID:1848319
A;Accession: T10427
A;Accession: T10427
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Residues: 1-158 <KEN>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Thesus papillomavirus
C; Species: Thesus papillomavirus
C; Species: S1-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C; Accession: A38503
Virology 181, 424-429, 1991
Virology 181, 424-429, 1991
Virology 181, 424-429, 1991
Virology 181, 424-429, 1991
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                                                 A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032 R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: papillomavirus E6 protein
C;Kaywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
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Editorein - human papillomavirus type 18
C; Species: human papillomavirus type 18
C; Species: human papillomavirus type 18
C; Species: human papillomavirus type 18
C; Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C; Accession: A26165; G26251
Expecies: A26165; G26251
Expecies: A26165; G26251
Expecies: A3714Le: identification of early proteins of the human papilloma viruses type 16 (HPV 1 A; Reference number: A91068; MUID:87218459; PMID:3034571
A; Accession: A26165
A; Accession: A26165
A; Residues: 1-158 cSES
A; Residues: 1-158 cSES
A; Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877
B; Cole. S.T.; Danos, O.
J. Mol. Biol. 193, 559-608, 1987
A; Title: Nucleotide sequence and comparative analysis of the human papillomavirus type A; Accession: G26251
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A,Residues: 1-188 <DEL:
A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g397
C,Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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A;Contents: annotation; identification of the protein
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A; Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
A; Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
B; Matlashewski, G.; Banks, L.; Mu-Liao, J.; Spence, P.; Pim, D.; Crawford, L. J. Gen. Virol. 67, 1909-1916, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Es protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
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Pred. No. 5.4;
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                                              DB 1; Length 151
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                                        Score 38; DB 1
Pred. No. 5.2;
1; Mismatches
                                                                         . 5.2;
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                                           77.6%;
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66.7%;
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Best Local Similarity 66...
6, Conservative
                                        Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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65 QCLLFYSKI 73
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R;Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502, MUID:91135017; PMID:1847266
A;Accession: A38502
A;Retence translation not shown
A;Retence translation not shown
A;Residues: 1-158 «VOL>
A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1
C;Superfamily: papillomavirus &E protein
C;Keywords: DNA binding: early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;05-141/Region: zinc finger CCCC motif
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C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
E;Reuter: 3.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5569, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma A;Reference number: A40509; MUID:91374616; PMID:1716694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6 protein - human papillomavirus type 51
C; Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: B40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4255, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus 1, A;Reference number: A40415; MUD:91303675; PMID:1649326
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A,Status: translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Kesiduss: 1-158 <REU>
A;Cross-references: UNIPROT:P27962; GB:M73258
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
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C; Superfamily: papillomavirus E6 protein
C; Reywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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Pred. No. 3.5;
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75.0%;
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A;Molecule type: DNA
A;Residues: 1-151 <LUN>
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68 CIKFYAKI 75
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Matches
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RESULT 9

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probable ATP/GTP-binding protein Cj1473c [imported] - Campylobacter jejuni (strain NCTC C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Pate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 R;Patkhill, J; Wren, Billi, K; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli, C. W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre Nature and Sequence of the food-borne pathogen Campylobacter jejuni reveals hy A;Reference number: A81259 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Accession: F8123 A;Access
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N,Alternate names: protein YM8010.12c; protein YMR182c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S55129; S17249
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Churcher, C.M.
R;Cession: S55129
A;Roclecule type: DNA
A;Residues: 1-211 <CHU>A;Residues: 1-211 <CHU>A;Residues: UNIPROT:Q00453; EMBL:Z49808; NID:g854440; PID:g854452; MIPS:YMR182c'
R;Estruch, F.
Nucleic Acids Res. 19, 4873-4877, 1991
A;Reference number: S17249; MUID:92020118; PMID:1923755
A;Roclession: S17249
A;Residues: 1-113, 'V', 115-211 <EST>A;Choss.references: EMBL:X59861; NID:g4317; PIDN:CAA42521.1; PID:g4318
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Pred. No. 10;
0; Mismatches 2; Indels
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C:Keywords: DNA binding; transcription factor; zinc finger
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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55 CLKFFSRI 62
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NyAlternate names: hypothetical protein YBR0224
Cispecies: Saccharomyces cerevisiae
Cipecies: Saccharomyces cerevisiae
Cipacession: 845872, 850812; 550321
Siberiam, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Bole submitted to the Protein Sequence Database, August 1994
A; Reference number: 845862
A; Accession: 845872
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A;Residues: 1-9: NEM.
A;Residues: 1-9: NEM.
A;Residues: 1-9: NEM.
A;Cross-references: UNIPROT: P38217; EMBL: Z35886; NID: 9536217; PIDN: CAA84959.1; PID: 95362
A;Experimental source: strain S288C
B;Schaaff-Gerstenschlaeger, I.; Schindwolf, T.; Lehnert, W.; Rose, M.; Zimmermann, F.K.
Yeast 11, 79-83, 1995
A;Title: Squence and functional analysis of a 7.2 kb fragment of Saccharomyces cerevisi
A;Reference number: S50812; MUID: 95282516; PMID: 7762304
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                                                                                                                                                                                                                                    Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                     hypothetical protein SPAC926.02 - fission yeast (Schizosaccharomyces pombe)
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A;Molecule type: DNA
A;Residues: 1-918 <SCW>
A;Cross-references: EMBL:X81324; NID:g587572; PIDN:CAA57104.1; PID:g587573
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C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC926.02
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Pred. No. 24;
1; Mismatches
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75.0%; Pred. No. 13;
iive 1; Mismatches
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KCLRFYOK 55
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Sequence 21, Appl Sequence 23, Appl Sequence 23, Appl Sequence 23, Appl Sequence 36, Appl Sequence 36, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl Sequence 27, Appl

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US-10-899-771-10
US-10-899-771-10
US-10-899-771-14
US-10-899-771-14
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US-10-899-771-14
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US-10-899-771-23
US-10-899-779-267-3

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Sequence Sequence Sequence

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Sequence 11, Applisequence 7, Applisequence 8, Applisequence 26253, Sequence 251917, Sequence 3927, Applequence 34, Applisequence 34, Applisequence 2248, Applisequenc

US-10-491-213-45 US-09-832-129-34 US-09-833-245-2248 US-10-733-368-34

ALIGNMENTS

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 US-10-476-570-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: artificial sequence
 US-10-476-570-11
  FEATURE:
  Sequence 11, Appl
Sequence 4, Appli
Sequence 50, Appli
Sequence 27, Appl
Sequence 27, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
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                                                                                  (without alignments)
64.268 Million cell updates/sec
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                                                                     June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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1: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
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4: \cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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7: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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16: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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S US-10-612-818-4

1 US-10-17-390-6

1 US-10-484-063-20

7 US-10-484-063-27

7 US-10-387-38-384-2

1 US-10-367-307-16

1 US-10-367-303A-1

1 US-10-899-771-4
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Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Sequence 27, Application US/10484063
; Sequence 27, Application US/10484063
; Publication No. USZO0S0048467A1
; GENERAL INFORMATION:
; APPLICANT: TORTOLENE O.LUNA, GUILLERMO
; APPLICANT: TORTOLENE, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING CIN
; FILE REPREMENT: POLLEN, MICHELE
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE OF INVENTION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 27
; LEWGTH: 151
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC: 560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR PILING DATE: 2002-07-19
PRIOR PILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO S: 27
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; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BUNGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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; ORGANISM: Human papillomavirus
US-10-484-063-20
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Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Impact Diagnostics
APPLICANT: Impact Diagnostics
APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
TITLE OF INVENTION: Associated Cancers
FILE REFERENCE: 3352-2-2
CURRENT APPLICATION NUMBER: US/10/612,818
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR FILING DATE: 2002-07-02
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.1
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APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021508w0/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
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; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
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US-10-484-063-20
; Sequence 20, Application US/10484063
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Sequence 6, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 4, Application US/10612818
Publication No. US20040110925A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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12 KCLKFYSKI 20
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             1 KCLKFYSKI 9
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Best Local Similarity
Matches 9; Conserv
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RESULT 3

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Gaps
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                                                                                                                                                                                                                                                                                   DB 16; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09367309A

Sequence 1, Application US/09367309A

Publication No. US20020081329A1

GENERAL INFORMATION:

APPLICANT: MACERALAN, RODERICK I.

APPLICANT: MALLIANS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR PILING DATE: 1999-02-19

PRIOR FILING DATE: 1997-02-19

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO I

LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 49; DB 9; Length 266; 100.0%; Pred. No. 0.68;
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Sequence 4, Application No. US2002018221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Delisse, Anne-Warie Eva Fernande
APPLICANT: Delisse, Anne-Warie Eva Fernande
APPLICANT: Delisse, Anne-Warie Ghislaine
APPLICANT: Dembardo-Benchaikh, Angela
TTTLE OF INVENTION: Vaccine
FILE REPERENCE: 1845107
CURRENT APPLICATION NUMBER: PCT/EP98/05285
FRIOR PLILING DATE: 1998-08-17
FRIOR PLLING DATE: 1998-08-17
FRIOR PLLING DATE: 1998-08-17
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR PLING DATE: 1998-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARR: FARENCE FLANCE OF WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                              100.0%; Score 49; DB 16
100.0%; Pred. No. 0.44;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
                                     NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 171
                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
               PRIOR FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 100..
Lag 9; Conservative
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Matches 9; Conservative
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US-10-000-903-4
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Publication No. US20040171806A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Modified HPV E6 and E7 genes and proteins useful for vaccination TILLE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR APPLICATION NUMBER: EP 01107271.7
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APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT PILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver: 3.2
SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10367057; Bequence 16, Application US/10367057; Publication No. US20050100554A1
GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Jewin, David A.;
APPLICANT: Devin, David A.;
APPLICANT: Ool, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same; FILE REFERENCE: 21402-559
CURRENT PEDLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
SPRIOR FILING DATE: 2002-02-14
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
LENGTH: 158
                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human Papillomavirus
US-10-858-384-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-367-057-16
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TYPE: PRT
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RESULT 13

US-10-899-771-10

JUS-10-899-771-10

Sequence 10, Application US/10899771

Publication No. US20050031638A1

GENERAL INFORMATION:

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide

PILE REFERENCE: B45124

CURRENT FILING DATE: 2004-07-27

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR PLING DATE: 2000-06-20

PRIOR PLING DATE: 1998-12-18

PRIOR PLING DATE: 1998-12-18

PRIOR PLING DATE: 1998-12-24

NUMBER OF SEQ ID NOS: 28

SEQ ID NO 10

LENGTH: 292
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100.0%; Score 49; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                            DB 13; Length 292;
                                                                                                                                                             0.74;
had 0; Indels
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Publication No. US20020182221A1

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Lombardo-Bencheikh, Angela

TITLE FOF INVENTION: Vaccine

FILE REFRENCE: B45107

CURRENT APPLICATION NUMBER: US/10/000,903

CURRENT FILING DATE: 1990-01

PRIOR FILING DATE: 1990-08-17

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                           0; Mismatches
                                                                                                                                    100.0%; Score 49;
100.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                   Query Match
Best Local Similarity 100.
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                                          TYPE: PRT
ORGANISM: Homo sapien
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SEQ ID NO 10
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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-06-20
PRIOR PILING DATE: 2000-6-20
PRIOR PLILOR DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR PLILOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SOFTHARE: FastSEQ for Windows Version 3.0
: SEQ ID NO 4:
LENGTH: 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                   DB 13; Length 273;
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                                                                                                                     Query Match 100.0%; Score 49; DB 13; Length 2
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cerard, Catherine Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE SEFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: 1997-08-22
NUMBER: FERENCE: 1997-08-22
NUMBER: FRENCE: 1997-08-22
SOFTWARE: FREUESEQ for Windows Version 3.0
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US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
                                                                                                                                                                                                                                                                                                                                                              US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                      TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
LENGTH: 273
                                                  ; ORGANISM: nx
US-10-000-903-4
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US-10-899-771-4
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US-10-899-771-6

Sequence 6, Application US/10899771

Publication No. US20050031638A1

GENERAL INFORMATION:

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Gerard, Catherine Marie Chislaine

TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide

FILE REFERENCE: B45124

CURRENT APPLICATION NUMBER: US/10/899,771

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR PILING DATE: 2000-06-20

PRIOR PILING DATE: 1998-12-18

PRIOR PILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NOS: 28
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CTHER INFORMATION: Chimaeric protein (protein D from Haemophilius)
CTHER INFORMATION: influenzae B and B6E7 fusion from Human papilloma
CTHER INFORMATION: virus type 16)
US-10-899-771-6
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Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels (
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6 LENGTH: 371
TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                               178 KCLKFYSKI 186
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US-10-000-903-6
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Db 178 KCLKFYSKI 186 Search completed: June 29, 2005, 05:48:14 JOb time : 54:8517 secs luis Page Blank (uspto)

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 11, Appl
Sequence 15345, A
Sequence 15345, A
Sequence 15345, A
Sequence 16345, A
Sequence 22699, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 25, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 162, Application US/08934915
Patent No. 5932412
GENERAL INPORMATION:
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHRNG, HWEE-MING
ITTLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
ITTLE OF INVENTION: DAPILLOMAVIRUS 1, 5, 6, 8,
ITTLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SECUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: MASON & ASSOCIATES, P.A.
STREET: 1755 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COMPUTER FRADABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: MICROSOFT WOR'S 0.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION DATE:
APPLICATION NUMBER: 07/949,836
FILING DATE: ATTORWATION:
APPLICATION NUMBER: 37,133
REGISTRATION DATE:
ATTORDAY APPLICATION NUMBER: 37,133
REGISTRATION NUMBER: 37,133
US-08-347-492B-2
US-08-141-2
PCT-US95-15484-2
PCT-US95-07111-2
PCT-US95-07171-3
US-09-459-7490-11
US-09-248-796A-15345
US-09-248-796A-15345
US-09-249-016-11532
US-09-949-016-11532
US-09-270-767-32699
US-09-270-767-32699
US-08-460-309-10
US-08-4155-077-10
US-08-4155-077-10
US-08-415-077-10
US-08-315-844A-23
US-09-315-949-016-7517
US-09-961-403-7
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Pred. No. 0.029;
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TELECOMMUNICATION:
TELEPHONE: 813-538-3820
TELEFAX: 813-538-3820
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100.0%;
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INFORMATION FOR SEQ ID NO:
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LENGTH: 20 amino acid
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Best Local Similarity
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       137, App
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Sequence 2, Appli
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Sequence 4, Appli
                                                                                                                    June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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Sequence 14,
Sequence 21,
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Sequence 10,
Sequence 10,
Sequence 1,
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Sequence 12,
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-980-5233-2
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-09-359-382-12
US-09-359-382-12
US-09-359-382-10
US-09-359-382-10
US-09-357-392-10
US-09-357-392-10
US-09-367-309A-1
US-09-485-885-4
US-09-485-885-4
US-09-485-885-14
US-09-485-885-14
US-09-485-885-14
US-09-159-339A-137
US-08-167-768-4
US-08-17-083-14
US-08-17-083-14
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US-08-17-083-14
US-08-18-333A-74
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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49
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Match I
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Score

Result No.

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Sequence 4, Application US/08316239B
Sequence 4, Application US/08316239B
Sequence 4, Application US/08316239B
Servent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
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ZIP: 20120-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: FORM:

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,239B

FLING DATE: 30-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: JGGIAIN, 435

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: UNME-0001

TELEPRATION NUMBER: JAY A.

REGISTRATION NUMBER: UNME-0001

TELEPRATION NUMBER: 31-9453

TELEPRAM: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: ALION ACID
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
NAME: Jagtiani, Ajay A.

REGIGSTRATION NUMBER: 35,205
REPERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: not relevant
not relevant
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MOLECULE TYPE: protein
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Best Local Similarity 100.
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Best Local Similarity 100.0
Matches 9; Conservative
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GENERAL INFORMATION:

APPLICANT: Wheeler, Cheryl A.

APPLICANT: Wheeler, Cheryl A.

TITLE OF INVENTION: Methods and a Diagnostic Aid for

TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer

TUTLE OF INVENTION: Cervical Cancer

TUTLE OF INVENTION: Cervical Cancer

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jagtiani & Associates
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                                                                                                                                                                                       Sequence 2. Application US/0990523A

| Sequence 2. Application US/0990523A
| Patent No. 6/03/03
| GENERAL INFORMATION:
| APPLICANT: GROPEN, JEANNINE
| APPLICANT: GUILLET, JEAN-GERARD
| APPLICANT: GUILLET, JEAN-GERARD
| APPLICANT: COUNTAN, FRANCINE
| APPLICANT: COUNTAN, FRANCINE
| TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: PARTICULARLY IN VACCINATION
| FILE REFERENCE: WOBL AO INS
| CURRENT APPLICATION NUMBER: US/09/980,523A
| CURRENT APPLICATION NUMBER: POT/FR00/01513
| PRIOR PILING DATE: 2000-05-31
| PRIOR FILING DATE: 2000-05-31
| PRIOR FILING DATE: 1999-06-03
| NUMBER OF SEQ ID NOS: 24
| SEOFTWARE PATENTIN VET. 2.1
      Gaps
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      Indels
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COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
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      Mismatches
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STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08316239B Patent No. 5679509
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ORGANISM: Human Papillomavirus
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      9; Conservative
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Best Local Similarity
                                                   1 KCLKFYSKI 9
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                                                                                                                                                                                     US-09-980-523A-2
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US-08-316-239B-3
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Partent No. 6306397

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBS, Elizabeth Ann
APPLICANT: WEBS, Elizabeth Ann
APPLICANT: WEBS, Islandeth Ann
APPLICANT: PRAZER, Islandeth Ann
APPLICANT: PRAZER, Islandeth Ann
APPLICANTON NUMBER: US 08/860,165
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
SEARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTHARE: PAPELIT VET. 20
NUMBER PAPELICATION VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/09359382
; Sequence 14, Application US/09359382
; Batent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: WEBB. Elizabeth Ann
; APPLICANT: WEBB. Elizabeth Ann
; APPLICANT: WEBB. Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT PERLICE 107227/0148
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: US/09/359,00868
; EARLIER PELICATION NUMBER: PCT/AU95/00868
; EARLIER PILING DATE: 1997-09-22
; EARLIER PELICATION NUMBER: AU PN0157/94
; EARLIER PILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOSTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12
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                                                                                                                                                                     Sequence 12, Application US/09359382
Patent No. 6306397
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Best Local Similarity 100.C
...rhes 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                  141 KCLKFYSKI 149
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1 KCLKFYSKI 9
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LENGTH: 172
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                                                                                                                                                                                   Sequence 12, Application US/08860165A
Fatent No. 6004557
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION WUMBER: US/08/860,165A
CURRENT APPLICATION WUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER APPLICATION NUMBER: AU PNO157
NUMBER OF SEQ ID NOS: 1995-12-20
SOFTWARE: PRECENTING NOS: 2.0
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APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT PILING DATE: 1997-09-22
BARLIER PILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER APPLICATION NUMBER: AU PNO157
SARLIER APPLICATION NUMBER: AU PNO157
SARLIER APPLICATION NUMBER: AU PNO157
SAPTWARE: PATENT OF AU PNOS: 12-20
SOFTWARE: PATENT OF AU PNOS: 12-20
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; Sequence 14, Application US/08860165A
; Eatent No. 6004557
; GENERAL INPORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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                  KCLKFYSKI
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LENGTH: 172
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LENGTH: 172
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Sequence 1, Application US/09367309A

Sequence 1, Application US/09367309A

Batent No. 6428807

GENERAL INFORMATION:
APPLICANT: MACIFARLAN, RODERICK I.
APPLICANT: MALLIANGS, JIM
ITTLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERRNCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1997-02-19

NUMBER: OF SEQ ID NOS: 6

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 1

LENGTHE 266
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100.0%; Score 49; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.31;
:ive 0; Mismatches 0;
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1996-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 273
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ORGANISM: Human papillomavirus type 16
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US-09-485-885-10
; Sequence 10, Application US/09485885
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     72 KCLKFYSKI 80
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 9; Conserva
                                                                          RESULT 11
US-09-367-309A-1
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US-09-485-885-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GRNERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper;
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: WARDS, Ian
; TITLE OF INVENTION: VALIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT FILING DATE: 1999-00-23
; EARLIER APPLICATION NUMBER: US 089/860,165
; EARLIER PILING DATE: 1999-00-23
; EARLIER PILING DATE: 1999-00-23
; EARLIER PILING DATE: 1999-00-23
; EARLIER PILING DATE: 1999-10-23
; EARLIER PILING DATE: 1999-10-23
; EARLIER PILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 2.0
                                                                                                                                                                                                                APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS,
APPLICANT: COX, John Cooper
APPLICANT: WEBB. Blizabeth Ann
APPLICANT: RAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILLE REPERENCE: 1227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
BARLIER FILING DATE: 1997-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
BARLIER APPLICATION NUMBER: AU PN0157
BARLIER APPLICATION NUMBER: AU PN0157
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                Sequence 10, Application US/08860165A Patent No. 6004557 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Matches 9; Conservative
72 KCLKFYSKI 80
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bruck. Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Guislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107-18
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GR 9717953.5
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FREESEQ for Windows Version 3.0
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GANERAL INFORMATION:

APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anna-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: BC7/EP98/05285
FRIOR APPLICATION NUMBER: PC7/EP98/05285
PRIOR FILING DATE: 1996-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-485-885-6; Sequence 6, Application US/09485885; Sequence 6, Application US/09485885; Patent No. 6342224; GENERAL INFORMATION:
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Best Local Similarity 100.03
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US-09-485-885-6
                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 10
LENGTH: 292
TYPE: PRT
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE REPERBUG: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 1998-08-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
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Best Local Similarity 100..
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; ORGANISM: Homo sapien
US-09-485-885-14
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14515; AAB60569.2;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IRR001334; E6.
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STRAIN=HPV16; TISSUB=Cervical;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U1451; AAB60565.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                   E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Q9WMP3
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01-OCT-2003 (TrEMBLrel. 25,
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NCBI_TaxID=10566;
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NCBI_TaxID=10566;
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C STRAIN=HPVI6; TISSUE=Cervical tissue;
A Haegert D.G., Galutira D.F., Younghusband B.H.;
A Haegert D.G., Galutira D.F., Younghusband B.H.;
L Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

EMBL; U14514; AAB60568 2.; -
DR GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.
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                                                     Length 90;
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STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1;
                                                                                                                                                                                                                                                                                              Humān papillomavirus.
viruses, deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
vicBI_TaxID=10566;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
                                                    100.0%; Score 55; DB 2; 100.0%; Pred. No. 0.049;
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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SEQÜENCE 91 AA; 11136 MW.
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NCBI_TaxID=10566;
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STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
RMBL; U14512; AAB60566.1; -.
RMBL; U14512; AAB60566.1; -.
GO; GO:0003677; FDNA binding; IEA.
InterPro; IPR001334; E6.
R Ffam; PF00518; E6; 1.
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                                                                                             100.0%; Score 55; DB 2; Length 84; 100.0%; Pred. No. 0.046; tive 0; Mismatches 0; Indels
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STRAIN=HPV16; TISSUE-Cervical tissue;
Aragert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513; AAB60567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IFR001334; E6.
Pfam; PF00518; E6; 1.
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Q80883;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1993 (TrEMBLrel. 25, Last sequence update)
O1-CT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; GBDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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                                                                    84 AA; 10177 MW; SAB6B896468E1CAA CRC64;
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Q80884;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
 GO; GO:0003677; F:DNA binding; IEA.
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Best Local Similarity 100...
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Best Local Similarity 100.
Matches 9; Conservative
          InterPro; IPR001334; E6. Pfam; PF00518; E6; 1. NON_TER 1
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MEDINE=2186229; PubMed=11857370;
Watte K.J. Thompson C.H., Coseart Y.E., Rose B.R.;
Watte K.J. Thompson C.H., Coseart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:866-874(2002)
Int. J. Cancer 97:866-874(2002)
Int. J. Cancer 97:866-874(2002)
GO: GO:00042025; C:host cell nucleus; IEA.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
SCQUENCE 130 AA; 15792 MW; BGC2147D227EEDDC CRC64;
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404701; AAL01359.1; -
GO; GO:0042025; C:host cell nucleus; IEA.
GG; GO:0003677; F:DNA binding; IEA.
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100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.056;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 procein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; PubMed=11857370;
                Best Local Similarity 100.
Matches 9; Conservative
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NCBI_TaxID=10581;
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 971.68-874 (2002).
EMBL; AR404704; AAL01365.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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NON_TER 99 99
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MEDLINE=21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cobsart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AALO1342.1; --.
GO; GO:0042025; C.Hoot cell nucleus; IEA.
GO; GO:0042025; C.Hoot cell nucleus; IEA.
FEMPL; PROSSIS; E6: 1.
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SEQÜENCE 103 AA; 12422 MW; 6F90CBAFIF25449B CRC64;
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                                 Query Match 100.0%; Score 55; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 0.05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 100.0%; Score 55; DB 2; Length 99; Similarity 100.0%; Pred. No. 0.054; 9; Conservative 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Es protein (Fragment).
Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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                                                                                                                                                                                                                                                         99 AA
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MEDLINE=21846229; PubMed=11857370;
                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                      35 PYAVCDKCL 43
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Best Local Similarity
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NCBI TaxID=10581;
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Matches

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Query Match

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Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                            RESULT 13
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MEDLINE=211046229; PubMed=11857370;

Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868=874(2002).

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.

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MEDIJNE=21846229; PubMed=11857370;
MATER K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Mater K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868=874(2002).
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0018; E6; 1.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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(TrEMBLrel. 25, Last annotation update)
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Matches 9; Conserv
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NCBI_TaxID=10581;
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97.868-874 (2002).
EMBL; AF404696; AAL01349.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:001877; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
NON TER.
SEQÜENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer 19:868-874(2002).
EMBL; AF404695; AAL01347.1;
GO; GO:00025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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                     0919C8,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
E6 protein (Fragment).
Viruses; daDMA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 proctein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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130 AA.
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PRT;
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE COT-2003 (TrEMBLrel. 25, Last annotation update)
DE BE protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; debnA viruses, no RNA stage; Papillomaviridae;
OC Viruses; debnA viruses, no RNA stage; Papillomaviridae;
OC NCBI_TAXID=10581;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA WEDLINE=21846229; PubMed=11857370;
RA WEDLINE=21846229; PubMed=11857370;
RA WATTER K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT cervical cancer isolates from Australia and New Caledonia.";
RT cervical cancer 97:888-874 (2002).
Cervical Cancer 97:888-874 (2002).
DR GO; GO:00042025; C:host cell nucleus; IEA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; B6; 1.
FT NON TER 1 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESAEA90895FCZ CRC64;
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100.0%; Score 55; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels
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46 PYAVCDKCL 54
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Search completed: June 29, 2005, 01:34:48 Job time : 54.2473 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-68 55 1 PYAVCDKCL 9 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	Ω	Description
1	55	100.0	158	-	Wewlas	protein E6 - human
7	44	80.0		-	W6WL51	E6 protein - human
m	43	78.2	153	٦	S15621	protein -
4	42	76.4		Н	W6WL35	
Ŋ	42	76.4		~	S36503	E6 protein - human
9	42	76.4	1891	~	T13594	
7	42	76.4	1920	~	T13893	ᄺ
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11	40	72.7	155	~	A44890	E6 protein - human
12	40	72.7	605	7	G70409	
13	40	72.7	951	7	T45726	
14	39	70.9		н	W6WL31	E6 protein - human
15	38	69.1	123	~	D72856	AcOrf-52 protein -
16	38	69.1	150	~	S36544	E6 protein - human
17	38	69.1	154	~	S36584	
18	38	69.1	187	~	T32826	hypothetical prote
19	38	69.1	194	7	T41796	~
20	38	69.1	401	~	A96941	hypothetical prote
21	38	69.1	552	~	S45886	
22	37	67.3	149	-	W6WL58	
23	37	67.3	158	-	W6WL18	E6 protein - human
24	36	•	101	~	E71607	metal binding prot
25	36	•	117	~	E64628	hydrogenase expres
26	36	65.5	148	~	A61237	E6 protein - human
27	36	•	148	~	S36532	E6 protein - human
28	36	65.5		ď	w	E6 protein - human
29	36	65.5	152	~	836550	E6 protein - human

W6WISI

B6 protein - human papillomavirus type 51
C/Species: human papillomavirus type 51
C/Species: human papillomavirus type 51
A/Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 3.J.
J. Virol. 65, 4216-4225, 1991
A;Piune: Biologic properties and nucleotide sequence analysis of human papillomavirus the A;Accession: B40415
A;Accession: B40415
A;Accession: B40415
A;Status: translation not shown

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Gaps

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0; Indels

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Conservative

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1 PYAVCDKCL

||||||||| 66 PYAVCDKCL 74

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RESULT 2

E6 protein - human	E6 protein - human	E6 protein - human	E6 protein - human	E6 protein - rhesu	DNA excision repai	hypothetical prote	transporter bindin	SEN1 protein - yea	hypothetical prote	E6 protein - human	zinc uptake regula	E6 protein - human	E6 protein - human	E6 protein - human	hypothetical prote
836555	S36527	S15614	S36497	W6WLR1	JQ1325	T24396	G69834	S53416	H84339	836509	AE3531	W6WL42	Wewle	836561	A75191
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154	154	159	159	191	296	510	575	2231	84	142	145	150	150	158	199
65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	65.5	63.6	63.6	63.6	63.6	63.6	63.6	63.6
36	36	36	36	36	36	36	36	36	32	32	35	35	32	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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protein B6 - human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Sedoff, K; Krammer, G; Durst, M; Suhai, S; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Cross-references: UNIPROT:P0316; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:KO2718; NID:g333031; PIDN:AAA46939.1; PID:g333032 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 55; DB 1; Length 158; 100.0%; Pred. No. 0.069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Superfamily: papillomavirus E6 protein
C.Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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us-08-170-344-68.rpr

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A;Molecule type: DNA
A;Residues: 1-153 <DBL.
A;Cross-ternecs: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396
C;Superfamily: papillomavirus E6 protein
C;Kcywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:077275; EMBL:AL031227; NID:e1330103; PID:e1316856; PIDN:CAA C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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C;Species: Drosophila melanogaster
C;Date: 13-6491999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13594
R;Perraz, C:; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
submitted to the BMBL Data Library, October 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17692
A;Accession: T13594
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1891 <FER.
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C,Species: Drosophila melanogaster
C,Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                            E6 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42, DB 2, Length 153;
Pred. No. 8;
1; Mismatches 1; Indels
                                                                                                            Length 149;
                                                                                                                                                                  Indels
C;Keywords: DNA binding; early protein; zinc finger F;30-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
                                                                                                               ij
                                                                                                          76.4%; Score 42; DB
ilarity 77.8%; Pred. No. 7.8;
Conservative 0; Mismatches
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A;Cross-references: FlyBase:FBgn0003053
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Best Local Similarity 77.8%;
Matches 7; Conservative 1
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                         59 PYGVCMKCL 67
                                                                                                                                                                                                                       1 PYAVCDKCL 9
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                                                                                                                                      Best Local Similarity
Matches 7; Conserv
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                                                                                                               Query Match
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C; Date: 30-Jun-1992 #sext_change 09-Jul-2004
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: #40824; 336521
R; Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A; Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A; Reference number: A40824; MUID:92124753; PMID:1310198
A; Accession: E40824
A; Accession: E40824
A; Residues: 1-149 cMAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P22158; EMBL:X55965; NID:g60882; PIDN:CAA39430.1; PID:g60883
C;Superfamily: papillomavirus E6 protein.
C;Keywords: DNA binding; aarly protein; transforming protein; zinc finger
F;29-65/Region: zinc finger CCCC motif
F;102-138/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15621
K;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: S15614; MUID:91188699; PMID:1964523
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A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
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                                                                                                                                                                                                                            Length 151;
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                                                                                                                                                                                                                                                                            Indels
                         A,Residues: 1-151 <LUN>
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding: early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                       80.0%; Score 44; DB 177.8%; Pred. No. 3.8; ive 1; Mismatches
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Pred. No. 5.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein - human papillomavirus type 35 Species: human papillomavirus type 35
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66.7%;
                                                                                                                                                                                                                                                   77.88;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                       Query Match 80.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: $36469
A;Accession: $36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <DEL>
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59 PYAVCKQCL 67
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A; Residues: 1-153 < HIR>
        A; Molecule type: DNA
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Riklenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodsc.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Tille: The complete genome sequence of the hyperthermophilic, sulfate-reducing archac A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Reference number: A69250; Muldisserved action not shown
                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-740 <KLLS.
A;Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AAB89876.1; PID:g26492
C;Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation fal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: human papillomavirus type 66
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A44890
R;Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of A;Reference number: A44890; MUID:92129556; PMID:1663515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 56
C;Species: human papillomavirus type 56
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Date: 31-Dec-1991 #sefs79
R;Locrincz, A.T.; Ouinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A;Reference number: A33377, MuID:90063558; PMID:2555440
  C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X74483; NID:9397053; PIDN:CAA52596.1; PID:9397054 C;Superfamily; papillomavirus B6 protein C;Superfamily; papillomavirus B6 protein and C;Superdes DNA binding; early protein; transforming protein; zinc finger CCC motif F;33-69/Region: zinc finger CCC motif F;106-142/Region: zinc finger CCCC motif
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*Residues: 1-155 <LOES
*A;Residues: 1-155 <LOES
*A;Cross-references: UNIPROT:P24836
*B;Delius, H.; Hofmann, B.
*Bubmitted to the EMBL Data Library, August 1993
*A;Description: Primer-directed sequencing of human papillomavirus types.
*A;Reference number: $336469
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Pred. No. 17;
0; Mismatches
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B6 protein - human papillomavirus type 66
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nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 PYAVCRVCL 70
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A; Residues: 1-155 <DEL>
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A;Status: preliminary
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                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1920 < YIP>
A; Residues: 1-1920 < YIP>
A; Cross-references: UNIPROT: 0-46205; EMBL: U86010; NID: 92769709; PID: 92769710; PIDN: AAB956
C; Genetics:
A; Gross-references: FlyBase: FBgn0003053
C; Function:
A; Description: probably function as a transcription factor
C; Keywords: nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R/Yip, M.L.R.; Lamka, M.L.; Lipshitz, H.D.
Development 124, 2129-2141, 1997
A; Title: Control of germ-band retraction in Drosophila by the zinc-finger protein HINDSI
A; Recension: T13893
A; Accession: T13893
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrogenase expression/formation regulatory protein (hypF) homolog - Archaeoglobus fulgi
C;Species: Archaeoglobus fulgidus
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100.0%; Pred. No. 55;
vative 0; Mismatches
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Pred. No. 12;
2; Mismatches
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112 PFLICDKC 119
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747 PYAVCDK 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PYAVCDK 7
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
C; Accession: T13893
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59 PHGVCTKCL 67
                                        PYRVCDDC 693
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  1 PYAVCDKC 8
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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A; Residues: 1-123 <AYR>
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                                            989
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:9819666; PMID:9537320

A;Reference undber: A70300; MUID:9819666; PMID:9537320

A;Accession: G70409

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Rossiues: 1-605 < AQP>
A;Cross-references: UNIPROT:067306; GB:AE000732; NID:g2983704; PIDN:AAC07275.1; PID:g298

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hvgr

C;Superfamily: integral membrane protein HP0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: G70409
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: 145726
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sasubmitted to the Protein Sequence Database, November 1999
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                                                            A,Cross-references: UNIPROT:Q80955
A,Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:78638)
S,Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
E;33.69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                     Length 155
                                                                                                                                                                                                                                                               2; Indels
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A;Accession: 145726
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-951 <CHO>
A;Cross-references: UNIPROT:Q9SN72; EMBL:AL132955
A;Experimental source: cultivar Columbia; BAC clone F1P2
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A;Introns: 16/3; 45/3; 75/3; 102/3; 163/3; 883/3; 932/3
A;Note: FIP2.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                          high affinity sulfate transporter - Aquifex aeolicus
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                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                72.7%;
77.8%;
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77.88;
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Best Local Similarity
7; Conserv?
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Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-155 <TAW>
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Ed protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A3244
R;Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-asso A;Reference number: A94398; MUD:89299478; PMID:2545036
                                                                                                                                                                                                                                                                                                                                            A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Kosidues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g45991
C;Comment: This protein may be involved in the oncogenic potential of this virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
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ACOFF-52 protein - Autographa californica nuclear polyhedrosis virus
Cispecies: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: dSDNA virus
C;Date: 12-NOV-1999 #sequence_revision 12-NOV-1999 #text_change 09-Jul-2004
C;Accession: D72856
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Status: preliminary A; Cross-references: UNIPROT: P41456; GB: L22858; NID: g510708; PIDN: AAA66682.1; PID: g55912 C; Genetics:

Gaps ö 69.1%; Score 38; DB 2; Length 123; 75.0%; Pred. No. 29; 2; Indels Pred. No. 29; 0; Mismatches 6; Conservative

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Search completed: June 29, 2005, 01:38:44 Job time: 12.2747 secs

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Sequence 11, Appl
Sequence 6, Appli
Sequence 20, Appl
Sequence 27, Appl
Sequence 2, Appl
Sequence 16, Appl
Sequence 1, Appli
Sequence 1, Appli
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                                                                                                                       (without alignments)
64.268 Million cell updates/sec
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                                                                                                   June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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| Cgn2_6/ptodata1/pubpaa/USO7_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
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| Cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO9_PUBCOMB.ppp:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-344-824-237
S US-10-44-824-237
US-10-612-818-4
I US-10-177-390-6
7 US-10-484-063-27
V US-10-484-063-27
V US-10-858-384-2
I US-10-858-384-2
I US-10-367-057-16
I US-10-367-057-16
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                                                                                                                                                                                                                                                                                                       1717557 segs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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No.
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Sequence 10, Appl
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 265840,
Sequence 205655,
Sequence 306006,
Sequence 306006,
Sequence 21356,
Sequence 22512,
Sequence 22512,
Sequence 22512,
Sequence 22512,
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Sequence 22512,
Sequence 131317,
Sequence 16162,
Sequence 16163,
Sequence 16163,
Sequence 16163,
Sequence 16163,
Sequence 16661,
Appli
Sequence 1667, Appli
Sequence 167, Appli
Sequence 167, Appli
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Sequence 228359,
Sequence 41187, A
Sequence 27, Appl
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Sequence 6, Application US/10484063

Sequence 6, Application US/10484063

Publication No. US20050048467A1

GENERAL INFORMATION:

APPLICANT: TORTOLERO-LUNA, GUILLERMO

APPLICANT: FOLIEN, MICHELE

TITLE OF INVENTION: PRE-CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2004-01-16

PRIOR FILING DATE: 2002-07-19

PRIOR FILING DATE: 2002-07-19

PRIOR FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SOUTHWARE: PARCHILING VET: 2.1
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3 US-10-000-903-4
7 US-10-899-771-4
7 US-10-899-771-4
3 US-10-899-771-10
3 US-10-000-903-10
7 US-10-899-771-10
7 US-10-899-771-14
7 US-10-899-771-14
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8 US-10-424-599-265840
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6 US-10-427-199-262512
6 US-10-427-199-262614
6 US-10-437-963-1150694
6 US-10-437-963-126044
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US-10-767-701-41187
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US-10-873-332-66
US-10-425-114-38299
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                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
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ORGANISM: Human papillomavirus
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  US-10-484-063-6
   SEQ ID NO 6
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TYPE: PRT ORGANISM: artificial sequence
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PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 20
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US-10-177-390-6
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LENGTH: 151
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FUDIcation No. US20040170644A1
GENERAL INFORMATION:
APPLICANT: OWMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGABLE-VORATILLE, Sandra
APPLICANT: POUNCELE-WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: MAXLURE OF ÉPEPTIONE BOUNCALLET, Sandra
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
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                    JASOBAR 4-824-237

Sequence 237, Application US/08344824

Sequence 237, Application US/08344824

Publication No. Usz0030152580A1

PEDERAL INFORMATION:
APPLICANT: SITHE, Alessandro
APPLICANT: SIDNEY, John

TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
NUMBER OF SEQUENCES: 399

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Clock
CITY: San Francisco
STRATE: California
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MEDLUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824

FILING DATE: 23-NOV-1994

CLASSIFICATION NUMBER: US 08/278,634

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REFERENCE/DOCKET NUMBER: 14137-80-1

TELEPHONE: (415) 543-9600

TELEPHONE: (415) 543-9600

TELEPRATION FOR SEQ ID NO: 237:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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Matches 9; Conserval
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US-10-476-570-11
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Sequence 4, Application US/10612818

Sequence 4, Application US/10612818

Bublication No. US20040110925A1

GENERAL INFORMATION:

APPLICANT: Impact Diagnostics

TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus

TITLE OF INVENTION: Associated Cancers

TITLE OF INVENTION: Associated Cancers

FILE REFERENCE: 3352-2-2

CURRENT FILING DATE: 2003-07-01

PRIOR APPLICATION NUMBER: US 60/394,172

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80 US-10-476-570-11
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Publication No. US2003014374341
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: Schuler, Improved Transfection of Eucaryotic Cells with Linear TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 02L505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                               ö
                                                                                                                                           Query Match 100.0%; Score 55; DB 16; Length 20; Best Local Similarity 100.0%; Pred. No. 0.058; Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 2, Application US/10858384

Publication No. US20050033025A1

GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: FERRIES, ESTELE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRACMENTS OF THE E6 PROTEIN

TITLE OF INVENTION: OR PROJUCTION AND THEIR USE

TITLE OF INVENTION: OR PROJUCTION AND THEIR USE

TITLE OF INVENTION: OR STOOK 100/058, 384

CURRENT FILING DATE: 1999-06-03

FRIOR APPLICATION NUMBER: FR 9907012

       Gaps
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Publication No. US20050100554A1

GENERAL INFORMATION:

APPLICANT: Cuthill, Scott;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Complexes and Methods of Using Same;

TITLE OF INVENTION: Complexes and Methods of Using Same;

FILE REFERENCE: 21402-559

CURRENT APPLICATION NUMBER: 2003-02-14

PRIOR APPLICATION NUMBER: 60/256,911

PRIOR FILING DATE: 2002-02-14
        Indels
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        Mismatches
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
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US-10-858-384-2
     9; Conservative
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Best Local Similarity
Matches 9; Conserv
                                                        1 PYAVCDKCL
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERN
APPLICANT: TORTOLERN
INTERO-LUNA, GUILLERNO
TITLE OF INVENTION: MFTHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: MFTHODS AND CANCEROUS GROWTHS, INCLUDING CIN
TITLE OF INVENTION: WREEC SOUR
TITLE OF INVENTION: WREEC SOUR
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT PILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: G0/306,809
PRIOR FILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLER, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HEV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR FILING DATE: 2004-01-19
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2001-07-20
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                                                                           Query Match
100.0%; Score 55; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.35;
                                                                                                0.35;
----- 0; Indels
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
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                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/10484063
Publication No. US20050048467A1
GENERAL INFORMATION:
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; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
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; ORGANISM: Human papillomavirus
US-10-484-063-20
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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LENGTH: 151
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Sequence 4, Application US/10899771
; Sequence 4, Application US/10899771
; Sequence 4, Application US/20050031638A1
; Publication No. US20050031638A1
; GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR PLILNG DATE: 2000-06-20
; PRIOR PLILNG DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius ) OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type OTHER INFORMATION: 16) US-10-899-771-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 13; Length 273; 100.0%; Pred. No. 0.58; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 55; DB 17; Length 273; 100.0%; Pred. No. 0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
              Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
        APPLICANT: Delisse, Anne-Marie Eva Fernande APPLICANT: Gerard, Catherine Marie Ghislaine APPLICANT: Gerard, Catherine Marie Ghislaine APPLICANT: Lombardoo-Bencheikh, Angela TILLE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 4
SEQ ID NO 5: 20
LENGTH: 273
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Sequence 10, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
Cabezon Silva, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-10-899-771-4
                                                                                                                                                                                                                                                                                                                                                          US-10-000-903-4
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APPLICANT: MACERLIAN, RODERICK I.
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES;
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR PILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 55; DB 9; Length 266; 100.0%; Pred. No. 0.57; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09367309A, Publication No. US20020081329A1 GENERAL INFORMATION:
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US-10-000-903-4
Sequence 4, Application US/10000903
Publication No. US2002182221A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-09-367-309A-1
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Sequence 10, Application US/10899771
| Publication No. US20050031638A1
| GENERAL INFORMATION NO. US20050031638A1
| GENERAL INFORMATION NO. US2005003163BA1
| APPLICANT: Dalemans, Wilfried L.J.
| APPLICANT: Dalemans, Wilfried L.J.
| APPLICANT: Dalemans, Wilfried L.J.
| APPLICANT: Dalemans, Wilfried L.J.
| TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
| TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
| TITLE OF INVENTION NUMBER: US/099,771
| CURRENT PILING DATE: 2004-60-20
| PRIOR APPLICATION NUMBER: PC7/EP98/08563
| PRIOR PILING DATE: 1998-12-14
| PRIOR FILING DATE: 1998-12-14
| PRIOR FILING DATE: 1998-12-24
| NUMBER OF SEQ ID NOS: 28
| SOFTON NUMBER PRESEQ for Windows Version 3.0
| SEQ ID NO 10
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: WHERE: US/10/000,903
CURRENT FILING DATE: 2001-10-01
FRIOR PILING DATE: 1998-08-17
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR FILING DATE: 1997-08-22
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9, Conservative
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US-10-000-903-10
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7517, Ap
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Sequence
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Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: Has Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                      US-09-485-885-21
US-09-485-885-23
US-09-949-016-8725
US-09-949-016-8726
US-09-949-016-8728
US-09-949-016-8729
US-09-949-016-8729
US-09-949-016-8730
US-09-949-016-7517
US-09-9561-403-7
US-09-562-702A-8
US-09-562-702A-6
US-09-562-702A-6
US-09-562-702A-6
US-09-562-702A-6
US-09-562-702A-6
US-09-562-702A-6
US-09-562-702A-6
US-09-949-016-5937
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDLIM TYPE: DISKETCE
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DISKETCE
COMPUTER: US 008/159,339A
FILING DATE: US 000-1993
CLASSIFICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1993
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 31,762
REFERENCE/DOCKET NUMBER: 31,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
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TYPE: amino acid
STRANDEDNESS: aingle
TOPOLLGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CA
USA
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STATE:
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Sequence 2, Appli
Sequence 3, Appli
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Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
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Sequence 1169, Ap
Sequence 561, App
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                                                                                                                                                                 June 28, 2005, 23:37:59; Search time 16.8626 Seconds (Without alignments) 39.842 Million cell updates/sec
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Sequence 18,
Sequence 18,
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Sequence 14,
Sequence 12,
Sequence 10,
Sequence 10,
Sequence 1,
Sequence 1,
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Sequence 6
Sequence 1
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Sequence
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-980-523A-2
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-09-359-382-14
US-09-359-382-12
US-09-359-382-14
US-09-359-382-14
US-09-367-309A-1
US-09-367-309A-1
US-09-485-885-4
US-09-485-885-10
US-09-485-885-10
US-09-485-885-10
US-09-485-885-10
US-09-485-885-10
US-09-385-334A-1162
US-08-129-339A-1163
US-09-315-339A-1163
US-09-375-314-18
US-09-375-314-18
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US-09-375-314-18
US-09-375-339A-249
US-08-159-339A-249
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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55
1 PYAVCDKCL 9
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Match 1
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Result

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; HYPOTHETICAL: NO
US-08-316-239B-4
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Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
STREET: Glacky Way Court
CITY: Centreville
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APPLICANT: CHOPPIN, TEANNINE
APPLICANT: GUILLET, JEBAN-GERARD
APPLICANT: GUILLET, JEBAN-GERARD
APPLICANT: GUILLET, JEBAN-GERARD
APPLICANT: GUILLET, JEBAN-GERARD
APPLICANT: GUILLET, JEBAN-GERARD
TITLE OF INVENTION: POLYTEPITOPIC PROTEIN FRACHENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: MOBIA O. INS
CURRENT APPLICATION NUMBER: PCT/FR00/01513
FRIOR FILING DATE: 2002-04-29
FRIOR PLILING DATE: 2000-05-31
FRIOR PLLING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN OF: 2.1
SOFTWARE: PATENTIN OF: 2.1
                                                                                   Gaps
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                                      100.0%; Score 55; DB 3; Length 11; 100.0%; Pred. No. 0.0053; tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             Sequence 2, Application US/09980523A Patent No. 6783763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human Papillomavirus
                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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1 PYAVCDKCL 9
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Matches 9; Conserv
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US-08-159-339A-1170
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GENERAL INFORMATION:
APPLICANT: Wheeler, Coette M.
APPLICANT: Warmener, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REGISTRATION NUMBER: 35,205
REGISTRATION NUMBER: UNNE-0001
TELEPHONE: (703) 817-9453
TELEPHONE: (703) 817-9453
TELEPHONE: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                       ATTORNEY AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION UNDRER: 35.205
REFERENCE/DOCKET UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPHONE: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08316239B
Patent No. 5679509
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TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                LENGTH: 162 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-3
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TYPE: amino acid
STRANDEDNESS: not releve
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66 PYAVCDKCL 74
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| Sequence 14, Application US/09359382
| Patent No. 6306397
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: COX, John Cooper
| APPLICANT: COX, John Cooper
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: WEBE, Ian
| APPLICANT: WEBER, Ian
| APPLICANT: WEBER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANTON NUMBER: US/09/359,382
| FILE REFERENCE: 017227/0148
| CURRENT FILING DATE: 1990-07-23
| EARLIER PILING DATE: 1990-07-23
| EARLIER FILING DATE: 1990-109-22
| EARLIER FILING DATE: 1990-109-22
| EARLIER FILING DATE: 1990-109-22
| FARLIER FILING DATE: 1990-109-22
| SARLIER PILING DATE: 1990-109-20
| SARLIER PILING DATE: 1990-109-30
| SARLIER PILING DATE: 1990-100-30
| SARLIER PILING DATE: 1990-300-30
|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: RAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 01722/1019
FILE REFERENCE: 01727/0193
CURRENT APPLICATION NUMBER: US 08/860,165
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER PILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PT/AU95/00668
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PT/AU95/00668
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER PILING DATE: 1997-09-22
EARLIER PILING DATE: 1997-09-22
EARLIER PILING DATE: 1997-09-22
EARLIER PILING DATE: 1997-09-22
SOFTWARE: DATE: 1997-09-22
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100.0%; Score 55; DB 3; Length 172;
100.0%; Pred. No. 0.076;
ive 0; Mismatches 0; Indels
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ORGANISM: Human papillomavirus type 16
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ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09359382; Patent No. 6306397; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                     9; Conservative
                                                                                                                                                                                                     135 PYAVCDKCL 143
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                             Best Local Similarity
Matches 9; Conserv
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   Query Match
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US-08-860-165-12
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US-08-860-165-14

US-08-860-165-14

US-08-860-165-14

Sequence 14, Application US/08860165A

GENERAL INFORMATION:
APPLICANT: EDWANDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Islandshin Interpretation TITLE OF INVENTION: UNAINTS OF HUMAN PAPILLOMA
TITLE OF INVENTION: UNAINTS OF HUMAN PAPILLOMA
CURRENT FRAZER; Island
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20

EARLIER PILING DATE: 1994-12-20

WUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

LENGTH: 172
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US-08-860-165-12

Sequence 12, Application US/08860165A

Patent No. 6004557

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS

FILE REFERENCE: 17227/130

CURRENT PALLORION NUMBER: US/08/860,165A

CURRENT PALLORION NUMBER: PCT/AU95/00868

EARLIER APPLICATION NUMBER: AU PNO157

EARLIER PILING DATE: 1995-12-20

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15
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                     Query Match 100.0%; Score 55; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 0.071; Matches 9; Conservative 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
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SEQ ID NO 12
LENGTH: 172
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Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                          GENERAL INCORMATION:
APPLICANT: MACHARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
FITTLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 266
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ORGANISM: Human papillomavirus type 16
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Patent No. 6428807
9; Conservative
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ORGANISM: Homo sapien
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US-09-367-309A-1
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Sequence 10, Application US/09359382

Patent No. 6306397

GENERAL INFORNATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Ilizabeth Ann

APPLICANT: WEBB, Ilizabeth Ann

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER FILING DATE: 1997-09-22

EARLIER FILING DATE: 1997-09-22

EARLIER FILING DATE: 1997-09-22

EARLIER FILING DATE: 1994-12-20

MUMBER OF SEQ ID NOS: 27

SOFTWARDE: DESCAIL ON SEC 12 NOS: 27

SOFTWARDE: DESCAIL ONS: 27
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| Sequence 10. Application US/08860165A |
| Patent No. 6004557 |
| Patent No. 6004567 |
| Patent No. 600468 |
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| Patent Patent No. 600468 |
| Patent Raphication Number: 1997-09-22 |
| Patent Raphication Number: Patent No. 600468 |
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100.0%; Pred. No. 0.076; ative 0; Mismatches 0; Indels
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SEQ ID NO 10
LENGTH: 266
                            9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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US-09-359-382-10
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RESULT 13
US-09-486-885-10
Sequence 10. Application US/09485885
Patent No. 6342224
Jatent No. 63424
Jatent No. 63434
Jatent No. 6344

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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Combardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT FILING DATE: 2000-2-18
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 371
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Patent No. 6342224
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Best Local Similarity 100.
Matches 9; Conservative
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US-09-485-885-6
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RESULT 15 US-09-485-885-14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE=Cervical tissue;
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14515; AAB60569.2; -.
GO; GO:000477; F. Chost cell nucleus; IEA.
GO; GO:000377; F: DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; Galutira D.F., Younghushand B.H.;
Submitted (GEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                          E6 protein (Fragment).

Human papillomavirus.

Yiruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

NCBI_TaxID=10566;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
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Last sequence update)
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               098B21
0988C3
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098MP3
098MP4
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01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
E6 protein (Fragment).
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Best Local Similarity
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Q80886;
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Maximum Match 100%
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MEDINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874[2002].
Int. J. Cancer 97:868-874[2002].
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1; -.
GO; GO:000477; F.INA binding; IEA.
InterPro; IPR001334; E6.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; debny viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10566;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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90 AA; 10964 MW; BC2531643ACBA76C CRC64;
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NCBI_TaxID=10581;
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SEQUENCE FROM N.A.
STRAINSHPVI6; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
BMBL, U14513; AB80567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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STRAIN-HPV16; TISSUE-Cervical tissue;
STRAIN-HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14514; AAB60568.2; -.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPrc; IPR001314; E6.
PFam; PF00518; E6; 1.
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Papillomavirus.
NCBI_TaxID=10566;
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Papillomavirus.
NCBI_TaxID=10566;
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90 Aa; 10904 MW; 5D3ADF843AD6060B CRC64;
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01-NOV-1996 (TYEMBLrel. 01, Created)
01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
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E6 protein (Fragment).
Human papillomavirus.
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Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874[2002].
EMBL; AF404700; AAL01357.1; ---
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
FFam; PF00518; E6; 1.
NON TER
SEQÜENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses, deput viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
        Pred. No. 0.13;
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Best Local Similarity 100.
Matches 9; Conservative
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21 VYDFAFRDL 29
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Best Local Similarity
Matches 9; Conserva
                                                                                   1 VYDFAFRDL
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MEDLINE=21846229; PubMed=11857370;

MEDLINE=21846229; PubMed=11857370;

Matts K.J.; Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868=874 (2002).

GO; GO:0044703; AAL01363.1;

GO; GO:0044703; P.DNA binding; IEA.

GO; GO:0003677; P.DNA binding; IEA.

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                                                     Query Match 100.0%; Score 48; DB 2; Length 99; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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99 AA; 12005 MW; C2B96025EC370E38 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NON TER 1
SEQÜENCE 130 AA; 15775 MW; 92D3C07BF9
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MEDLINE=21846229; PubMed=11857370;
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NCBI_TaxID=10581;
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NCBI TaxID=10581;
SEQUENCE
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34 VYDFAFRDL 42
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002)
EMBL; AF404694; AAL01345-1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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B6 protein (Fragment).

Human papillomavirus type 16.

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

Papillomavirus.

NCBI_TaxID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OF-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment 25, Last annotation update)
Human papillomavirus type 16.
Viruges, dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                                                                                                                                                                           (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; Pubmed=11857370;
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Best Local Similarity 100.
Matches 9; Conservative
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21 VYDFAFRDL 29
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29 VYDFAFRDL 37
                              21 VYDFAFRDL 29
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1 VYDFAFRDL 9
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01-DEC-2001
01-DEC-2001
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; Ap4047025; AL01361.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404698; AAL01353.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 48; DB 2; Length 143; 100.0%; Pred. No. 0.15; ive 0; Mismatches 0; Indel8
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01-DEC-2001 (TTENBLrel. 19, Created)

01-DEC-2001 (TTENBLrel. 19, Last sequence update)

01-OCT-2003 (TTENBLrel. 25, Last annotation update)

E6 protein (Fragment).

Human papillomavirus type 16.

Viruses; deNNA viruses, no RNA stage; Papillomaviridae;

Papillomavirus.
                                                                                                                             E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
                                               (TremBlrel. 19, Created)
(TremBlrel. 19, Last sequence update)
(TremBlrel. 25, Last annotation update)
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143 AA.
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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nes 9; Conservative
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PRELIMINARY;
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RESULT 15

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O12335
PRELIMINARY; PRT; 151 AA.

AC 012335
DT 01-JUL-1997 (TrEMELrel. 04, Last sequence update)
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OC Viruses; depote of TrEMELrel. 15, Last annotation update)
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CO VIRUSES; depote of Tremellomavirus
CO VICTI TAXID-10581;
RA TOTTGES-10 M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
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RA TOTTGES-10 M.L., Buonaguro P.M., Meglio M., BEP32ABB016CC88B CRC64;

Query Match
RA TOTTGES-10 M.L., Buonaguro M., Mismatches D., Indels D., Gaps D.,
RA TOTTGES-10 M.L., Buonaguro M., Mismatches D., Indels D., Gaps D.,
RA TOTTGES-10 M.L., Buonaguro M., Mismatches D., Indels D., Gaps D.,
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RA TOTTGES-10 M.L., Buonaguro M., Mismatches D., Indels D., Gaps D.,
RA TOTTGE-10 M.L., Buonaguro M., Mismatches D., Indels D.,
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Search completed: June 29, 2005, 01:34:48 Job time : 55.2473 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-67 Title: Perfect score:

1 VYDFAFRDL 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SUMMERTES	
Result		Query				
No.	Score	Match	Match Length	BB	QI	Description
1	48	100.0	158	г	WEWLHS	protein E6 - human
8	43	89.6	148	~	836515	ein -
n	42	87.5	149	7	W6WL33	
4	39	81.2	158	~	836561	E6 protein - human
S	38	79.2	149	н	W6WL58	E6 protein - human
9	38	79.2	158	н	W6WL39	E6 protein - human
7	37	77.1	158	-1	W6WL18	6 protein -
80	37	77.1	158	-	W6WLPR	E6 protein - human
6	36	75.0	128	7	A81153	type I restriction
10		72.9	246	~	B69230	conserved hypothet
11		72.9	324	~	A97919	3-oxoacyl-[acyl-ca
12		72.9	324	~	C95048	3-oxoacyl-(acyl-ca
13	35	72.9	483	~	A97295	fusion of Uroporph
14	34	70.8	149	-	W6WL31	E6 protein - human
15	34	70.8	154	7	836527	E6 protein - human
16	34	70.8	155	Н	W6WL43	ı
17	34		195	0	A96779	hypothetical prote
18	34	70.8	285	7	B64712	ç
19	34	•	285	~	E71803	
20	34	70.8	544	7	C42653	
21	33	68.8	88	7	AF1937	hypothetical prote
22	33	68.8	149	ч	W6WL35	
23	33	68.8	174	7	T50419	hypothetical prote
24	33	68.8	193	7	T16662	
25	33	68.8	270	~	D90542	conserved hypothet
56	33	8	290	~	T47991	
27	33	œ.	325	~	C86721	
28	33	٠	432	7	A84798	hypothetical prote
29	33	68.8	434	7	AD0061	>

S36515
B6 protein - human papillomavirus type 34
C;pspcies: human papillomavirus type 34
C;pspcies: human papillomavirus type 34
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C;pacession: S36515
R;belius, H.; Hofmann, B.
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R;belius, H

RESULT 2

aminopeptidase C [cysteine aminopept	DNA nucleotidylexo	hypothetical prote	hypothetical prote	insulin precursor	hypothetical prote	E6 protein - human	carbonic anhydrase	competence transcr	hypothetical prote		hypothetical prote	hypothetical prote	hypothetical prote
B95033 B97904	S48143	B23595	F84646	G90581	IPCA	H71905	836503	B69078	843611	C71013	F86471	H96702	E90298	T47992
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4 4 4 4 4 4 4	445	529	697	1228	108	133	153	176	192	203	231	232	244	278
68.8	68.8	68.8	8.8	68.8	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
33	33	33	33	33	32	32	32	32	32	32	32	32	32	32
30	32	33	4.4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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but an appillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: as-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
Vixology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Recension: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT: P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Readidues: 1-158 dSEE>
A;Cross-references: UNIPROT: P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the levaluation: preliminary; translated from GB/EMBL/DDBJ
A;Resesion: T10427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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C;Superfamily: papillomavirus E6 protein
C;Superds: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
E;110-146/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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A, Residues: 1-149 <KIR>
A, Cross-references: UNIPROT: P26555; GB: D90400; NID: 9222386; PIDN: BAA31845.1; PID: 933370
C, Superfamily: papillomavirus E6 protein
C, Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.
C;Superfamily: papillomavirus ES protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: host Homo_sapiens (man)
C;Date: 11-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502
R;Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.2%; Score 38; DB 1; Length 158; 77.8%; Pred. No. 1.8;
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C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Title: Human papillomavirus type 58 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                         79.2%; Score 38; DB 77.8%; Pred. No. 1.6; Live 0; Mismatches
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C,Species: human papillomavirus type 39
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Matches 7; Conservative
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A;Status: translation not shown
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Matches 7; Conservative
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42 VYDFVFADL 50
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44 VYEFAFSDL 52
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A,Reaidues: 1-158 <DEL:
A,Creasures: 1-158 <DEL:
A,Creasures: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970
C,Superfamily: papillomavirus E6 protein
C,Reywords: DNA binding; early protein; nucleus; zinc finger
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A,Readdues: 1-149 <CCD.>
A,Readdues: 1-149 <CCD.>
A,Readdues: 1-149 <CCD.>
A,Cross-references: UNIPROT: P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C,Superfamily: papillomavirus E6 protein
C,Superfamily: papillomavirus E6 protein
C,ScWywords: DNA blinding; early protein; zinc finger
E;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
  A;Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g3969
                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
B;Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, NA Feference number: A33020; MUID:86200464; PMID:3009902
A;Accession: A03683
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C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: human papiilomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36561
                                                                                                                                                        Gaps
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36561
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Pred. No. 1.1;
1; Mismatches 1; Indels
                                                                                                  89.6%; Score 43; DB 2; Length 148; 88.9%; Pred. No. 0.15; ive 0; Mismatches 1; Indels
                            C;Superfamily: papillomavirus B6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                            Local Similarity 88.9
nes 8, Conservative
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VYQFAFKDL 52
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DB 2; Length 128;

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Query Match 75.0%; Score 36; Best Local Similarity 75.0%; Pred. No. 3 Matches 6; Conservative 1; Mismatcl
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87.5%;
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Best Local Similarity 87.5'
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6, Conservative
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217 VFDFAIRDV 225
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108 IYDFAFDD 115
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C.Species: Neisseria meningitidis
C.Species: Neisseria meningitidis
C.Species: Neisseria meningitidis
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A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Date: 30-0m-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
B;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: C40509
A;Accession: c40509
A;Accession: pape: DNA
A;Residues: L-158 <REU>
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A;Experimental source: serogroup B, strain MC58
C;Genetics:
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                      Affections: 1-158 CCCL>
Affections: 1-158 CCCL>
Affections are references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
Affections are references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
B;Matlashewski, G:, Banks, L:, Mu-Liao, J:, Spence, P.; Pim, D.; Crawford, L.
Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacterie A;Rontenran number: A92791; MUID:8630665; PMID:3018129
A;Contents: annotation; identification of the protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding: early protein; transforming protein; zinc finger
F;105-141/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2.8;
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C;Superfamily: papillomavirus B6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.1%; Score 37; DB 1; 66.7%; Pred. No. 2.8;
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77.8%; Pred. No. ....
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44 VFEFAFKDL 52
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44 VYEFAFGDL 52
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Matches 6; Conserv
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A; Molecule type: DNA
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Conserved hypothetical protein MTH972 - Methanobacterium thermoautotrophicum (strain D. Cispecies: Methanobacterium thermoautotrophicum (cispecies: Methanobacterium 186920) (cispecies: Methanobacterium 186920) (cispecies: Mismith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Mismith, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, P.K.; S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 (Methanobacterium thermoautotrophicum Delta H: funch Reference number: A69000; MUID:98037514; PMID:9371463 (Misminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-246 (MTH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:027053; GB:AE000871; GB:AE000666; NID:g2622069; PIDN:AAB85^
A;Experimental source: strain Delta H
C;Genetics:
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A;Residues: 1-324 «KUR»
A;Cross_references: UNIPROT:Q93NA1; GB:AE007317; PIDN:AAK99181.1; PID:g15457938; GSPDB
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Pred. No. 17;
2; Mismatches 1; Indels
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Pred. No. 12;
0; Mismatches
1; Mismatches
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C;Superfamily: 3-oxoacyl-[acyl-carrier-protein]
C;Keywords: acyltransferase
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A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-149 cGCL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g45991
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: $36469
A;Accession: $35627
A;Accession: $35627
A;Accession: $35627
A;Accession: $35627
A;Residues: 1-154 <DEL>
A;Residues: 1-154 <DEL>
C;Superfemences: UNIPRROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397
C;Superfemences: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397
C;Superfemences: UNIPROT Protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
836527
EG protein - human papillomavirus type 53
C;Species: human papillomavirus type 53
C;Species: human papillomavirus type 53
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 83627
R;Delius, H; Hofmann, B.
Bibmitted to the EMBL Data Library, August 1993
A;Degoription: Primer-directed sequencing of human papillomavirus types.
                                                                                                                                                                                                                                                                                                                                                          Query Match 70.8%; Score 34; DB 1; Length 149; Best Local Similarity 77.8%; Pred. No. 11; Matches 7; Conservative 0; Mismatches 2; Indels
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Job time : 12.2747 secs
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Best Local Similarity 66.7
Matches 6; Conservative
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46 VYNFAYTDL 54
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R;Tettelin, H: Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: C95048
A;Accession: C95048
A;Molecule type: DNA
A;Residues: 1-324 akuna
A;Residues: 1-324 akuna
A;Residues: 1-324 akuna
A;Cross-references: UNIPROT:Q93NA1; GB:AE005672; PIDN:AAK74580.1; PID:g14971886; GSPDB:C
C;Genetics:
A;Gene: SP0417
C;Superfamily: 3-oxoacy1- [acy1-carrier-protein] synthase III
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R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
                                    3-oxoacyl-(acyl-carrier-protein) synthase III [imported] - Streptococcus pneumoniae (str
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
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A;Cross-references: GB:AE001437; PIDN:AAK81148.1; PID:g15026284; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
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A,Note: host Homo sapiens (man)
C,Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
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Pred. No. 17;
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72.9%;
Best Local Similarity 66.7%;
Matches 6; Conservative
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Matches 7; Conservative
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Sequence 16, Appli Sequence 2, Appli Sequence 15, Appli Sequence 157, Appl Sequence 158, Appl Sequence 160, Appl

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Sequence 4, Al Sequence 10, Sequence 10, Sequence 6, Al Sequence 14, Sequence 14, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 29, Sequence 29, Sequence 29, Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Sequence 6, Al Sequence 27, Seq

us-08-170-344-67.rapb

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Run on:

Sequence:

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GS-10-751-845-84

| Sequence 84, Application US/10751845 |
| Sequence 84, Application No. US20050100928A1 |
| Sequence 84, Application No. US20050100928A1 |
| SENERAL INFORMATION: |
| APPLICANT: Hedley, Mary Lynne |
| APPLICANT: Chicz, Roman M. |
| TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES |
| FILE REPERENCE: 08191-013001 |
| CURRENT APPLICATION NUMBER: US/10/751,845 |
| FILE REPERENCE: 2004-01-05 |
| PRIOR APPLICATION NUMBER: US 60/169,846 |
| PRIOR APPLICATION NUMBER: US 60/169,846 |
| PRIOR APPLICATION NUMBER: US 60/154,665 |
| PRIOR PILING DATE: 1999-12-09 |
| PRIOR FILING DATE: 1999-09-16 |
| NUMBER OF SEQ ID NOS: 163 |
| SOFTWARE: FASTERE for Windows Version 4.0 |
| SEQ ID NOS: 163 |
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US-09-758-759-111
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US-10-484-063-27
US-10-883-184-2
US-10-367-057-16
US-10-472-724-2
US-10-751-845-159
US-10-751-845-158
US-10-751-845-168
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US-10-899-771-4
US-10-899-771-10
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US-10-899-771-14
US-10-899-771-14
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US-10-899-771-14
US-10-899-771-14
US-10-368-046-10
US-10-368-046-10
US-10-368-046-10
US-10-476-570-29
US-10-476-570-29
US-10-800-023-27
US-10-800-023-21
US-10-899-771-21
US-10-899-771-21
US-10-899-771-23
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      Query Match
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Matches 9
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64.268 Million cell updates/sec
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Sequence 2
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                                                                                                                                          June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.pep:*
| Cgn2_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*
                 GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-239-113A-291
US-10-444-063-5
US-10-751-845-94
US-10-451-645-94
US-10-458-384-6
US-10-751-845-65
US-10-751-845-65
US-10-777-390-6
US-10-77-390-6
US-10-484-063-20
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                                                                                                                                                                                                                                                                                                                                                                           1717557 segs, 384547976 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Searched:

Sequence 41, Appl Sequence 65229, A Sequence 111, App Sequence 13357, A

Sequence 21, Sequence 21, Sequence 23, Sequence 23,

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KESULT 2
US-10-239-313A-291
Sequence 291, Application US/10239313A
Sequence 291, Application US/10239313A
Sequence 291, Application No. US20030175285A1
GENERAL INFORMATION:
APPLICANT: CREMIA, Mathalie
APPLICANT: CREMIA, Mathalie
APPLICANT: CREMIA, Liliane
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: MOLECULE OF PARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: NO-TERMINAL A GLUTAMINE IN THE FORM
TITLE OF INVENTION: NO-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: NO-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
TITLE OF INVENTION: NO-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: FR 00/03711
PRIOR PLICATION NUMBER: FC 01/70772
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR PLING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SEQ ID NO 291
LENGTH: 10
LENGTH: 10
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LENGTH: 10
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US-10-484-063-5
i Sequence 5, Application US/10484063
i Publication No. US20050048467Al
i Berlian No. US20050048467Al
i GENERAL INFORMATION:
i APPLICANT: SASTRY, K. JAGANNADHA
i APPLICANT: TORTOLERO-LUNA, GUILLERMO
i TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
i TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
i FILE REFERENCE: UTSC: 560US
i CURRENT APPLICATION NUMBER: US/10/484,063
i CURRENT PILING DATE: 2004-01-16
i PRIOR PILING DATE: 2002-07-19
i PRIOR PILING DATE: 2001-07-20
i NUMBER OF SEQ ID NOS: 27
i SOFTHARE: PATENTING DATE: 2001-07-20
i NUMBER OF SEQ ID NOS: 21
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ORGANISM: Human papillomavirus
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2 VYDFAFRDL 10
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 10
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RESULT 4 US-10-751-845-92

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; Sequence 94, Application US/10751845
; Publication No. US2050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Urban, Robert G.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT FILING DATE: 2004-01-05
; PRIOR FILING DATE: 2004-01-05
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; RIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; RIOR APPLICATION NUMBER: US 60/169,846
; RIUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
Sequence 92, Application US/10751845
Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TILLE OF INVENTION: UUCLEIC ACIDS ENCODING POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/09/664,225
FILE REPLIANTO NUMBER: US/09/664,225
FRICH APPLICATION NUMBER: US 60/169,846
FRICH FILING DATE: 1999-12-09
FRIOR FILING DATE: 1999-12-09
FRIOR FILING DATE: 1999-01-6
FRIOR FLING DATE: 1999-01-6
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION NUMBER: US 60/154,665
FRIOR APPLICATION OF SEQ ID NOS: 163
FRIOR APPLICATION OF SEQ ID NOS: 163
FRIOR FILING DATE: 1999-09-16
FRIOR PLING DATE: 1999-09-16
FRIOR APPLICATION OF SEQ ID NOS: 163
FRIOR PLING DATE: 1099-09-16
FRIOR APPLICATION OF SEQ ID NOS: 163
FRIOR PLING DATE: 1999-09-16
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; ORGANISM: Human Papilloma virus
US-10-751-845-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 9; Conservative
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US-10-751-845-94
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US-10-484-063-4
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Sequence 126, Application US/10751845
| Sequence 126, Application US/10751845
| Publication No. US20050100928A1
| GENERAL INFORMATION:
| APPLICANT: Hedley, Mary Lynne
| APPLICANT: Urban, Robert G.
| APPLICANT: Urban, Robert G.
| APPLICANT: Orlicz, Robert G.
| PRICE REFERENCE: 0819-013001
| CURRENT APPLICATION NUMBER: US/09/664,225
| PRIOR PILING DATE: 2000-08-18
| PRIOR FILING DATE: 1999-12-09
| PRIOR FILING DATE: 1999-12-09
| PRIOR FILING DATE: 1999-09-16
| NUMBER OF SEQ ID NOS: 163
| NUMBER OF SEQ ID NOS: 163
| SEQ ID NO 126
| SEQ ID NO 126
| MANDER OF SEG ID NOS: 163
                        APPLICANT: Chicz, Roman M.

ITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR PELING DATE: 2000-08-18
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR PILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 48; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0: Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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APPLICANT: Schuler, Gerold; APPLICANT: N.V. Antwerps Innovatiecentrum
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
             Urban, Robert G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 9; Conservative
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US-10-177-390-6
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OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
OTHER INFORMATION: for E6 of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Publication No. US20050033025A1

GRERAL INFORMATION:

APPLICANT: GROPPIN, JEANNINE

APPLICANT: GUILET, JEAN-GERAED

APPLICANT: GUINERINO: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

CURRENT APPLICATION NUMBER: US/10/858,384

CURRENT FILING DATE: 2004-06-02

PRIOR FILING DATE: 1990-06-03

NUMBER OF SEQ ID NOS: 24

SOUTWARE: PATENTIN VET. 3.2
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REPRENCE: USC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PLANTANT NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human papillomavirus US-10-484-063-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 9; Conservative
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US-10-858-384-6
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LENGTH: 22
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NUMBER OF SEQ ID NOS: 27
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LENGTH: 158
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US-10-858-384-2
                                                                                   LENGTH:
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| GENERAL INFORMATION:
| APPLICANT: SASTRY, K. JAGANNADHA
| APPLICANT: POLICAN MICHELE
| APPLICANT: FOLLEN MICHELE
| TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HEV-ASSOCIATED
| TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN
| FILE REPERBINE: UTSC:560US
| TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
| FILE REPERBINE: 2004-01-16
| PRIOR APPLICATION NUMBER: PCT/US02/23198
| PRIOR APPLICATION NUMBER: FOT/US02/23198
| PRIOR PLING DATE: 2001-07-19
| PRIOR FILING DATE: 2001-07-20
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: PATENTIN VET: 2.1
| SEQ ID NO 20
| LENGTH: 151
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| Sequence 27, Application US/10484063
| Publication No. US20050048467A1
| GENERAL INPORMATION:
| APPLICANT: SASTRY, K. JAGANNADHA
| APPLICANT: FOLLEN, MICHELE
| TILLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
| TILLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN
| FILE REPRERENCE: UTSC:560US
| CURRENT APPLICATION NUMBER: US/10/484,063
| CURRENT FILING DATE: 2004-01-16
| PRIOR PILING DATE: 2002-07-19
| PRIOR PILING DATE: 2002-07-19
| PRIOR FILING DATE: 2001-07-20
| PRIOR FILING DATE: 2001-07-20
TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear TITLE OF INVENTION: POLymucleotides by Blectroporation FILE REFERENCE: 021505w/JH/ml.
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 151
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Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                           ORGANISM: Human papillomavirus type 16
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; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
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US-10-484-063-20
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                                                                                                                                                                                                                                                  TYPE: PRT
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100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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Sequence 16, Application US/10367057

Sublication No. US20050100554A1

GENERAL INFORMATION:

APPLICANT: Cuthill, Scott;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Cool, Chean Eng A.;

TITLE OF INVENTION: Complexes and Methods of Using Same;

FILE REFERENCE: 21402-559

CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/256,911

PRIOR APPLICATION NUMBER: 60/256,911

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CuraSeqList version 0.1
                                                    ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                           42 VYDFAFRDL 50
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ORGANISM: Homo sapiens
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RESULT 15

US-10-472-724-2

Sequence 2, Application US/10472724

Publication No. US2004011806A1

GENERAL INFORMATION:
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFRENCE: 4121-154

CURRENT FILING DATE: 2003-09-17

PRIOR APPLICATION NUMBER: US/10/472,724

CURRENT FILING DATE: 2002-03-22

PRIOR APPLICATION NUMBER: EP 01107271.7

PRIOR APPLICATION NUMBER: EP 01107271.7

PRIOR APPLICATION NUMBER: EP 01107271.7

SOFTWARE: Patentin Version 3.2

SOFTWARE: Patentin Version 3.2

SOFTWARE: Patentin Version 3.2

SEQ ID NO 2

LENGTH: 171

TYPE: PRT

ORGANISM: Artificial Sequence

CREATURE:
CREATURE:
COTHER INFORMATION: Synthetic Construct
US-10-472-724-2
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                                          Query Match 100.0%; Score 48; DB 17; Length 158; Best Local Similarity 100.0%; Pred. No. 0.56; Matches 9; Conservative 0; Mismatches 0; Indels (
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Job time : 53.8517 secs
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54 VYDFAFRDL 62
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COMPUTER: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: TASTSCE for Windows Version 2.0

SOFTWARE: TASTSCE for Windows Version 2.0

SURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,339A

FILING DATE: O'-AUG-1993

APPLICATION NUMBER: US 07/926,666

FILING DATE: O'-AUG-1992

APPLICATION NUMBER: US 08/027,746

FILING DATE: O'-AUG-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: O'-AUG-1993

APPLICATION NUMBER: US 08/103,396

FILING DATE: O'-AUG-1993

APTORNEY/AGENT INPORMATION:
NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/POCKET NUMBER: 018623-005030US

TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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Sequence 14, Appl
Sequence 14, Appl
Sequence 161, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 564, App
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Sequence 276, App
Sequence 3, Appli
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17543, A
                                                                                      June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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Sequence 14, 7
Sequence 10, 7
Sequence 10, 7
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-159-339A-564
US-07-990-122-4
US-09-980-523A-6
US-09-980-523A-2
US-09-980-523A-2
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-09-359-382-14
US-09-359-382-14
US-09-359-382-10
US-09-485-885-4
US-09-485-885-4
US-09-485-885-4
US-09-485-885-14
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 2, Appli
Sequence 8, Appli
Sequence 36699, A
Sequence 51916, A
Sequence 5878, Ap
Sequence 4486, Ap
Sequence 6351, Ap
Sequence 6351, Ap
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                                                                                                                                                                                          44, Appl
46, Appl
41497, A
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                       Sequence
US-08-746-797-2
US-08-927-387-2
US-08-918-058-2
US-09-810-836B-8
US-09-270-767-51916
US-09-107-5328-5878
US-09-107-5328-5878
US-09-107-5328-6878
US-09-583-110-4066
US-09-583-110-4066
US-09-583-110-4066
US-09-583-110-4066
US-09-452-239-44
US-09-452-239-46
US-09-452-239-46
US-09-270-767-41497
US-09-228-991A-16878
US-09-228-991A-16878
US-09-248-7966-18343
US-09-248-7966-18343
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SSULT 1 5-08-159-339A-246	Sequence 246, Application US/08159339A	Patent No. 6037135	GENERAL INFORMATION:	APPLICANT: Kubo, Ralph T.	APPLICANT: Grey, Howard M.	APPLICANT: Sette, Alessandro	APPLICANT: Celis, Esteban	TITLE OF INVENTION: HLA Binding peptides an	TITLE OF INVENTION: Uses	NUMBER OF SEQUENCES: 1254	CORRESPONDENCE ADDRESS:

ALIGNMENTS

NAKESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STEBT: Two Embarcadero Center, Eighth Floor
CITY: San Francisco

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids

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RESULT 4
US-09-980-523A-6
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                                     100.0%; Score 48; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Gette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FLLING DATE: 29-NOV-1993
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFLALLIUN: 4-2-4
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,7622
                                                                                                                                                                                                                                                   Sequence 564, Application US/08159339A
Patent No. 6037135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564:
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TELECOMONDIVERION: 17ELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                   Query Match
Best Local Similarity 100.
Matches 9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                          ||||||||||
1 VYDFAFRDL 9
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                                                                                                                 1 VYDFAFRDL 9
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US-08-159-339A-246
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RESULT 3

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Patent No. 341595

GREGALIA INCOMANIA, CARN K.
APPLICANT. GROWNING.
ATCORNY. AGAIN. TO GROWNING.
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PRIOR FILING DATE: 1999-06-03
                         NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYDFAFRDL 57
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                                                                          SEQ ID NO 2
LENGTH: 158
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US-09-601-729-276

US-09-601-729-276

Sequence 276, Application US/09601729

Patent No. 6683052

GENERAL INFORMATION:

APPLICANT: THIAM, KADER

APPLICANT: GRAS-MASSE, HELENE

APPLICANT: GRAS-MASSE, HELENE

APPLICANT: GOINVERTION:

APPLICANT: GOINVERTION:

APPLICANT: GOINVERTION: LIPPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES

TITLE OF INVENTION: LIPPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT TITLE OF INVENTION: LIPPOPEPTIDES

PILE REFERENCE: USB-97-AU-IN

CURRENT FILING DATE: 2000-11-2/0

PRIOR APPLICATION NUMBER: PCT/FR99/00259

PRIOR PELING DATE: 1999-02-05

PRIOR PILING DATE: 1999-02-05

PRIOR PILING DATE: 1999-02-05

PRIOR PILING DATE: 1999-02-05

PRIOR PLOS: 281

SEQ ID NOS: 281

SEQ ID NO 276

LENGTH: 23

TAVED: 1077

LENGTH: 23

TAVED: 1077
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APPLICANT: CHOTFIN, USANNINE
APPLICANT: COURTER, PRANCINE
APPLICANT: COUNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USF
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USF
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USF
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: FR 99/07012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
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                                                                                                                     Query Match 100.0%; Score 48; DB 4; Length 22; Best Local Similarity 100.0%; Pred. No. 0.0097; Matches 9; Conservative 0; Mismatches 0; Indels
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                       ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6
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APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                   5 VYDFAFRDL 13
                                                                                                                                                                                                                       1 VYDFAFRDL 9
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US-09-980-523A-2
LENGTH: 22
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Sequence 3, Application US/08316239B
Sequence 3, Application US/08316239B
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                      ö
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                                                                                     100.0%; Score 48; DB 4; Length 158; 100.0%; Pred. No. 0.079; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 48; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 0.081; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER RADDALE FOOM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FITTING DATE: 30-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION: (703) 817-9453
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 162 amino acids STRANDEDNESS: not relevant
                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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118 VYDFAFRDL 126
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US-08-117-083-10
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       LENGTH: 172
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Sequence 4, Application US/08316239B

Patent No. 5679509

GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SUGURNCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Aggliani & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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15-00-16 / Application US/08860165A

15 Sequence 14, Application US/08860165A

16 GENERAL INPORMATION:
1 APPLICANT: EDWARDS, Stirling John
1 APPLICANT: COX, John Cooper
1 APPLICANT: COX, John Cooper
1 APPLICANT: FRAZER, Ian
2 APPLICANT: FRAZER, Ian
2 TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
3 FILE REFERENCE: 1722/130

5 CURRENT APPLICATION NUMBER: DCT/AU95/00868

5 EARLIER APPLICATION NUMBER: PCT/AU95/00868

5 EARLIER APPLICATION NUMBER: AD PROSTON NUMBER: A
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MEDIUM TYPE: Plopy disk

COMPUTER: ISP POCOMPATIBLE

COMPUTER: ISP POCOMPATIBLE

COMPUTER: ISP POCOMPATIBLE

COMPUTER: ISP POCOMPATIBLE

COMPUTER: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/316,239B

FILING DATE: 30-SEP-1994

CLEASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jagtiani, Ajay A.

REFERENCE/DOCKET NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFONE: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOPOLOGY: not relevant
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Best Local Similarity
Matches 9; Conserv
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   US-08-316-239B-4
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STATE:
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US-09-389-382-14

i Sequence 14, Application US/09359382

j Batent No. 6306397

i GENERAL INPORMATION:

APPLICANT: EDWANDS, Stirling John

APPLICANT: EDWANDS, Stirling John

APPLICANT: EDWANDS, Stirling John

APPLICANT: ELZABER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 01727/0148

CURRENT FILING DATE: 1999-07-23

CURRENT FILING DATE: 1999-07-23

EARLIER FILING DATE: 1995-07-25

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-112-20

MUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 14

LENDERTH: 172

LENDERTH: 172
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; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursonell, Michael E.
APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CONTY: San Francisco
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-14
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                                                                                                     Query Match 100.0%; Score 48; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.087; Matches 9; Conservative 0; Mismatches 0; Indels
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US-09-359-382-14
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Gapa
                                                                        GENERAL INFORMATION:
APPLICANT: EDMARDS, Stirling John
APPLICANT: EDMARDS, Stirling John
APPLICANT: EDMARDS, Stirling John
APPLICANT: WEBS, John Cooper,
APPLICANT: WEBS, Elizabeth Ann
APPLICANT: WEBSER, Ian
TILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 01722/10148
CURRENT FILING DATE: 1999-00-23
CURRENT FILING DATE: 1999-00-22
ERALIER PILING DATE: 1997-09-22
ERALIER FILING DATE: 1995-12-20
ERALIER FILING DATE: 1994-12-20
ERALIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.0
SOFTWARE: PATENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: 1870/367, 309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHIN OF: 2.1
SEQ ID NO: 260
LENGTH: 266
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
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; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
                                       Sequence 10, Application US/09359382 Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09367309A
; Patent No. 6428807
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US-09-485-885-4
Sequence 4, Application US/09485885
Patent No. 634224
GENERAL INFORMATION:
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Best Local Similarity 10v...
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                        US-09-359-382-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
LOCATIONS: 1..182
OTHER INFORMATION: Anote= "Xaa refers to stop codon in
OTHER INFORMATION: the open reading frame."
              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                A-58783
PC-DOS/MS-DOS
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: 3-587
TELEPHONE: 415-781-1989
TELEPHONE: 415-781-1989
TELEFRX: 910 277299
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TTYPE: amino acids
TTYPE: amino acids
TTYPE: amino acids
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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Matches 9; Conserv
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LENGTH: 266
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Gaps

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### APPLICANT: Bruck, Claudine
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Teresa
| APPLICANT: Cabezon Silva, Angela
| TITLE OF INVENTION: Vaccine
| TITLE OF INVENTION: Vaccine
| TITLE OF INVENTION: Vaccine
| TITLE REPERENCE: B45107
| CURRENT FILING DATE: 2000-02-18
| PRIOR APPLICATION NUMBER: PCT/EP98/05285
| PRIOR PLING DATE: 1999-08-17
| PRIOR PLING DATE: 1997-08-22
| NUMBER OF SEQ ID NOS: 23
| NUMBER OF SEQ ID NOS: 23
| NUMBER OF SEQ ID NOS: 23
| TYPE: PRT
| ORGANISM: Homo sapien
| UND ORGANISM: Homo sapien
| ORGANISM: Homo sapien
| UND ORGANISM: Homo sapien
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds Run on:

(without alignments) 76.805 Million cell updates/sec

US-08-170-344-66 46 1 LLRREVYDF 9 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* 4 3 2 1. .. Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	protein E6 - human	Q)	cobyrinic acid a,c	hypothetical prote	Н	ш		replicative DNA he	replicative DNA he	probable replicati	hypothetical prote	ribonucleoside-dip	ribonucleoside-dip	hypothetical prote	hypothetical prote	E6 protein - human	E6 protein - human	E6 protein - human	conserved hypothet	heptosyltransferas	alcaligin synthesi	hypothetical prote	hypothetical prote	erythroid cell tra	xanthophyll epoxid	w	¤	probable RNA helic	aconitate hydratas
SUMMARIES	ΙΩ	W6WLHS	C75514	E69528	T27014	B81293	E86567	D72056	E81610	H81665	G71503	T05117	B48687	A49412	T01377	C85018	W6WL33	W6WL35	W6WL58	G70231	B81001	JC4556	D70542	A71273	150224	T09537	S69548	T07754	S63453	S50387
	DB		7	7	~	~	N	~	7	'n	~	~	~	~	7	~		-	-	N	0	~	~	~	~	~	~	~	~	0
	Length	158	299	458	635	254	449	449	468	472	472	487	804	847	991	1117	149	149	149	190	322	461	469	479	582	99	663	699	737	778
a	Query Match	100.0	78.3	78.3	78.3	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9	73.9		73.9	73.9
	Score	46	36	36	36	35	35	32	32	35	35	32	35	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34
	Result No.	п	7	Ю	4	ഗ	9	7	œ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

E6 protein - human	E6 protein - human	E6 protein - human	E6 protein - rhesu	hypothetical prote	YghA protein [impo	×	hypothetical prote	oligo-1,6-glucosid	conserved hypothet	oligo-1,6-glucosid	type I restriction	spore cortex synth			ribosomal protein
A61237	S36515	836573	W6WLR1	877228	F87705	C89903	T19319	JQ0535	H90608	D70034	E75221	A84232	S28292	F87330	F75534
2	~	~	-	~	N	N	N	~	~	~	~	N	7	~	~
148	148	148	191	199	229	265	503	509	537	561	623	099	772	824	142
71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	9.69
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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protein E - human papillomavirus type 16
C;Species: human papillomavirus type,16
C;Species: human papillomavirus type,16
C;Species: human papillomavirus type,16
C;Species: human papillomavirus type,16
C;Accession: A03682; T10427
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g33303
A;Nolocule type: DNA
A;Residues: 1-168 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:1848319
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev A;Reference number: 217014; MUID:91162763; PMID:1848319
A;Reference number: 217014; MUID:91162763; PMID:1848319
A;Residues: 1-168 <KEN>
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
A;Genetics:
A;Genetic
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Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
RESULT 1
W6WLHS
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Gaps ö Query Match 100.0%; Score 46; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.049; Matches 9; Conservative 0; Mismatches 0; Indels

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1 LLRREVYDF 9 셤 ð

RESULT 2

C75514 Conserved hypothetical protein - Deinococcus radiodurans (strain R1) C)Species Deinococcus radiodurans C)Species Deinococcus radiodurans C)Bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C)Accession: C75514 R)White, 0; Elsen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J., K) Shein, M.; Vomathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; I S, Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 A)Fitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A)Reference number: A75250; MUID:20036896; PMID:10567266

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A;Gene: dnaB
C;Superfamily: phage P22 gene 12 protein
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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207 LLKRKIYDY 215
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413 LLNREIFDF 421
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                    6
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A, Molecule type: DNA
A, Residues: 1-449 <STO>
                    1 LLRREVYDF
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A,Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.

A,Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A,Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-458 eKLE>
A;Festdues: 1-458 eKLE>
A;Cross-references: UNIPROT:028054; GB:AE000951; GB:AE000782; NID:g2689274; PIDN:AAB8902
C;Superfamily: cobyrinic acid a,c-diamide synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-635 <WIL>
A;Cross-references: UNIPROT:O18199; EMBL:293393; PIDN:CAB07691.1; GSPDB:GN00020; CESP:Y4
A;Experimental source: clone Y48ElB
                    A;Molecule type: DNA
A;Residues: 1-299 <WHI>
A;Cross-references: UNIPROT:Q9RX35; GB:AE001907; GB:AE000513; NID:g6458162; PIDN:AAF1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Introns: 77/3; 140/3; 143/2; 209/2; 236/2; 413/3; 437/1; 473/3; 510/1; 525/1; C; Superfamily: Caenorhabditis elegans hypothetical protein Y48E1B.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Y48E1B.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27014
R;McMurray, A.
                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                      Length 299;
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                                                                                                                                                                                                                                                                                        1; Indels
                                                                                       A; Experimental source: strain R1
C; Genetics:
A; Gene: DR0480
A; Map position: 1
C; Superfamily: conserved hypothetical protein MJ1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.3%; Score 36; DB 2; 75.0%; Pred. No. 18;
                                                                                                                                                                                                                                         Score 36; DB 2;
Pred. No. 11;
1; Mismatches
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A;Reference number: Z20299
                                                                                                                                                                                                                                         78.3%;
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Best Local Similarity 75.v.
''^a 6; Conservative
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Best Local Similarity 77.8<sup>3</sup>
Matches 7; Conservative
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256 LLDRELYDF 264
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317 LRNEIYDF 324
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A;Status: preliminary
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hypothetical protein Cj1467 [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;CAccession: Bl1293
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A;Recference number: A81259; MUD:20150912; PMID:10688204
A;Status: preliminary
A;Mcsedule type: DNA
A;Residues: 1-254 cPRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q9PMJ3; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB738
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E86567

replicative DNA helicase [imported] - Chlamydophila pneumoniae (strain J138)

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I

Nucleic Acids Res. 28, 2311-2314, 2000

A;Fitche: Comparison of whole genome sequences of chlamydia pneumoniae J138.

A;Accession: E86567
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C;Genetics:
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: D72056
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
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Pred. No. 15;
4; Mismatches 0; Indels
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probable replicative DNA helicase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
probable replicative DNA helicase - Chlamydia trachomatis
C;Species Chlamydia trachomatis
C;Species Chlamydia trachomatis
C;Species Chlamydia trachomatis
C;Species C;Species Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: G71503
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MU1D:99000809; PMID:9784136
A;Accession: G71503
A;Accession: G71503
A;Accession: G71503
A;Residues: 1-472 <ARN>
A;Cross-references: UNIPROT:084505; GB:AE001323; GB:AE001273; NID:g3328931; PIDN:AAC680
C;Genetics:
A;Gene: dnaB
C;Superfamily: phage P22 gene 12 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F7H19.40 - Arabidopsis thaliana
()Species: Arabidopsis thaliana (mouse-ear cress)
()Species: Arabidopsis thaliana (mouse-ear cress)
()Species: Arabidopsis thaliana (mouse-ear cress)
()Accession: T05117
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Me Bubmitted to the Protein Sequence Database, July 1998
A;Reference number: Z1539
A;Accession: T05117
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-487 cBEV>
A;Cross-references: UNIPROT: O82736; EMBL: ALO31018
A;Experimental source: cultivar Columbia; BAC clone F7H19
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: B48687
R;Rubin, H.; Salem, J.S.; Li, L.S.; Yang, F.; Mama, S.; Wang, Z.; Fisher, A.; Hamann, C Proc. Natl. Acad. Sci. U.S.A. 90, 9280-9284, 1993
A;Title: Cloning, sequence determination, and regulation of the ribonucleotide reductas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 4
A;Introns: 59/1; 112/1; 141/1; 185/2; 222/3; 239/3; 272/2; 297/3; 318/3; 343/3; 363/2;
A;Note: F7H19.40
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Pred. No. 30;
0; Mismatches 1; Indels
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   Indels
      1;
   Mismatches
   ;
0
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Best Local Similarity 87.5%;
Matches 7; Conservative
   7; Conservative
                                                                                                                421 LLRREYYD 428
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                                                                            A;Accession: E81610
A;Status: preliminary
A;Status: preliminary
A;Moldoule type: DNA
A;Residues: 1-468 «REA>
A;Cross-references: UNIPROT:Q9K2D6; GB:AE002174; GB:AE002161; NID:g7189059; PIDN:AAF3801
A;Experimental source: strain AR39, HL cells
C;Genetics: A;Genetics: CP0131
C;Superfamily: phage P22 gene 12 protein
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A,Status: preliminary
A,Molecule type: DNA
A,Residuse: 1-472 <TET>
A,FCSOSA-references: UNIPROT:Q9PJP4, GB:AE002346; GB:AE002160; NID:g7190805; PIDN:AAF3958
A,Experimental source: strain Nigg (MOPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: E81610
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID: 20150255; PMID: 10684935
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Accession: H81665
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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A; Reference number: A72000; MUID: 99206606; PMID: 10192388
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Pred. No. 28;
0; Mismatches
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Pred. No. 29;
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C,Superfamily: phage P22 gene 12 protein
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87.58;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity
                                                         Status: preliminary
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                                                                                                                                         A; Residues: 1-804 cMB>
A; Residues: 1-804 cMB>
A; Cross-references: UNIPROT: P50647; GB: L22057; NID: g349791; PIDN: AAA29755.1; PID: g349792
C; Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain
C; Superfamily: herpesvirus ribonucleoside biosynthesis; oxidoreductase; redox-active disulfide
F; 217-442,799-802/Disulfide bonds: redox-active #status predicted
F; 429, A29/Active site: Asn, Glu #status predicted
F; 429/Active site: Cys (cysteine thiyl radical intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain - malaria parasite (Plasm
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A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Plasmodium falciparum
Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
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Jate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
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Pred. No. 66;
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53;
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Pred. No. 56;
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A; Reference number: A48687; MUID: 94022359; PMID: 8415692
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Pred. No. 53;
2; Mismatches
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A;Molecule type: DNA
A;Residues: 1-991 <COR>
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Best Local Similarity 66...
6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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114 LISKEVYDF 122
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154 LISKEVYDF 162
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Best Local Similarity
                                   A; Accession: B48687
A; Status: preliminary
A; Molecule type: DNA
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A; Introns: 450/1
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C65018
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spri Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: C85018
A;Accession: C85018
A;Accession: C85018
A;Accession: C85018
A;Retaines: 1-1117 < C700>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9M133; GB:NC_001268; NID:g7267637; PIDN:CAB80949.1; GSPDB: C;Genetics: A;Gene: A74g01400 A;Map position: 4
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                                                                                                                                                                                                                     hypothetical protein AT4g01400 [imported] - Arabidopsis thaliana
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Pred. No. 75;
3; Mismatches
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55.6%;
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Best Local Similarity 55.6
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Run on:

Sequence:

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Result

Searched:

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MEDLINE-21846229; PubWed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404704; AL01365.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
PFGm; PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
                                                                                        Q8 jmu8
Q8 ghn0
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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NCBI_TaxID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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E6 protein (Fragment).
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MEDLINE-21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OFC-2003 (TrEMBLrel. 25, Last annotation update)
15 protein (Fragment 12)
16 protein (Fragment 12)
17 Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                          SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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                                                                                 Query Match
Best Local Similarity 100.0
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Matches 9; Conservative
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16 LLRREVYDF 24
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NCBI TaxID=10581;
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Q919C2;
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Q919C8
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Q919C2
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AA6040701; AAL01359.1; ---
EMBL, FA6040701; AAL01359.1; ---
GO; GO:0042025; Chost cell nucleus; IEA.
GO; GO:003677; P.DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL, AF404700, AAL01357.1; -.
GO, GO:0042025, C:host cell nucleus; IEA.
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Q91989;
Q1-BG.
G1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2003 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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0919C0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; debna viruses, no RNA stage; Papillomaviridae;
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   EMBL, AF404703; AAL01363.1; -.

GO; GO:0042025; C:host cell mucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.

Pfam; PF00518; E6; 1.

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SEQÜENCE 130 AA; 15792 MW; B6C2147D22'
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MEDLINE=21846229; PubMed=11857370;
                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
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nes 9; Conservative
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16 LLRREVYDF 24
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16 LLRREVYDF 24
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MEDLINE=21846229; PubMed=11857370;
Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; #AF040698; AAL01353.1; ---
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
NON TER
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SEQÜENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
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MEDLINE-97437474; PubMed-9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.,
Bath-Giraldo E., Giraldo G.,
Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
EMBL; AP003015; AABY0732.1; -.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein.
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Best Local Similarity 100.0
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Best Local Similarity 100.
Matches 9; Conservative
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29 LLRREVYDF 37
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NCBI_TaxID=10581;
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002)
EMBL; AF404702; AL01361.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; daDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus.
130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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SEQÜENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
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143 AA; 17272 MW; 071F14EB3E6BE2AC CRC64;
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24 LLRREVYDF 32
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NCBI_TaxID=10581;
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208 (1997).
EMBL, AF003016, AAB70733.1;
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34114; AAA91661.1; -.
EMBL; U34130; AAA91672.1; -.
EMBL; U34130; AAA91677.1; -.
EMBL; U34131; AAA91678.1; -.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10581;
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
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SEOUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=96079021; Pubmed=7494284;
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MEDLINE=20112892; PubMed=10644829;

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MEDLINE=20112892; PubMed=10644829;

MEDLINE=20112892; PubMed=1064829;

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

Nanalysis of human papillomavirus type 16 E6 variants in relation to gray coden 72 polymorphism genotypes in cervical carcinogenesis.";

J. Gen. Virol. 81:117-325 (2000).

REMBL, AJ388061; CAB45104.1; -..

REMBL, AJ388061; CAB45124.1; -..

REMBL, AJ388065; CAB45124.1; -..

ROJ, GO:0042025; C:host cell nucleus; IEA.

GOJ, GO:0043025; C:host cell nucleus; IEA.

InterPro. IPRO01834; E6.

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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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STRAIN-Xinjiang;
Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
"Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang.";
Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 ccoon 72 polymorphism genotypes in cervical carcinogenesis.";
Gen. Virol. 81:317-355 (2000).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
MEDLINE=22242222; Ayala F.J., Villarreal L.P.;
DeFlippis V.R., Ayala F.J., Villarreal L.P.;
"Evidence of diversifying selection in human papillomavirus type 16 Fbut not E7 oncogenes.";
J. Mol. Evol. 55:491-499(2002).
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
EMBL; AP469197; AA015691.1;
EMBL; AJ380663; CAB45118.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; OF312A8BDBA6CF1F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6 variant (Transforming protein E6).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Cruz M.R., Martins C.R.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF32781, AAG45540.1; -.
EMBL; AJ388057; CAB45106.1; -.
EMBL; AJ388069; CAB45106.1; -.
EMBL; AY089951, AAM11875.1; -.
EMBL; AY089954; AAM11875.1; -.
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                                                                                                            June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10P_RUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US10P_RUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US10P_RUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10P_RUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US10P_RUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-476-570-28
US-10-484-063-4
US-10-476-570-27
US-10-751-845-65
US-10-71-845-126
US-10-177-390-6
US-10-484-063-27
US-10-484-063-27
US-10-858-384-2
US-10-367-057-16
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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6, Appli
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Sequence 160, App
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Sequence 82, Application US/10751845

Publication No. US20050100928A1

GENERAL INFORMATION:
APPLICANT: Heddley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Order, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT PILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-01-6
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665

PRIOR APPLICATION NUMBER: US 60/154,665

NUMBER OF SEQ ID NOS: 163

SOFTWARE: FRAESEQ for Windows Version 4.0

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.larity 100.0%; Pred. No. 1.5e+06;
Conservative 0; Mismatches 0;
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US-10-751-845-82
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RESULT 5
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; Sequence 4, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
    APPLICANT: ADSIRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
    APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2002-01-19
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR PPLING DATE: 2001-07-19
; SOFTWARE: PALENTIN VOR: 27
; SEQ ID NOS: 27
; SEQ ID NO 4
; LENGTH: 15
                                                                                        APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: MOURGLE-MORATILLE, Sandra
APPLICANT: BOUNGLIE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: MINERINON: MARINER: Sandra
FILE REFERENCE: 45536-5071-US
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER: OF SEQ ID NOS: 63
SOFTWARE: PATCHIN Ver. 2.1
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                Sequence 28, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human papillomavirus
US-10-484-063-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Sequence 27, Application US/10476570

Sequence 27, Application US/2044A1

BUDLication No. US20040170644A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT:
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APPLICANT:
MAILLERE, Bernard
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; Sequence 65, Application US/10751845
; Publication No. US20550100928A1
; GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
TITLE OF INVERTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
; CURRENT PAPLICATION NUMBER: US/09/664,225
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-12-09
; PRIOR FILING DATE: 1999-09-16
; RIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 46; DB 16; Length 23; 100.0%; Pred. No. 0.091;
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ORGANISM: Human Papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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TYPE: PRT
ORGANISM: Human papillomavirus
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Best Local Similarity 100.0
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9, Conservative
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Sequence 6, Application US/1017390

Publication No. US2030143743A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT PEPLICATION NUMBER: US/10/177,390

CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.1
Sequence 126, Application US/10751845

PUBLICATION NO. US20050100928A1

GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: UNMER: US/10/751,845

CURRENT APPLICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIOR APPLICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIOR APPLICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIOR APPLICATION NUMBER: US/09/664,225

PRIOR PELICATION NUMBER: US/09/664,225

PRIO
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100.0%; Score 46; DB 17; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.49;

Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-126
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; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
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US-10-484-063-20
'Sequence 20, Application US/10484063
'Publication No. US20050048467Al
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 100.
Matches 9; Conservative
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Sequence 27, Application US/10484063
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENREAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT PILING DATE: 2004-01-16
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2002-07-20
; NUMBER: OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 27
LIBRICH: 151
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: MICHELE
TITLE OF INVENTION: METHODIS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REPERBRES: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT APPLICATION NUMBER: PCT/US02/23198
PRIOR PLILING DATE: 2002-01-16
PRIOR PLILING DATE: 2002-07-19
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 151
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100.0%; Pred. No. 0.64;
iive 0; Mismatches 0; Indels
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Publication No. US20050033025A1
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOUNGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: FORNINE
APPLICANT: FERRIES, ESTELLE
APPLICANT: FERRIES, ESTELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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Sequence 157, Application US/10751845

| Sequence 157, Application US/10751845
| Publication No. US20050100928A1
| GENERAL INFORMATION:
| APPLICANT: Urban, Pobert G. |
| APPLICANT: Urban, Roman M. |
| TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPTIDES FILE REFERENCE: 08191-013001
| CURRENT APPLICATION NUMBER: US/09/664,225
| PRIOR PILING DATE: 2004-01-05
| PRIOR FILING DATE: 1999-12-09
| PRIOR FILING DATE: 1999-12-09
| PRIOR FILING DATE: 1999-09-16
| NUMBER OF SEQ ID NOS: 163
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Score 46; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                   Query Match
100.0%; Score 46; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-157
                                                                                                        FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
        SOFTWARE: PatentIn version 3.2
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21 LLRREVYDF 29
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US-10-751-845-157
                         SEQ ID NO 2
LENGTH: 17
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US-10-472-724-2

Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Sequence 2, Application Occupance 2, Application US/10472724

Sequence 2, Application US/10472724

GENERAL INFORMATION: Modified Hov E6 and E7 genes and proteins useful for vaccination FILE REFERENCE: 4121-154

CURRENT APPLICATION NUMBER: US/10/472,724

CURRENT APPLICATION NUMBER: PCT/EP02/03271

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 27
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TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
PRIOR APPLICATION NUMBER: R 9907012
PRIOR APPLICATION NUMBER: R 9907012
NUMBER OF SEQ ID NOS: 24
SOFTMARE: PATENTIN DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-367-057-16

Sequence 16, Application US/10367057

Publication No. US20050100554A1

GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Oci, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same;
FILE REFERENCE: 21402-559;
CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT PILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/256,911

PRIOR PLING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                              LENGTH: 158
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9; Conservative
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44 LLRREVYDF 52
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 158
TYPE: PRT
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Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
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APPLICANT: Urban, Rob
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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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100.0%; Score 46; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Artificial fusion sequence US-10-751-845-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
CONTER INFORMATION: Artificial fusion sequence
US-10-751-845-160
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 158
LENGTH: 237
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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46 LLRREVYDF 54
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US-10-751-845-160
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Search completed: June 29, 2005, 05:48:13 Job time : 54.8517 secs 🎨 Blank (nsbto)

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds

(without alignments)
39.842 Million cell updates/sec

Title:
US-08-170-344-66
Sequence:
1 LLRREVYDF 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched:
513545 segs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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ise: Issued_Patents_AA:*

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2: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*

4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*

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8: /cgn2_6/ptodata1/iaa/Packfiles1.pep:*

9: /cgn2_6/ptoda

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

and is derived by analysis of the total score distribution.

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	Description	Sequence 252, App		m	4	Sequence 14, Appl	14,	Sequence 10, Appl	Sequence 10, Appl	10,	1, 4	4	Sequence 10, Appl	9	Sequence 14, Appl	4	7	_	ĭ	48,	48,	654,	618,	4, A			4	Sequence 24, Appl
SUMMARIES	ID	US-08-159-339A-252	US-09-980-523A-2	US-08-316-239B-3	US-08-316-239B-4	US-08-860-165-14	US-09-359-382-14	US-08-117-083-10	US-08-860-165-10	US-09-359-382-10	US-09-367-309A-1	US-09-485-885-4	US-09-485-885-10	US-09-485-885-6	US-09-485-885-14	US-07-909-122-4	US-09-601-729-276	US-09-980-523A-6	US-08-934-915-160	US-09-585-858-48	US-10-270-878-48	US-09-198-452A-654	US-09-438-185A-618	US-08-136-743B-4	US-08-159-339A-135	US-09-248-796A-17266	US-09-328-352-4631	US-09-691-270A-24
	DB		4	ч	Н	e	Ю	н	e	m	4	е	٣	က	m	н	4	4	7	4	4	4	4	7	М	4	4	4
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	91.3	91.3	82.6	76.1	76.1	76.1	76.1	76.1	76.1	73.9	73.9	73.9	73.9
	Score	46	46	46	46	46	46	46	46	46	46	46	46	46	46	42	42	38	35	35	32	35	32	35	34	34	34	34
	Result No.	-	~	m	4	S	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 18475, A Sequence 388, App Sequence 2450, Ap Sequence 2111, Ap Sequence 1725, Ap Sequence 1109, Ap Sequence 19185, A Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 214, App Sequence 21634,		
34 73.9 792 4 US-09-902-540-16475 33 71.7 264 4 US-09-710-279-388 32 69.6 85 4 US-09-248-70012-64919 32 69.6 169 4 US-09-248-70012-6919 32 69.6 362 4 US-09-248-7012-5 32 69.6 376 4 US-09-107-532A-5211 32 69.6 457 4 US-09-248-796A-19185 32 69.6 473 4 US-09-248-796A-19185 32 69.6 473 4 US-09-790-838-5 32 69.6 4872 4 US-09-790-838-7 32 69.6 4872 4 US-09-790-838-7 32 69.6 4872 4 US-09-790-838-7 31 67.4 208 3 US-08-961-083-214 31 67.4 273 4 US-09-58-714-783-3 31 67.4 273 4 US-09-58-110-3517 31 67.4 273 4 US-09-58-110-3517	ALIGNMENTS	Sequence 22. Application US/08159339A Sequence 22. Application US/08159339A Bettent No. 6037135 CENERAL INFORMATION: APPLICANT: Sette, Alessandro APPLICANT: Sette, Alessandro APPLICANT: Celis, Esteban TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: Uses NUMBES OF SEQUENCES: 1254 ADDRESSE: Townsend and Townsend and Crew LIP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CITY: San Francisco STREET: Two Embarcadero Center, Eighth Floor CITY: Ban Francisco STREET: LA SAN FRANDALE FORM: MEDIUM TYPE: Diskette COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: Patacts OF Windows Version 2.0 CURRENTING SYSTEM: DOS SOFTWARE: 129-NOV-1993 CLASSIFICATION NUMBER: US 07/926,666 FILING DATE: 05-AUG-1922 CLASSIFICATION NUMBER: US 08/027,746 FILING DATE: 05-AUG-1933 APPLICATION NUMBER: US 08/103,396 FILING DATE: 05-AUG-193 APPLICATION NUMBER: US 08/103,396 FILING DATE: 05-AUG-193 ATTORNEY/AGENT INFORMATION: TELECOMMUNICATION INFORMATION: TEL
00000000000000000000000000000000000000		RESULT 1 US-08-139A- Sequence 252, Sequence 252, Sequence 252, Sequence 252, Sequence 252, Sequence 252, Sequence 252, Septicant: APPLICANT: APPLICANT: TITLE OF ITTLE

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GENERAL INFORMATION:
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Patent No. 5679509
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOUGGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FEANCINE
APPLICANT: CONNAN, FEANCINE
TITLE OF INVENTION: PROTEENTO FROUDCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOBL AO INS
CURRENT APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-06-31
PRIOR FILING DATE: 2000-06-31
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PAGENTIN VET: 21
SOFTWARE: PAGENTIN VET: 21
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                                      100.0%; Score 46; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                  0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                             Sequence 2, Application US/09980523A Patent No. 6783763 GENERAL INFORMATION: APPLICANT: CHOPPIN, JEANNINE APPLICANT: BOURGAULT VILLADA, ISABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                  9; Conservative
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1 LLRREVYDF 9
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Matches 9; Conserv
                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                             1 LLRREVYDF
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US-08-159-339A-252
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US-08-316-239B-3
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APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Locreased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 6126 Rocky Way Court
CITY: Centreville
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 30-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: JGGIAINI, AJAY A.

REGISTRATION NUMBER: 35.205

REGISTRATION NUMBER: 35.205

REFERENCE/DOCKET NUMBER: 35.205

REFERENCE/DOCKET NUMBER: 35.205

TELEPHAN: (703) 817-9453

TELEPHAN: (703) 803-9387

INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08316239B Patent No. 5679509
                                                                     ATTORNEY/ACENTING 130.

NAME: Jagtiani, Ajay A.
REGISTATION UNDHER: 35,205
REFERENCE/DOCKET UNDHER:
TELECOMMUNICATION INFORMATION:
TELEFRANG: (703) 817-9453
TELEFRANG: (703) 817-9453
TELEFRANG: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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APPLICATION NUMBER: US/00
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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Best Local Similarity 100.
Matches 9, Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
18-08-316-239B-3
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Gaps
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                                                                                                                                                                                                                                            Sequence 10, Application US/08117083
Fatent No. 5719054
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Boursnell, Michael E.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: Malter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CONTY: San Francisco
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Similarity 100.0%; Score 46; DB 3; Length 172; Similarity 100.0%; Pred. No. 0.12; 9; Conservative 0; Mismatches 0; Indels
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the open reading frame."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION PATA:
APPLICATION DATA:
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
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GENERAL INFORMATION: APPLICANT: EDWARTION: APPLICANT: EDWARDS, Stirling John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58
TELEPHONE: 415-781-1989
TELEFAX: 415-38-3249
TELEK: 910 277299
INFORMATION FOR SEQ. ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 182 maino acids
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Best Local Similarity 100.
Matches 9; Conservative
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113 LLRREVYDF 121
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OTHER INFORMATION:
OTHER INFORMATION:
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STRANDEDNESS: sir
TOPOLOGY: linear
  Query Match
Best Local Similarity
Matches 9; Conserv
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-359-382-14

; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
; APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
; APPLICANT: FRAZER, Ian
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILLE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER PILING DATE: 1999-07-23
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1995-12-20
; EARLIER FILING DATE: 1994-12-20
; SOFTMARE: PATENTIN DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTMARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                     US-08-860-165-14

Sequence 14, Application US/08860165A

Patent No. 6004557;
Batent No. 600457;
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Blizabeth Ann
APPLICANT: WEBB, Blizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
TITLE APPLICATION NUMBER: US/08/860,165A
CURRENT PILING DATE: 1997-09-22
CURRENT PAPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157
BARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 155
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                     Score 46; DB 1; Length 162;
Pred. No. 0.11;
; Mismatches 0; Indels
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                  Query Match
100.0%; Score 46; DE
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 9; Conservative 0; Mismatches
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ORGANISM: Human papillomavirus type 16
US-09-359-382-14
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LENGTH: 172
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US-09-485-885-10
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LENGTH: 273
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                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09359382

Patent No. 6306397

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPLILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION: VARIANTS OF HUMAN PAPLILLOMA VIRUS ANTIGENS
FILE REFERENCE: 099-07-23
FEARLIER FILING DATE: 1999-07-23
EARLIER FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER RELING DATE: 1994-12-20
EARLIER RELING DATE: 1994-12-20
EARLIER FILING DATE: 1994-12-20
EARLIER FILING DATE: 1994-12-20
EARLIER FILING DATE: 1994-12-20
              APPLICANT: WEB, Elizabeth Ann
APPLICANT: WEB, Elizabeth Ann
APPLICANT: WEB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/680,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 266
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100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
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Patent No. 6428807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
APPLICANT: COX, John Cooper
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44 LLRREVYDF
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US-09-359-382-10
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LENGTH: 266
TYPE: PRT
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US-09-367-309A-1
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; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES; FILE REFERENCE: 017227/0149; CURRENT APPLICATION NUMBER: US/09/367,309A; CURRENT FILING DATE: 1999-08-11; PRIOR APPLICATION NUMBER: PCT/AU98/00080; PRIOR FILING DATE: 1998-02-13; PRIOR PLILICATION NUMBER: AU PO 5178; PRIOR FILING DATE: 1997-02-19; NUMBER OF SEQ ID NOS: 6; SOFTWARE: Patentin Ver: 2.1; SEQ ID NO : 2.0.1; SEQ ID NO : 2.0.1; LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 46; DB 4; Length 266; 100.0%; Pred. No. 0.19; or Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: FRASESQ for Windows Version 3.0
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Combardo-Bencheikh, Angela
TILE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
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ORGANISM: Human papillomavirus type 16
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Patent No. 6342224
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Patent No. 6342224
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Best Local Similarity 100.
Matches 9; Conservative
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150 LLRREVYDF 158
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ORGANISM: Homo sapien
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APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALEFSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 155 Page Mill Road
                                                                                                                                                                                                                            100.0%; Score 46; DB 3; Length 390; 100.0%; Pred. No. 0.28; tive 0; Mismatches 0; Indel8
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CUREBLY APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRION NUMBER: 28,952
REFERENCE/DOCKET NUMBER: 28,00-20105.01
TELEPHONICATION INFORMATION:
TELEPHONICATION 11950RATION:
TELEPHONICATION 11950RATION:
TELEPHONICATION 11950RATION:
TELEPHONICATION 1494-0792
    ; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 14
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14
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COUNTY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
"WENTER: IBM PC compatible
"METHER: IBM PC compatible
"METHER: PC compatible
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Job time : 17.9126 secs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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169 LLRREVYDF 177
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STATE: California
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US-07-909-122-4
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100.0%; Pred. No. 0.27;
ive 0; Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TILLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: PCT/EP98/05285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09485885
Patent No. 634224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/EP98/05285

PRIOR FILING DATE: 1998-08-17

PRIOR APLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 292
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CURRENT FILING DATE: 2000-02-18
PRIOR PELING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6342224
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Matches 9; Conservative
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Matches 9; Conservative
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150 LLRREVYDF 158
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Colosu) AUDIA OCOA SIUI

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PIR; A03682; WGWLHS.
Incerpro; IPRO01334; E6.
Pfam; PPO0518; E6; 1.
DNA-binding; Barly protein; Nuclear protein; Oncogene; Zinc-finger.
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                                            June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds (without alignments) 84.958 Million cell updates/sec
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08grd9
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07qpj0
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069218
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     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                       1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                    Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                - protein search, using sw model
                                                                                                                                                                                                                                                                                        VE6_HPV16
08.03M0
08.03M0
08.04M0
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Gapop 10.0 , Gapext 0.5
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Q9GT91
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Q9N5J2
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
                                                                      US-08-170-344-65
48
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Match Length
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chlamydia m
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                                     rhodopseudo
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citrus
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              09pkp0
073n14
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09lby1
08ubx2
07cwe0
06sey1
08trj8
08trj8
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Q9PKP0
Q73N14
Q7R389
Q6NCR7
Q9LBY1
Q8UBX2
Q7CWE0
Q6SBY1
Q8TRJ8
Q96BA0
Q7QUR9
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
Du M., Fan X., Hong E., Chen J.J.;
"Interaction of oncogenic papillomatirus E6 proteins with fibulin-1.";
Biochem. Biophys. Res. Commun. 296:962-969(2002).
-I-FUNCTION: This protein has transforming activity in vitro.
-I-FUNCTION: Exhibits a strong, but non specific affinity for double stranded DNA (in vitro).
-I-SUBUNIT: Interacts with FBLN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Nuclear matrix-associated.
-i- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90218027; PubMed=2157796; Schneider-Maumoury S., Pehau-Arnaudet G., Breitburd F., Orth G.; Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia."; J. Gen. Virol. 71:809-817(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rowekamp W.G.;
                                                                                                                                                                                                                                                   Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85246220; PubMed=2990099;
Seedorf K., Krammer G., Durst M., Suhai S., Ro
Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                                       Last sequence update)
Last annotation update)
    158 AA
PRT;
                                                                                 Created)
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Query Match
Best Local Similarity 100.v.
Best Local Similarity 100.v.
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nes 9; Conservative
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  SEQUENCE FROM N.A.
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                                                                                    SEQUENCE FROM N.A.
                                                                                                        Cruz M.R., Cer
Martins C.R.F.
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STRAIN-E-350G, and Af2-a;
STRAIN-E-350G, and Af2-a;
STRAIN-E-350G, and Af2-a;
STRAIN-E-2182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
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                                                                                                                              Gaps
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                                                                                Query Match 100.0%; Score 48; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 9; Conservative 0; Mismatches 0; Indels
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY098922; AAM2910.1; -.
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
SEQUENCE 158 AA; 19145 MW; CB70F51C00F867DC CRC64;
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Martins C.R.F.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                       01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transforming protein B6.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Virnses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus
                     Potential.
01FEF5ADCFDB37EB CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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37 73 PC
110 146 PC
158 AA; 19187 MW;
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Matches 9; Conservative 0
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NCBI_TaxID=10581;
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ZN_FING
SEQUENCE
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QBJMUB;
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                                                                                                             Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
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100.0%; Pred. No. 0.014;
ive 0; Mismatches 0; Indels
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-UNA-2002 (TrEMBLrel. 21, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
E6 procein.
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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SEQUENCE 158 AA; 19160 MW; AFF015533FC7FAF7 CRC64;
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SEQUENCE 158 AA; 19157 MW; F140F509DAC794F6 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transforming protein E6.
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BMBL; AF472509; AAA015705.1; --
EMBL; AF486324; AAA015705.1; --
EMBL; AY098918; AAM29166.1; --
EMBL; AY098918; AAM29166.1; --
EMBL; AY0987055; C:host cell nucleus; IEA.
GO; GO:00042025; C:host cell nucleus; IEA.
InterPro; IPR001334; B6.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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Best Local Similarity 100.
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Best Local Similarity luv...
9, Conservative
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                                                               SEQUENCE FROM N.A.
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Q8QRD6;
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Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
Martins C.R.F.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
Martins C.R.F.;
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Teral M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF486299; AAL96604.1; -.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                            Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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EMBL, AF486302, AAL96611.1; --
EMBL, AF486308, AAL96613.1; --
EMBL, AF584061, AAL96613.1; --
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Ffam; PF00518; E6; 1.
SEQUENCE 158 AA; 19201 MW; 004EF5ADCE6B375B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Human papillomavirus type 16.
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Best Local Similarity
Matches 9; Conserv
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                                                                                     NCBI_TaxID=10581;
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                                                         Papillomavirus
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A CTUZ M.K. Martins C.R.F.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF408325; AAL96630.1; -.
R EMBL; AF402678; AAM085408.1; -.
R EMBL; AY1089923; AAM08517.1; -.
R EMBL; AY112662; AAM51853.1; -.
R GO; GO:0003677; F.Nost cell nucleus; IEA.
R GO; GO:0003677; F.DRO binding; IEA.
R FOUENCE 158 AA; 19208 MW; B8E47F57F22EC2EI CRC64;
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Viruses; daBNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10581;
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Viruses; dapillomaviruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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Cheung J.L.K., Xu L.Y., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheung A.F.;

"Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China.";

J. Infect. Dis. 186:656-700(2002).

BMBL; AP4863017; AL96612.1;

GO; GO:0003677; R.DNA binding; IEA.

GO; GO:0003677; F.DNA binding; IEA.

InterPro; IPRO1334; E6.

Pfam; PP00518; E6; 1.

SEQUENCE 158 AA; 19187 MW; 005E2FC1E617C55B CRC64;
                                                                                                               MEDLINE=2282962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.;
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type l6 intratypic variant infection and risk for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
BMBL; AFR48309; AAL96614.1; ---
GO; GO:000357; F:DNA binding; IEA.
GO: GO:000357; F:DNA binding; IEA.
GO: GO:000357; F:DNA binding; IEA.
FINTERPOOLIS; E6.
FFAM: PPF00518; E6; 1.
SEQUENCE 158 AA; 19173 MW; 161AD3EFAA4D636B CRC64;
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01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 proctein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=22182962; PubMed=12195358;
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Best Local Similarity luv...
9; Conservative
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NCBI_TaxID=10581;
NCBI_TaxID=10581;
                                                               SEQUENCE
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Q8QRE1
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                                                                                                            Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).

EMBL, AF486318; AAL96623.1; -.. GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003877; F:DNA binding; IEA.
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MEDLINE=22182952; PubMed=12195358;

Chan P.K.S., Law C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

Cheung J.L.K., Xu L.Y., Cheng A.F.;

"Human papillomavirus type 16 intratypic variant infection and risk

for cervical neoplasia in southern China.";

J. Infect. Dis. 186:696-700(2002).

BMBL, ARP4861B; ALP4651.1;

GO; GO:0042025; C:hOSt cell nucleus; IEA.

InterPro; IRR001334; E6.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 19173 MW; 14EBF5ADCFDB3640 CRC64;
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PFGNUENCE 158 AA; 19188 MW; 01FEF5B1D21AF7EB CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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                                                                                            MEDLINE=22182962; PubMed=12195358;
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                               SEQUENCE FROM N.A.
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Gaps

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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF187899; AAF133991; --
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPRO01334; E6.
Pfam; PF00518; E6; 1.9210 MW; 004EF5ADD6FABESB CRC64;
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EMBL, AF187086; AAF187081.; --
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPro; IRRO01334; E6.
Pfam; PP00518; E6; 1.
SEQUENCE 158 AA; 19195 MW; 00564EIA8994CB0B CRC64;
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                                                                                                                                     Query Match 100.0%; Score 48; DB 2; Length 158; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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Job time : 56.2473 secs
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NCBI TaxID=10581;
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                                                                                     chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Chenng A.F.;

"Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China.";

J. Infect. Dis. 186:686-700(2002).

EMBL, AF486303; AAL96608.1;

GO, GO.00032025; Chost cell nucleus; IEA.

GO, GO.000377; F.DNA binding; IEA.

InterPro: IPRO/134; EG.

Pfam; PPF00518; E6; 1.

SEQUENCE 158 AA; 19146 MW; CB6EF5A91548727C CRC64;
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Terai M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF536179 AQ10712.1;
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transforming protein E6.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 158 AA; 19074 MW; 9EBCF5B6DB95D75E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA.
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                                                            STRAIN=A8-C131;
MEDLINE=22182962; PubMed=12195358;
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Best Local Similarity 100...
9, Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
Papillomavirus.
NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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Q71BI7;
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Q9QDH3
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Gaps

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds

(without alignments)

76.805 Million cell updates/sec
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Title:

Perfect score: 48
Sequence: 1 MHOKRTAMF 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

4: pir4:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote DedA-family integr hypothetical prote hypothetical prote hypothetical prote conserved hypothet prote protein E6 - human monooxygenase-rela hypothetical prote tetrahydrofolylpol tetrahydrofolylpol folylpolyglutamate dtdp-6-deoxy-1-man hypothetical prote hypothetical prote hypothetical prote ahl receptor (AF33 linalool 8-monooxy cytochrome-c oxida nodule-specific hy prote transcription regu hypothet hypothetical prote hypothetical prote probable PHD-type protein hypothetical nypothetical 1ypothetical Description conserved gene 26 SUMMARIES AF2911 D97686 A48495 T20233 S63583 B81936 C81170 T40911 OSHU7B G98140 164035 AI0886 E91115 G65087 D83425 H82045 T49843 T41621 H36790 E85960 B82522 T02277 WZBEB8 128025 Query Match Length DB 492 521 891 Score Result ş

Cjaccesion: C81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodoson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Status: preliminary

monocyygenase-related protein TC0425 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

RESULT 2

hypothetical prote hypothetical prote	cytochrome-c oxida ferredoxin [import	ferredoxin II (AF2 hynotherical prote	hypothetical prote	hypothetical prote	glucose inhibited	glucose-inhibited	hypothetical prote	conserved hypothet	endothelial cell p	hypothetical prote	hypothetical prote	probable deoR-fami
T32016 T20513	S65387 AB3120	E98167 T26664	E70849	T02816	B71942	G64652	E69999	AI3239	A55365	T39184	T47020	AE0236
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62.5	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4	60.4
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30	33 33	9.8 4.8	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SEE>
A; Cross-terences: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G33303
A; Cross-terences: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G33303
B; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                  C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Sedoorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
A;Title: Human papillomavirus type 16 DNA sequence.
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
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Keywords: DNA binding; early protein; zinc finger
F;37-73 Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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protein E6 - human papillomavirus type 16
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Best Local Similarity
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linalool 8-monooxygenase (EC 1.14.99.28) - Pseudomonas incognita
C;Species: Pseudomonas incognita
C;Species: Pseudomonas incognita
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A46495
R;Ropp, J.D.; Gunsalus, I.C.; Sligar, S.G.
B;Ropp, J.D.; Gunsalus, I.C.; Sligar, S.G.
A;Title: Cloning and expression of a member of a new cytochrome P-450 family: cytochrome A;Reference number: A46495; MUID:93388536; PMID:8376348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q59723; GB:L23310; NID:g405542; PIDN:AAA25810.1; PID:g40554
C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology
C;Keywords: oxidoreductase
F;242-377/Domain: cytochrome P450 homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q18847; EMBL:Z75533; PIDN:CAA99815.1; GSPDB:GN00019; CESP:C'A;Genetics:
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A;Variety: strain MS11
C;Date: Z8-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Date: Z8-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accesion: S63583
R;Fussenegger, M.; Meyer, T.F.
A;Fussenegger, M.; Meyer, T.F.
A;Title: Cloning and characterization of the Neisseria gonorrhoeae MS11 folC gene.
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T20233
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A;Introns: 76/3; 172/3; 272/2; 312/1; 367/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C54G4.2
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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submitted to the EMBL Data Library, June 1996
A;Reference number: 219241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 62.5
Matches 5, Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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tetrahydrofolylpolyglutamate
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MHRKRASVF 130
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293 LHMRRTAM 300
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1 MHQKKTVV 8
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-406 <ROP>
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: D97666
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: AF2911
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
i Karo, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
Biter, B.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
                                                 A;Cross-references: UNIPROT:Q9PKPO; GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF3928
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription regulator, LuxR family Atu2727 [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: il-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-245 <KUR>
A;Residues: 1-245 <KUR>
A;Cross-references: UNIPROT:Q8UBX2; GB:AE008688; PIDN:AAL43708.1; PID:g17741237; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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                                                                                                                                                                                              Score 33; DB 2;
Pred. No. 22;
1; Mismatches
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Pred. No. 17;
3; Mismatches
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                                                                                                                                                                                              68.8%;
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Best Local Similarity 55.6%;
Matches 5; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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338 VHQKRTA 344
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A;Molecule type: DNA
A;Residues: 1-267 <KUR>
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Indels

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A;Cross-references: UNIPROT:094400; EMBL:AL034490; PIDN:CAA22476.1; GSPDB:GN00068; SPDF
A;Experimental source: strain 972h-; cosmid c126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-80 <SAD>
A;Cross-references: UNIPROT:P24311; EMBL:Z14244; NID:g30150; PIDN:CAA78613.1; PID:g3015
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CCOmplex: part of a 13 chain complex spanning the inner mitochondrial membrane and con
(see PIR:OTHUSA), VD (see PIR:OTHUSS), VIa (see PIR:OGHUGA), VIb (see PIR:OGHUGB), VIC
m dimers within the mitochondrial inner-membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: cytochrome- oxidase chain VIIb
C;Superfamily: cytochrome- oxidase chain VIIb
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran
F;L23/Domain: transit peptide (mitochondrion) #setatus predicted <TNP>
F;24-80/Product: cytochrome-c oxidase chain VIIb #status predicted <MAT>
F;33-59/Domain: transmembrane helix #status predicted <TR01>
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C;Dacession: S29856
R;Sadlock, J.E.; Lightowlers, R.N.; Capaldi, R.A.; Schon, E.A.
Biochim. Biophys. Acta 1172, 223-225, 1993
A;Title: Isolation of a cDNA specifying subunit VIIb of human cytochrome c oxidase.
A;Reference number: S29856; WUID:93176819; PMID:8382530
                                                                                                                                                                                                                                                                                     probable PHD-type zinc finger - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40911
R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
A;Reference number: Z21956
A;Reference number: Z21956
A;Reference number: T40911
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 16;
0; Mismatches 2; Indels
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69;
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     Pred. No. 51;
1; Mismatches
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     85.7%;
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Matches 5; Conservative
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Best Local Similarity 75.v.
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A;Cross-references: GDB:138315
                                Conservative
                                                                                                                                               329 QKRTAVF 335
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475 MHQRRTS 481
  Best Local Similarity
Matches 6; Conserve
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                                                                                      3 OKRTAMF 9
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A; Residues: 1-571 <MUR>
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C;Species: Neisseria meningitidis
C;Species: OS-May-2000 #sequence_revision OS-May-2000 #text_change O9-Jul-2004
C;Accession: B81936
R;Parkhill, J:, Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Axture 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
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A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID: 20175755; PMID: 10710307
                                                                                                                                      A;Cross-references: UNIPROT:Q50990; GB:Z68205; NID:g1237075; PIDN:CAA92428.1; PID:g12370
C;Superfamily: folylpolyglutamate synthase
C;Keywords: ligase
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A;Rebidues: 1-424 <PAR>
A;Residues: 1-524 <PAR>
A;Experimental source: Serogroup A, strain 22491
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A;Cross-references: UNIPROT:Q9K0C1; GB:AE002423; GB:AE002098; NID:g7225913; PIDN:AAF4111
A;Experimental source: serogroup B, strain MC58
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Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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                                                        A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
                                                                                                                                                                                                                                                             Length 424;
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A; Reference number: S63582; MUID:96180644; PMID:8602142 A; Accession: S63583
                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                          Score 31; DB 2; Pred. No. 51; 1; Mismatches
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51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: folC, NMA0896
Superfamily: folylpolyglutamate synthase
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C;Superfamily: folylpolyglutamate synthase
                                                                                                                                                                                                                                                             64.6%;
85.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                            329 OKRTAVF 335
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                                                                                                                 A; Residues: 1-424 <FUS>
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A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
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                                Accession:
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Best Local Similarity 62.5
Matches 5; Conservative
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nes 5; Conservative
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144 IHQELTALF 152
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137 MHHRRTAV 144
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A;Molecule type: DNA
A;Residues: 1-219 <PAR>
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A;Status preliminary
A;Status DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9P9YO; GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF8552
A;Experimental source: strain ga5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
Chado, M.A.; Madeira, A.M.B.N.; Matchia, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunse, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; da Silva, M.M.; Silva, Sawasak
A;Authors: da Silva, A.C.R.; da Silva, A.M.; Silva, Jr., W.A.; da Silva, A.D.; Z
A; Contago, W., Status, A.D.; Sawasak
A; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.D.; Z
                                                                                                                                                                           C;Accession: G98140
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Residues: 1-181 «KUR»
A,Cross-references: UNIPROT:Q8U6K8; GB:AE007870; PIDN:AAK88649.1; PID:g15158372; GSPDB:G
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                                                                                                                                                        dtdp-6-deoxy-1-mannose-dehydrogenase [imported] - Agrobacterium tumefaciens (strain C58
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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A;Map position: linear chromosome
C;Superfamily: dTDP-4-dehydrorhamnose 3,5-epimerase
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Best Local Similarity 62.5
Matches 5; Conservative
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                     HOKRIPDF 33
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A; Molecule type: DNA
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession. 164035
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, G;Gcayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: 164035
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A;Cross-references: UNIPROT:P44251; GB:U32830; GB:L42023; NID:g1574389; PIDN:AAC23210.1
C;Superfamily: Haemophilus influenzae hypothetical protein H11552
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A10886
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher h. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: A10886
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hypothetical protein HI1552 - Haemophilus influenzae (strain Rd KW20)
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Pred. No. 44;
1; Mismatches 2; Indels
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Job time : 13.2747 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Sequence 2, App...
Sequence 16, Appl
Sequence 16, Appl
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Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
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Sequence 2, Appli
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Sequence 154256,
                                     June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds (without alignments) 64.268 Million cell updates/sec
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'(gnz_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*
'(gnz_6)ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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'(gnz_6)ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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7 US-10-858-384-2

10S-10-367-057-16

US-10-367-058-10

5 US-10-367-095-10

5 US-10-368-066-10

6 US-10-368-066-10

7 US-10-918-337-10

6 US-10-472-724-2

6 US-10-029-386-32092

6 US-10-029-386-32092
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Maximum Match 100%
Listing first 45 summaries
OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                           Searched:
                                               Run on:
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Sequence 130, App Sequence 130, App Sequence 17933, Sequence 178972, Sequence 20, Appl Sequence 20, Appl Sequence 168323, Sequence 3, Appl Sequence 3, Appl Sequence 3107, A Sequence 3107, A Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 2125, Sequence 241203, Sequence 241203, Sequence 241203, Sequence 262525, Sequence 262525,	equence 348, equence 400, equence 20578 equence 905, equence 52503 equence 1490, equence 1196,
US-10-424-599-263544 US-10-038-854-130 US-10-424-599-129338 US-10-424-599-178972 US-10-424-599-178972 US-10-424-599-168951 US-10-424-599-168951 US-10-424-599-168323 US-10-955-017-9 US-10-955-017-9 US-10-955-017-9 US-10-437-963-195412 US-10-437-963-195412 US-10-425-115-300764 US-10-425-115-300764 US-10-425-115-30764 US-10-425-115-30764 US-10-425-125-30764 US-10-424-599-262525 US-10-424-599-262525 US-10-424-599-262525 US-10-424-599-262525 US-10-424-599-262525 US-10-424-599-262525 US-10-424-599-265525 US-10-424-599-265525	363-616-3 408-765A- 425-115-2 083-357-9 156-761-1 767-701-5 017-161-1
1125 125 126 126 126 126 126 126 126 126 126 126	11 4 4 4 1 1 1 2 2 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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OTHER INFORMATION: Description of the artificial sequence: peptide E6 1-22
                                                                                                                      GREAT INCRMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAUIT-VILLADA, Isabelle
APPLICANT: POUVELLB-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of Deptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of Deptides derived from E6 and/or E7
TITLE OF INVENTION: MIXTURE US/10/476,570
CURRENT FILING DATE: 2002-03-11-04
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATCHIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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100.0%; Score 48; DB 16; Length 22;
Best Local Similarity 100:0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels
                          Sequence 59, Application US/10476570 Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: artificial sequence
                                                                                                          GENERAL INFORMATION
US-10-476-570-59
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LENGTH: 22
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 13 SOFTWARE: FastSEQ for Windows Version 4.0
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JERNEKALI INFOURNATION:

TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line
FILE REFERENCE: 44149-11US1
CURRENT PERFERENCE: 44149-11US1
CURRENT PELING DATE: 2003-02-14
PRIOR PELING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 48; DB 15; Length 536;
                                                                                                      APPLICANT: MACHELAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVESTION: CRELATING IMMUNOSTIMULATING COMPLEXES
TITLE OF INVESTION: CRELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR PILLING DATE: 1997-02-13
PRIOR RILING DATE: 1997-02-19
FILING PILLING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 48; DB 9; Length 266; 100.0%; Pred. No. 0.076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Human papillomavirus type 16
                  ; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10367095; Publication No. US20030228696A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 536
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LENGTH: 266
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APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: PERRIES, BSTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE EG PROTEIN
TITLE OF INVENTION: PARTICILARLY IN VACCINATION
TITLE OF INVENTION: PARTICILARLY IN VACCINATION
FILE REPERRICE: 5060-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR PILING DATE: 2004-06-02
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Complexes and Methods of Using Same TITLE OF INVENTION: Complexes and Methods of Using Same FILE REPERENCE: 21402-2559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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PRIOR APPLICATION NUMBER: 60/256,911

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 16

LENGTH: 158
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Publication No. US20050100554A1
GENERAL INFORMATION:
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Publication No. US20050033025A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                               APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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                                  Best Local Similarity
Matches 9; Conserv
MHOKRTAMF
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US-10-367-057-16
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Gaps

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100.0%; Score 48; DB 17
100.0%; Pred. No. 0.15;
  APPLICATION NUMBER: US 60/356,161
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Publication No. US20050118191A1
                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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US-10-918-337-10
                                                                                                                                                                                                                                                                                                                            LENGTH: 536
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                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Virus-Like Particles for Expression in Insect Cells
FILE REFERENCE: 44149-2031
CURRENT APPLICATION NUMBER: US/10/367,367
CURRENT FILING DATE: 2003-02-15
                            Gaps
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                                                                                                                                                                                                                                                                                                               APPLICANT: Robin A. Robinson
APPLICANT: Vittoria Cioce
TITLE OF INVENTION: Method for Isolation and Purification of
TITLE OF INVENTION: Expressed Gene Products In Vitro
FILE REFERENCE: 44149-3051
                            Indels
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; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-368-046-10
Pred. No. 0.15;
Best Local Similarity 100.0%; Pred. No. 0.1
Matches .9; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PELLING DATE: 2003-02-15

PRIOR PELLING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR PILING DATE: 2002-02-14

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PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                            Sequence 10, Application US/10368046 Publication No. US20040063188A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-367-367-10; Sequence 10, Application US/10367367; Publication No. US20040121465A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Best Local Similarity
9, Conserve
                                                                        1 MHOKRTAMF
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LENGTH: 536
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GRUERAL INFORMANION:
GRAIN INFORMANION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Optimization of Gene Sequences of
TITLE OF INVENTION: Chimeric Virus-Like Particles for Expression in Insect Cells
TITLE OF INVENTION: Chimeric Virus-Like Particles for Expression in Insect Cells
CURRENT APPLICATION NUMBER: US/10/918,337
CURRENT APPLICATION NUMBER: US/10/918,337
CURRENT FILING DATE: 2004-02-14
FRIOR APPLICATION NUMBER: US 60/356,119
FRIOR PELING DATE: 2002-02-14
FRIOR PELING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR PILING DATE: 2002-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
```

DB 17; Length 536;

```
Squence 154256, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPRENCE: 38-21 (5323) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

SEQ ID NO 154256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 263544, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                        0; Indels
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US-10-424-599-154256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_7C.1.pep
US-10-424-599-263544
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Pred. No. 77;
0; Mismatches 1
    Pred. No. 13;
1; Mismatches
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    85.78;
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Best Local Similarity 85.,
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Matches 6; Conservative
                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 HWKKTAMF 46
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ORGANISM: Glycine max
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Best Local Similarity
Matches 6; Conserva
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17 HOKRTSM 23
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US-10-424-599-263544
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LENGTH: 190
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                                                                                                                                                                  Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Sequence 2, Application US/10472724

Sequence 2, Application US/040171806A1

Sequence 2, Application US/040171806A1

Fublication No. US20040171806A1

GENERAL INFORMATION: Modified HPV E6 and E7 genes and proteins useful for vaccination of TILE REFERENCE: 4121-154

CURRENT APPLICATION NUMBER: US/10/472,724

CURRENT FILING DATE: 2002-03-09-17

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2001-03-23

NUMBER OF SEQ ID NOS: 27

NUMBER OF SEQ ID NOS: 27

SOSTWARE: Patentin version 3.2
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Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICAMT: Penn, Sharron G.
APPLICAMT: Rank, David R.
APPLICAMT: Rank, David R.
APPLICAMT: Hanzel, David R.
APPLICAMT: HANZEL INFORMATION: EXPRESSION ANALYSIS TWO
FILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32092
LENGTH: 51
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N: EXPRESED IN ADULT LIVER, SIGNAL = 2.2
N: EXPRESED IN PLACENTA, SIGNAL = 1.9
N: EXPRESED IN BRAIN, SIGNAL = 1.9
N: EXPRESED IN HELA, SIGNAL = 0.35
N: EXPRESED IN HELA, SIGNAL = 0.35
N: EXPRESED IN HOUG, SIGNAL = 2.1
N: EXPRESED IN LUNG, SIGNAL = 2.7
N: EXPRESED IN LUNG, SIGNAL = 2.6
N: EXPRESED IN HEART, SIGNAL = 2.6
N: EXPRESED IN HEART, SIGNAL = 4.30e-01
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      Indels
      ö
      Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 8; Conservative
      9; Conservative
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OTHER INFORMATION: EXPRES
OTHER INFORMATION: EXPRES
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                                                1 MHQKRTAMF 9
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Sequence 47963, Application US/10425114

Sequence 47963, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Soreen, Yihua

APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwai

TITLE OF INVENTION: Nacleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53313) B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 47963

LENGTH: 94
     Sequence 159338, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53233)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 159338
LENGTH: 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
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US-10-424-599-159338
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Pred. No. 44;
0; Mismatches 2
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Job time : 53.8517 secs
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: Glycine max
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APPLICANT: Miller, Isabelle
APPLICANT: Miller, Isabelle
APPLICANT: Miller, Isabelle
APPLICANT: Miller, Isabelle
APPLICANT: Miller, Isabelle
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFRENCE: 21402-230
CURRENT APPLICATION NUMBER: 60/258,928
PRIOR PELING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR PELING DATE: 2001-01-02
PRIOR PELING DATE: 2001-01-02-20
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-02-20
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-03-29
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PRIOR PELING DATE: 2001-03-29
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-13
PRIOR PELING DATE: 2001-04-25
PRIOR PELING DATE: 2001-04-25
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PRIOR PELING DATE: 2001-04-35
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Application US/10038854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burgess, Catherine E
Edinger, Shlomit R
Ellerman, Karen
Gunther, Erik
                                                                                                                       Wolenc, Adam R
Vernet, Corine
Eisen, Andrew J
Liu, Xiaohong
Malyankar, Uriel M
Shimkets, Richard A
Tchernev, Vellzar
Spaderna, Steven K
Gorman, Linda
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Staphylococcus aureus
US-10-038-854-130
                      Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
                                                                                                                                                                                                                                                                                                                                                                                                     Patturajan, Meera
Gusev, Vladimir Y
Gangolli, Esha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shenoy, Suresh G
Rastelli, Luca
Casman, Stacie J
Boldog, Ferenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 68.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guo, Xiaojia S
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APPLICANT:
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APPLICANT:
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Sequence 263, App Sequence 9242, App Sequence 9242, App Sequence 6713, Ap Sequence 24480, A Sequence 24480, A Sequence 2514, A Sequence 2518, A Sequence 27, Appli Sequence 2, Appli Sequence 4947, Appli Sequence 475, Appli Sequence 475, Appli

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Sequence 220, Application US/0815939A

Patent No. 6037135

GENERAL INFORMATION:
APPLICANT: Grey, Howard M.
APPLICANT: Grete, Alessandro
APPLICANT: Gette, Alessandro
APPLICANTON: Uses
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: Ban Francisco
COMPUTER: LBM COMPATE: GA
COMPUTER: LBM COMPATIBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LBM COMPATIBLE
COMPUTER: LBM COMPATIBLE
COMPUTER: LBM COMPATIBLE
COMPUTER: LBM COMPATIBLE
COMPUTER: LSP-NOV-1993
CLASSIFICATION NUMBER: US 08/027,746
FILING DATE: 05-ANG-1992
APPLICATION NUMBER: US 08/103,396
FILING DATE: 05-ANG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
RESISTRACE/DOCKET NUMBER: 21 alouver
RESISTRACE/DOCKET NUMBER: 01 alouver
            US-09-201-945-263
US-09-201-945-263
US-09-134-000C-6713
US-09-252-991A-24484
US-09-270-767-43484
US-09-270-767-37468
US-09-270-767-37468
US-09-270-767-52685
US-09-270-767-52685
US-09-289A-2
US-08-884-20-2
US-08-884-20-2
US-09-9949-015-2
US-09-9949-016-6725
US-09-949-016-10136
                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-250
 Sequence 36, Appl
Sequence 36, Appl
Sequence 2944, Ap
Sequence 2944, Ap
Sequence 21873, A
Sequence 6391, Ap
Sequence 6391, Ap
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Sequence 50091, A
Sequence 10152, A
Sequence 43468, A
Sequence 44609, A
Sequence 36, Appl
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1, Appli
158, App
10, Appl
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Sequence 3, Appli
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                                                                                                  June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, A Sequence 14, A Sequence 10, A Sequence 10, A Sequence 11, A Sequence 158, Sequence 16, A
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-360-523A-2

US-09-316-239B-3

US-08-316-239B-4

US-08-360-165-14

US-08-360-165-10

US-08-360-165-10

US-09-359-382-10

US-09-359-382-10

US-09-359-382-10

US-09-360-165-10

US-09-360-165-10

US-09-360-165-10

US-09-270-767-34874

US-09-270-767-34689

US-09-270-767-44609

US-09-270-767-44609

US-09-270-767-44609

US-09-270-767-44609

US-09-270-76-44609

US-09-270-76-44609

US-08-222-616-36
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US-09-252-91A-21873
US-09-949-016-10407
US-09-949-016-6391
US-08-637-759B-263
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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No.
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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100.0%; Pred. No. 0.0023;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                       100.0%; Score 48; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
CITY: Mashington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPIRY: USAS

ZIP: 20005-3315

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION NUMBER: US 07/909,296
FILING DATE: 0-JUL-1992
APPLICATION NUMBER: B 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadder, Linda A: REGISTRATION NUMBER: 33,218
REGISTRATION NUMBER: 33,218
REGISTRATION NUMBER: 33,218
REGISTRATION NUMBER: 30.2481-1195-00000
TELECOMMUNICATION: NUMBER: 202-408-4000
                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-980-523A-2; Sequence 2, Application US/09980523A; Sequence No. 6783763; Patent No. 6783763; PATENT INFORMATION: APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                 Sequence 3, Application US/08363586 Patent No. 5629161 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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1 MHQKRTAMF 9
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    US-08-159-339A-250
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A PAPLICANT: BOTRGARIANT VILLAND: TARRELLE APPLICANT: BOTRGARIANT VILLAND: TARRELLE APPLICANT: TOWN, PRANCESAND APPLICANT: CONNAN, PRANCESAND APPLICANT: CONNAN, PRANCES OF HIS RESEARCE APPLICANT: CONNAN, PRANCES OF HIS RESEARCE APPLICANTON WINDERS: UND STATEMENT OF THE OFFI PRINCES FILLS PRODUCTION AND THEIR RESEARCE. NOT APPLICANTON WINDERS: UND STATEMENT OFFI PRODUCTION AND THEIR REPORTED APPLICANTON WINDERS: UND STATEMENT OFFI PRODUCTION AND THEIR REPORTED APPLICANTON WINDERS: UND STATEMENT OFFI PRODUCTION WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: UND WINDERS: U
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-14
            APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130

CURRENT APPLICATION NUMBER: US/08/860,165A

CURRENT FILING DATE: 1997-09-22

EARLIER FILING DATE: 1995-12-20

EARLIER PLICATION NUMBER: AU PNO157

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFUMARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09359382

Sequence 14, Application US/09359382

Batent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: EDWARDS, Stirling John

APPLICANT: EDWARDS, Stirling John

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION: VARIANTS OF 99/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER FILING DATE: 1995-12-20

EARLIER PELING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-20

EARLIER FILING DATE: 1994-12-20

SOFTWARE: PARCENTION NUMBER: AU PNO157/94

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 48; DB 3; Length 172; 100.0%; Pred. No. 0.017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/08860165A Patent No. 6004557
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
       Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 MHOKRTAMF 78
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US-09-359-382-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is Associated with an
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wheeler, Cosette M.

Parmenter, Cheryl A.

TITLE OF INVENTION: Methods and a Diagnostic Aid for

TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi

TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

TITLE OF INVENTION: Cervical Cancer

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
                                                                                                                       Gaps
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                                                                    100.0%; Score 48; DB 1; Length 162; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONTEXPONDENCESS:
CORRESPONDENCESS:
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BEATORIE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PAPE: Floppy disk
COMPUTER: PAPE: PO-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: AJ35
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, AJ34 A.
REFERENCE/DOCKET NUMBER: UNME-0001
TELEFAK: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08316239B
Patent No. 5679509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                 Ouery Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                  1 MHOKRTAMF 9
                                                                                                                                                                                                            1 MHOKRTAMF 9
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HYPOTHETICAL:
    ; HIFOLINGO US-08-316-239B-3
                                                                                                                                                                                                                                                                                                           US-08-316-239B-4
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100.0%; Score 48; DB 4; Length 266; 100.0%; Pred. No. 0.026; Live 0; Mismatches 0; Indels
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APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 31, 31 AND 56,
TITLE OF INVENTION: 11, 16, 18, 31, 31, 31 AND 56,
TITLE OF INVENTION: USFPUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USFPUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USFPUL IN IMMUNOASSAY FOR
TITLE OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: AASON & ASSOCIATES, P.A.
STREET: 11757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEPU. IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.6%; Score 43; DB 2; 100.0%; Pred. No. 0.022;
CURRENT APPLICATION NUMBER: US/09/367,309A;
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SEQ ID NO: 2.1
SEQ ID NO 1
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: FLORIDA
COMPUTER: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
RILING DATE: 22-SEP-1997
FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELEPOMYUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEPAX: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 158, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-934-915-158
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                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-359-382-10

| Sequence 10. Application US/09359382
| Patent No. (306397)
| Patent No. (306397)
| Patent No. (306397)
| Patent No. (306397)
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: FRAZER, Ian
| APPLICANT: FRAZER, Ian
| APPLICANT: FRAZER, Ian
| APPLICANT: FRAZER, Ian
| CURRENT PAPPLICATION NUMBER: US/09/359, 382
| CURRENT PAPPLICATION NUMBER: US/09/359, 362
| EARLIER APPLICATION NUMBER: US/09/359, 363
| EARLIER PALICATION NUMBER: US/09/359, 0666
| EARLIER PILING DATE: 1997-09-22
| EARLIER PILING DATE: 1997-12-20
| FARLIER PILING DATE: 1997-12-20
| FARLIER PILING DATE: 1994-11-20
| NUMBER: OF SEQ ID NOS: 2.0
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     APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLCMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
BARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 48; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 0.026; Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human papillomavirus type 16
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Patent No. 6428807
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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US-09-367-309A-1
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LENGTH: 266
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RELATING TO KLEBSIELLA
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SEQ ID NO SO091
LENGTH: 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1012, Application US/09489039A
; Sequence 1012, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: GATY Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; TITLE OF INVENTION: US/09/489, 039A
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT PILING DATE: 2000-01-27
; PRIOR PILING DATE: 1999-01-29
; RIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10152
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Pred. No. 31;
2; Mismatches
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Pred. No. 31;
2; Mismatches
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Pred. No. 45;
0; Mismatches
                                                                                                                                                                       ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-34874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-50091
   CURRENT APPLICATION NUMBER: US/09/270,767
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 50091, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                   TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Klebsiella pneumoniae
                 CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 34874
LENGTH: 249
                                                                                                                                                                                                                                   68.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 66.7%;
Similarity 85.7%;
6; Conservative
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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215 IHIKRTAMY 223
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215 IHIKRTAMY 223
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Best Local Similarity
Matches 6; Conserv
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
     Gaps
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APPLICANT: Boursnell, Michael E.
APPLICANT: Inglis, Stephen C.
APPLICANT: MULTO, Alan' J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCE: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Xaa refers to stop codon in
the open reading frame."
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Pred. No. 1.3;
   Indels
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ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/117,083
FILING DATE: 10-SEP-1993
TARGETICATION: 435
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 Mismatches
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                                                                                                                                 RESULT 12
1S-08-117-083-10
Sequence 10, Application US/08117083
Patent No. 5719054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFRENCE/DOCKET NUMBER: A-587
TELEPHONE: 415-781-1989
TELERX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..182
OTHER INFORMATION:
OTHER INFORMATION:
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                                       2 HOKRTAMF 9
                                                                         HOKRTAMF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
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US-09-270-767-34874
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 Matches
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2 HQKRTAM 8 |||| || 5 HQKRNAM 11

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Search completed: June 29, 2005, 01:44:23 Job time : 17.9126 secs

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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papillomavirus.
NCBI_TaxID=10566;
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NCBI_TaxID=10581;
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BMER_HUMAN
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VE7 HPV16
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32 41 75.9 95 2 Q9UZ74 Q9UZ74 PYTOCOCCUB
33 41 75.9 96 2 Q8UJ78 Q8U378 Q8U378 PYTOCOCCUB
34 41 75.9 250 2 Q8U378 Q8U378 Q8U378 PYTOCOCCUB
35 41 75.9 279 2 QPQ286 Q8U378 QR31US G31US
36 41 75.9 279 279 QPQ286 QPQ284 CHOMODACTE
37 41 75.9 1000 2 QPQZM4 QPQ29 QPQ29 CHTOMODACTE
39 40 74.1 126 2 QG5TR3 QG5TR3 CHOMODACTE
40 74.1 220 2 QG5TN0 QG5TR3 CHOMODACTE
41 40 74.1 221 2 QG5N01 QG5TR3 CHOMODACTE
42 40 74.1 221 2 QG5N01 QG5TR3 CHOMODACTE
43 40 74.1 223 2 QG5N01 QG5TR3 CHOMODACTE
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ALIGNMENTS

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J. Virol. 63:782-789(1989).
InterPro. IPRO0148; Papvi_B7.
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Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
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                                                                                                                      Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                            Last sequence update)
Last annotation update)
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26 AA
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                                         Created)
PRT;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
E7 ORF (Fragment).
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PRELIMINARY;
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Best Local Similarity
'Local 9; Conserv?
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SEQUENCE FROM N.A.
MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                                                                       SEGUENCE FROM N.A.
Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
Lee H.-P.;
                                                                                                                                             "Major sequence variants in E7 gene of human papillomavirus type 16 from cervical cancerous and noncancerous lesions of Korean women."; Gynecol. Oncol. 66:275-281(1997).
                                    SEQUENCE FROM N.A.
MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 54; DB 2; Length 98; 100.0%; Pred. No. 0.096;
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Teral M., Fu L., Ma Z., Burk R.D.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; U76404; AAC58243.1; -.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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InterPro; IPR000148; Papvi_E7
Pfam; PF00527; E7; 1.
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NCBI_TaxID=10581;
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"The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.",
cell 53:539-547 (1988).
-1- FUNCTION: E7 protein has both transforming and trans-activating
SEQUENCE FROM N.A.
MEDLINE=90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
"Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
J. Gen. Virol. 71:809-817(1990).
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InterPro; IPR000148; Papvi_E7.
Efam; PF000527; E7; 1.
DNA-binding; Early protein; Oncogene; Trans-acting factor; Transcription regulation.
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                                                                                                                                                                                                               SEQUENCE FROM N.A. Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Ol-JUL-1997 (TrEMBLrel. 04, Created)
Ol-JUL-1997 (TrEMBLrel. 04, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transforming protein B7.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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C-XX-C motif-2.
9BD612534CD2C9EB CRC64;
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SECUENCE FROM N.A.
MEDLINE=22182962; PubMed=12195358;
MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheung T.F.;
"Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
J. Infect. Dis. 186.696-700 (2002).
EMBL; AF486329; AAL96634.1; \...
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   Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplain as southern China.";
J. Infect. Dis. 186:696-700(2002).
EMBL; AF486345; AAL96650.1;
InterPro; IPPR000148; Papvi_E7.
Pfam; PR00527; E7; 1.
SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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100.0%; Pred. No. 0.096; Lindels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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EMBL; AF486344; AAL96649.1; -.
Interepro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; 1.

SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
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QBQRD3;
QBQBD3;
QBQBD3;
QBQBD3;
QBCT-2002 (TrEMBLrel. 21, Last sequence update)
QBCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
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NCBI_TaxID=10581;
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SEQUENCE FROM N.A.
MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL; AF003021; AAB70738.1; -.
Interpro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;
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MEDLINE-974317474; PubMed=2292007;
MEDLINE-974317474; PubMed=2292007;
TOTRESELIO M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jinhu X., Xinxing W., Yun T.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF003022; AAB70739.1; -.
EMBL; AF477385; AAM03025.1; -.
INTERPY; IRRO00448; Papvi E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Matches 9, Conservative
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NCBI_TaxID=10581;
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012338;
01-JUL-1997 (
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01-JUN-2002
01-JUN-2002
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and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL, ABCUGIT4; AAMO3984.1; -.
PÉmn; PPO3819; MazG; 1.
PIRSF; PIRSF006690; UCP006690_pph; 1.
                                                                                                                                                                                       Human papillomavirus type 16
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         Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Matches 8; Conservative
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                                                                90 VCPICSOKP 98
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Q8TT97
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EMBL, AJ388662; CAB45171.1; -.

InterPro; IPR00148; Papvi_E7.

Pfam, PR0027; E7.

NON TER 98

SEQÜENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;
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                                         100.0%; Score 54; DB 2; Length 98; 100.0%; Pred. No. 0.096;
                                                               0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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InterPro, IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E7 protein (Framment)
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Human papillomavirus type 16.
                                                Local Similarity 100.
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Papillomavirus.
NCBI_TaxID=10581;
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Papillomavirus
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Q778H3;
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SEQUENCE FROM N.A.

MEDLINE=21929760; PubMed=11932338; DOI=10.1101/gr.223902;

Allan N., Nashoru V., Roy A., Endrizzi M.G., Macdonald P.,

Allan N., Naylor J., Stange-Thomann N., Darzellano K., Johnson R.,

Linton L., Maylor J., Stange-Thomann N., Darzellano K., Johnson R.,

Linton L., McKernan R., Tarahama D.E., Grahame D.A., Guss A.M.,

A lengh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.M., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rery J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
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100.0%; Score 54; DB 2; Length 98; 100.0%; Pred. No. 0.096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.6%; Score 50; DB 2; Length 98; 88.9%; Pred. No. 0.46;
                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jinhu X., Xinxing W., Yun T.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF461264; AAL66736.1; -.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein MA0540.
                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
E7 protein.
                                                                                                                                                                                                                                                                                                                                                   98 AA
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                                                                Mismatches
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RESULT 13

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Nagase T., Kikuno R., Ohara O., "Prediction of the coding sequences of unidentified human genes. XXII. The complete sequences of 50 new cDNA clones which code for large
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Coles E.G., Christiansen J.H., Economou A., Bronner-Fraser M.,
Wilkinson D.G.;
A vertebrate crossveinless-2 homolog modulates BMP activity and
neural crest cell migration.";
Development 0:0-0(2004).
EMBL; AY731S07; AAU34017.1; -.
SEQUENCE 678 AA; 75031 MW; B4EF49FAAEDCCCAB CRC64;
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     01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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PROSITE; PS01208; VWFC 1; UNKNOWN 2
PROSITE; PS50184; VWFC 2; 2.
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EMBL, AB075845, BAB85551.1; -.

InterPro; IPR002919; Cysrich TIL.

InterPro; IPR0009041; PMP SGCI.

InterPro; IPR000294; VITK dep_GIA.

InterPro; IPR001007; VWF_C.
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                           KIAA1965 protein (Fragment).
Name=KIAA1965;
Homo sapiens (Human).
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Pfam; PF00093; VWC; 3.
Pfam; PF00094; VWD; 1.
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SMART; SM00216; VWD; 1
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=86181601; PubMed=3008427; Dartmann K., Schwarz E., Gissmann L., Zur Hausen H.; "The nucleotide sequence and genome organization of human papilloma
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DNA-binding; Early protein; Oncogene; Trans-acting factor;
Transcription regulation.
                                                                          Score 49; DB 2; Length 95;
Pred. No. 0.67;
0; Mismatches 1; Indels
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Pred. No. 3.3;
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C-XX-C motif-2.
AACA9A60C933E1F6 CRC64;
                           8A68E2F4EFA616BA CRC64;
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AC QBTF36; CTEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1986 (Rel. 02, Created)
23-OCT-1986 (Rel. 02, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name=E7;
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Complete proteome.
SEQUENCE 95 AA; 10875 MW;
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InterPro, IPR000148; Papvi_E7
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                                                                             90.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 11.
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77.8%;
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                                                                                                                                 8; Conservative
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                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
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tes 7; Conserv
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Papillomavirus
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P04020;
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MEDLINE=21846229; PubMed=11857370;

MALES K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, AF4043025, Cahost cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

NON TER

1 SEQUENCE 103 AA; 12422 MM; 6F90CBAFIF25449B CRC64;
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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Q8qhn0
Q8qhb5
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Q8qrd5
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Q8qrd6
Q8qrd9
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P03126
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0919D6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OFC-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein (Fragment):
Human papillomavirus type 16.
Viruges; deDNA viruses, no RNA stage; Papillomaviridae;
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                                    OSWMPS
VBC HPV16
QBJMU8
QBQHPO
QBQHTO
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Q9WMP4
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Best Local Similarity 100.
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404699; AAL01355.1;
GO; GO:0002677; F:DNA binding; IEA.
PFam; PF00518; E6; 11.
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404696; AAL01349.1; ---
GO; GO:0042025; C:host cell nucleus; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                     130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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                                                                       100.0%; Score 57; DB 2; 100.0%; Pred. No. 0.26;
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MEDLINE=21846229; PubMed=11857370;
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E6 protein (Fragment).
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Pfam; PF00518; E6; 1.

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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404701; AL01359-1; -
GO; GO:0003677; F:DNA binding; IEA.
Fam; PF00518; E6; 1.

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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart tate of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874[2002).

EMBL, AF404700; AAL01357.1;

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                          130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
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 EMBL, AF404703, AAL01363.1; -. GO, GO:0042025; C:host cell nucleus; IEA. GO; GO:0003477; F:DNA binding; IEA. Pfam; PF00518; E6; 1.
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SEQUENCE FROM N.A.
MEDLINE=21846229; PubMed=11857370;
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Matches 9; Conservative
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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RESULT 4 Q919C0

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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404702; AAL01361.1;
GO, GO:0002057; C:host cell nucleus; IEA.

GO, GO:0003677; F:DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(202).
EMBL; AF404698; AAL01353.1;
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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B6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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NCBI_TaxID=10581;
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404695; AAL01347.1; -..
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
NON TER
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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                  100.0%; Score 57; DB 2; Length 130;
100.0%; Pred. No. 0.26;
tive 0; Mismatches 0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQÜENCE 138 AA; 16696 MW; 481E5ARA901
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MEDLINE=21846229; PubMed=11857370;
  Query Match
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MEDLINE=20112892; PubMed=10644829; Van Duin M., Shijders P.J., Vosen M.T., Klaassen E., Voorhorst F., van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analyais of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).
BMBL, AJ388056; CAB45104.1; -
BMBL, AJ388066; CAB45114.1; -
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34125; AAA91661.1; -.
EMBL; U34130; AAA91677.1; -.
EMBL; U34131; AAA91677.1; -.
GO; GO:0040255; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
                                                                                                                                         151 AA
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133 TGRCMSCCR 141
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NCBI_TaxID=10581;
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NCBI_TaxID=10566;
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Q76TS0
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MEDLINE=9747474; PubMed=9292007;
MEDLINE=9747474; PubMed=9292007;
MEDLINE=9747474; PubMed=9292007;

Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).

EMBL, AF003016; AAB70733.1;
GO; GO:0003677; F:DNA binding; IEA.

InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9743744; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
Torneello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Torneello M.L., Giraldo G.,
Beth-Giraldo E., Giraldo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
D. Gen. Virol. 78:2199-2208(1997).
EMBL, AF003015; AAB70732.1;
GO, GO:0042025; C.Nost cell nucleus; IEA.
GO, GO:00402025; C.Nost cell nucleus; IEA.
InterPro; IPR001334; E6.
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100.0%; Pred. No. 0.3;
cive 0; Mismatches 0; Indels
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 proctein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 Aa; 18206 MW; 51C12A8B149C6D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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Matches 9; Conservative
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125 TGRCMSCCR 133
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EMBL; AJ388063; CAB45118.1; -. GO; GO:00042025; C:host cell nucleus; IEA.

GO; GO:000277; F:DNA binding; IEA.

InterPro; IPR00134; E6.

Pfam; PF00518; E6; 1.

SEQUENCE 151 AA; 18304 MW; OF312A8BDBA6CF1F CRC64;
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100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
                                                                                                                                                                                                                                                                05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
E6 oncoprotein (E6 protein).
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                                                                                                                    1 TGRCMSCCR 9
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Best Local Similarity
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Q77E16;
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Search completed: June 29, 2005, 01:34:43 Job time : 55.2473 secs

133 TGRCMSCCR 141

1 TGRCMSCCR 9

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-63 57 1 TGRCMSCCR 9 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir 79:*
1: pir1:*
2: pir2:*
: pir3:* Database

STIMMARTES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein E6 - human	- uis	-	E6 protein - bovin	muscarinic acetylc	muscarinic recepto	muscarinic acetylc	muscarinic acetylc	muscarinic acetylc	hypothetical prote	late embryogenesis	conserved hypothet	hypothetical prote	polyketide synthas	E6 protein - human	small hydrophobic	hypothetical prote	heme biosynthesis	cyc02 protein prec	hypothetical prote		collagen - nematod	hypothetical prote			Ð	· hypothetical prote		hypothetical prote
SUMMARIES	Ü	WEWLHS	W6WL35	W6WLEB	W6WLB2	A31897	151837	809508	A24325	A29514	E84560	G84839 .	H71363	E84542	T30283	W6WL31	JQ1625	T20906	B84274	300877	A72759	WGWLR1	A44984	T17980	C71460	T33488	S28098	T18975	T24272	T15651
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	Length	158	149	137	139	460	460	460	460	460	222	280	355	369	6420	149	174	305	305	101	143	191	295	310	591	747	911	152	164	188
ď	Query Match	100.0	75.4	73.7	73.7	71.9	71.9	71.9	71.9	71.9	70.2		70.2	70.2	70.2	68.4	68.4	68.4	67.5	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.9	64.9	64.9
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140 TGRCMSCCR 148

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WGWLSS

WE protein - human papillomavirus type 35

C;Species: human papillomavirus type 35

Z;Species: human papillomavirus type 35

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: E40824; 83551

R;Marich, J.E.; Ponteier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776 1992

Virology 186, 770-776

A;Accession: E40824; MUID:92124753; PMID:1310198

A; Status: translation not shown

hypothetical prote	probable membrane- hypothetical prote	conserved hypothet	laminin alpha-1 ch		E6 protein - human		E6 protein - human	hypothetical prote	fl8485 protein [im	zinc finger/leucin	laminin gamma 2 ch	laminin B2t chain	structural polypro	conserved hypothet
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30	31 32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SEE>
A; Cross-terences: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G333303
A; Cross-terences: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G33303
B; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Virol. 65, 2093-2097, 1991
A; A; Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A; Reference number: 217014; MUID: 91162763; PMID: 1848319
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protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: buman papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T1047 Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-158 <KEN>
A;Cross-references: EMBL:KO2718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
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Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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Indels

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A,Molecule type: DNA
A,Residues: 1-139 <480>
A;Residues: 1-139 <480>
A;Cross-references: UNIPROT:P11302; GB:M20219; GB:M19551; NID:g332996
C;Superfamily: papillomavirus E6 protein
C;Reywords: DNA binding; early protein; zinc finger
F;17-55/Region: zinc finger CCCC motif
F;90-129/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                          73.7%; Score 42; DB 1; Length 139; 75.0%; Pred. No. 31;
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0; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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A, Accession: H31169
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C.Species: bovine papillomavirus type 1
C.Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C.Accession: C10151
R.Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Abture 299, 529-534, 1982
A.A.Title: The primary structure and genetic organization of the bovine papillomavirus type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Contents: annotation
RiAndrophy, B.J.; Schiller, J.T.; Lowy, D.R.
Science 230, 442-445, 1985
A/Fitle: Identification of the protein encoded by the E6 transforming gene of bovine pag
A/Reference number: A94282, MUID:86018841; PMID:2996134
A/Rontents: annotation; identification of the protein
C;Comment: This protein is present in the cell nucleus and the cellular membrane.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Modecule type: DNA
A; Residues: 1-137 cCHE>
A; Cross-references: UNIPROT: P06931; GB: X02346; GB: J02044; GB: M24622; GB: X00473; NID: g609
A; Cross-references: UNIPROT: P06931; GB: X02346; GB: J02044; GB: M24622; GB: X00473; NID: g609
B; Danos, O.; Engel, L., Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Yirol. 46, 557-566; 1983
A; Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus genc
A; Reference number: A92993; MUID: 83189357; PMID: 6302319
                           A, Residues: 1-149 <MAR>
A, Residues: 1-149 <MAR>
A, Cross-references: UNIPROT: P27228; GB: M74117; NID: 9333050; PIDN: AAA46966.1; PID: 9333051
R, Delius, H.; Hoffmann, B.
Bubmitted to the EMBL Data Library, August 1993
A, Description: Primer-directed sequencing of human papillomavirus types.
A, Reference number: S36469
A, Accession: S36521
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C,Species: bovine papillomavirus type 2
C,Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 < CDEL>
A;Residues: 1-149 < CDEL>
A;Residues: 1-149 < CDEL>
A;Residues: 1-149 < CDEL>
A;Experimental source: grain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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Pred. No. 31;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.4%; Score 43; DB 1; Length 149; 100.0%; Pred. No. 24; o; Mismatches 0; Indels
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R,Groff, D.E.; Mitra, R.; Lancaster, W.D.submitted to GenBank, May 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.7%;
75.0%;
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Best Local Similarity
6; Conserv?
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Matches 7; Conserv
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A.Accession: A31897
A.Molacule type: DNA
A.Molacule type: DNA
A.Residues: 1-460 <SINA
A.Residues: 1-460 <SINA
A.Molacule the authors translated the codon ATC for residue 119 as Thr
A.Mote: the authors translated the codon ATC for residue 119 as Thr
B.Mote: A. Schaptro. N. M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A.Reference number: A92742
A.Reference number: A92742
A.Reference number: A92742
C.Superfamily: vertebrate rhodopsin
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosph
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C;Species: Rattus sp. (rat)
C;Date: 26-Uul-1996 #sequence_revision 26-Uul-1996 #text_change 24-Nov-1999
C;Accession: 151837
R;Lai, J; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roesk Adv. Exp. Med. Biol. 287, 313-330, 1991
A;Tile: The molecular properties of the MI muscarinic receptor and its regulation of C A;Reference number: 151837; MUID:92101806; PMID:1759615
A;Accession: 151837
A;Status: preliminary; translated from GB/EMBL/DDBJ
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muscarinic acetylcholine receptor M1 - mouse
C;Species: Mus musculus (house mouse)
C;Species: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999
C;Accession: A31897
R;Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
A;Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
A;Title: Isolation, sequence, and functional expression of the mouse M1 muscal
A;Reference number: A92694; MUID:89054021; PMID:2848036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A;Cross-references: GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:g241254
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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A) Experimental source: cerebral cortex
A;Note: only a part of the protein translation is given; none of the nucleotide sequen.
B;Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues inv.
A;Reference number: A37121; MUID:90337982; PMID:2380182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurotransmitter receptor; phospi
                                                                                                                               glycoprotein; neurotransmitter receptor; phospi
                                     Across-references: UNIPROT: P04761; GB:X04413; NID:g1863; PIDN:CAA28003.1; PID:g1866 C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate rhodopsin C; Superfamily: vertebrate receptor; glycoprotein; neurotransmitter receptor; phos F; 25-50/Domain: transmembrane #status predicted <TM1> F; 25-50/Domain: transmembrane #status predicted <TM2> F; 100-121/Domain: transmembrane #status predicted <TM3> F; 147-268/Domain: transmembrane #status predicted <TM5> F; 167-387/Domain: transmembrane #status predicted <TM5> F; 187-367/Domain: transmembrane #status predicted <TM5> F; 187-367/Domain: transmembrane #status predicted <TM6> F; 187-367/Domain: trans
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A Residues: 1-460 < ROL3.
A) Kresidues: 1-460 < ROL3.
A) Cross-references: UNIPROT: P08482
R; Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A; Tile: Identification of a family of muscarinic acetylcholine receptor genes.
A) Reference number: A94293; MUID:87263421; PMID:3037705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A94518; A94293; A37121; A29514
R;Bonner, T.I.
A;Reference number: A94518
A;Reference number: A94518
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Fi402-420/Domain: transmembrane #status predicted <TM7>
F:2.12/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 86;
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C; Keywords: G protein-coupled receptor; glycoprotein; ne
F; 25-50. Domain: transmembrane #status predicted <TM1>
F; 62-93/ Domain: transmembrane #status predicted <TM2>
F; 100-121/ Domain: transmembrane #status predicted <TM3>
F; 142-168/ Domain: transmembrane #status predicted <TM4>
F; 187-209/ Domain: transmembrane #status predicted <TM5>
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Pred. No. 86;
0; Mismatches
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C,Superfamily: vertebrate rhodopsin
C,Keywords: G protein-coupled recept
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75.0%;
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Similarity 75.0%;
6; Conservative
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A; Residues: 1-227;338-460 <BO2>
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Matches 6, Conserv
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Best Local Similarity
Matches 6; Conserv
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A;Residues: 1-460 <CHA>
A;Residues: 1-460 <CHA>
A;Cross-references: UNIPROT:P11229; EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451
A;Cross-references: UNIPROT:P11229; EMBL:X52068; NID:g34450; PIDN:CAA36291.1; PID:g34451
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
Nucleic Acids Res. 15, 10604, 1987
A;Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.
A;Reference number: S06327
A;Accession: S06327
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A24325
R;Kubo, T.; Fukuda, K.; Mikami, A.; Maeda, A.; Takahashi, H.; Mishina, M.; Haga, T.; Hag Nature 233, 411-416, 1986
A;Title: Cloning, sequencing and expression of complementary DNA encoding the muscarinic A;Reference number: A24325; MUID:87014801; PMID:3762692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-172,'M',174-460 <PER>
A;Cross-references: EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID:g32318
A;Cross-references: EMBL:X15263; NID:g32317; PIDN:CAA33334.1; PID:g32318
C;Superfamally: vertebrate thodopsin
C;Superfamally: vertebrate thodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
P;25-50/Domain: transmembrane #status predicted <TM1>
F;62-93/Domain: transmembrane #status predicted <TM2>
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;Residues: 1-460 (ALL.)

;Cross-references: GB:V00508; GB:W15128; NID:g297405; PIDN:CAA68560.1; PID:g297406

;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J

MBO J. 6, 3923-3929, 1987

**MRO J. 6, 3921-3929, 1987

**Title: Distinct primary structures, ligand-binding properties and tissue-specific expr

;Reference number: S04326; WUID:88166632; PMID:3443095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: 809508; 806327; 804326
R;Chapman, C.G.; Browne, M.J.
Nucleic Acids Res. 18, 2191, 1990
A;Title: Isolation of the human ml (Hml) muscarinic acetylcholine receptor gene by PCR
A;Reference number: 809508; MUID:90245684; PMID:2336407
A;Accession: 809508.
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Pred. No. 86;
0; Mismatches 2; Indels
            Length 460
                                                                                  2; Indels
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F;142-168/Domain: transmembrane #status predicted <TM4>
F;187-209/Domain: transmembrane #status predicted <TM5>
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    DB 2;
86;
                                                                              0; Mismatches
        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             muscarinic acetylcholine receptor M1 - human
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71.9%;
75.0%;
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75.0%;
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                                                                                                                                                                                                                                       257 GRCCRCCR 264
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                                             Local Similarity
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    Query Match
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Matches
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A;Molecule type: DNA
A;Residues: 1-355 <COL>
A;Cross-references: UNIPROT:083158; GB:AE001197; GB:AE000520; NID:g3322382; PIDN:AAC651
A;Experimental source: strain Nichols
C;Genetics:
A;Gene : TP0121
C;Superfamily: conserved hypothetical protein yodo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein At2g16650 [imported] - Arabidopsis thaliana C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C'Accession: E84442
R'Lin, X'; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R.Lin, X.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, I. Nature 402, N61-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Recession: E84542
A,Status: preliminary
A,Molecule type: DNA
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C;Species: Streptomyces sp.
A;Variety: strain MA6548
A;Variety: strain MA6548
C;Accession: T30283
E;Motamedi, H.; Cai, S.J.; Shafiee, S.J.; Elliston, K.O.
Bur. J. Biochem. 244, 74-80, 1997
A;Title: Structural organization of a multifunctional polyketide synthase involved in the structural organization of a multifunctional polyketide synthase involved in the structural organization of a MID:9717; PMID:9063448
A;Reference number: Z20806; MUD:97217427; PMID:9063448
A;Accession: T30283
A;Accession: T30283
A;Accession: T30283
A;Molecule type: DNA
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A; Cross-references: EMBL:Y10438; NID:e1014806; FID:e290681; PIDN:CAA71463.1
G; Genetics:
A; More: EkbA
C; Genetics:
A; Note: EkbA
C; Keywords: carrier protein
F; 51-433/Domain: 3-oxoacy1-[acy1-carrier-protein] synthase I homology cOAS1>
F; 3391-3462/Domain: 3-oxoacy1-[acy1-carrier-protein] synthase I homology cOAS2>
F; 3505-3900/Domain: acy1 carrier protein homology cACP1>
F; 3903-4254/Domain: acy1-carrier-protein] S-malonyltransferase homology cAMT1>
F; 5307-5378/Domain: acy1-carrier-protein homology cACP2>
F; 5307-5378/Domain: acy1-carrier-protein homology cACP2>
F; 5307-5378/Domain: acy1-carrier-protein] synthase I homology cAMT1>
F; 5307-5378/Domain: acy1-carrier-protein] synthase I homology cOAS3>
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                                                                                                                                                                                                                                            6; Conservative
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261 TGRCLSC 267
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A,Map position: 2
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84839
R;Lin, X.; Kaul S; Rounsley, S.D; Shea, T.P; Benito, M.I; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Recession: G84839
A;Recession: G84839
A;Recession: G84839
A;Recession: G84839
A;Residues: 1-280
A;Residues: 1-280
A;Cross-references: UNIPROT:Q98783; GB:AE002093; NID:g3894196; PIDN:AAC78545.1; GSPDB:GR
                                                                                                                                  CjAccesion: E84560
Rjun, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Riin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
ArTitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Recession: B84560
A; Accession: E84560
A; Residues: 1-22 <STO>
A; Residues: 1-22 <STO>
A; Cross-references: UNIPROT:Q95119; GB:AE002093; NID:g4874291; PIDN:AAD31354.1; GSPDB:GN
A; Map position: 2
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: H71363
                                     hypothetical protein At2g18120 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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Pred. No. 76;
2; Mismatches 1; Indels
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62.5%;
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-149 < GOL
A; Residues: 1-149 < GOL
A; Comment: 1-149 < GOL
C; Comment: This protein may be involved in the oncogenic potential of this virus.
C; Superfamily: papillomavirus E6 protein
C; Superfamily: papillomavirus E70 protein
F; Reywords: DNA binding; parly protein;
F; Reywords: DNA binding; parly protein;
F; Reywords: DNA binding; Pinger CCC motif
F; 103-139/Region: zinc finger CCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 366-311, 1989
A;Title: Nuclectide sequence of human papillomavirus type 31: a cervical neoplasia-assoc
A;Reference number: A94398; MUID:89299478; PMID:2545036
F;5932-6206/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2> F;6293-6364/Domain: acyl carrier protein homology <ACP3>
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar.1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
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                                                                                                  Score 40; DB 2; Length 6420;
Pred. No. 5.5e+02;
1; Mismatches 1; Indels
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                                                                                               Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Search completed: June 29, 2005, 01:38:37 Job time: 12.2747 secs

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US-10-484-063-9
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US-10-484-063-9
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUBL.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US11NEW PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US11NEW PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US11NEW PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US11NEW PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Compugen Ltd
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US-10-978-249-513
US-10-476-570-44
US-10-177-390-6
US-10-484-063-27
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US-10-367-057-16
US-10-367-057-16
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                                                                                                                                                                                                                                                                                                                              1717557 seqs, 384547976 residues
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 TGRCMSCCR 9
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Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 10, Appl
Sequence 214017,
Sequence 3195, Ap
                                                                                                                                                                                                          Sequence 266658, Sequence 155, App Sequence 155, App Sequence 155, App Sequence 124, App Sequence 115, App Sequence 118, App Sequence 118, App Sequence 1118, App Sequence 155, App Sequence 157, App Sequence 82,                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 513, App
Sequence 188, App
Sequence 6, Appli
Sequence 93, Appli
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Sequence 10, Appl
Sequence 22, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 513,
1 US-10-899-771-4
3 US-10-809-771-4
3 US-10-809-771-10
3 US-10-809-771-10
3 US-10-809-771-10
3 US-10-809-771-6
3 US-10-809-771-14
5 US-10-809-771-14
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5 US-10-809-771-14
6 US-10-809-771-14
7 US-10-809-804-245-155
6 US-10-809-804-245-155
7 US-10-809-86-155-155
8 US-10-809-86-155-155
8 US-10-809-86-155-155
8 US-10-809-86-155-155
8 US-10-139-76-31-18
8 US-10-139-76-31-18
8 US-10-319-76-31-18
8 US-10-39-88-31-11071
US-99-782-980-82
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US-10-225-567A-188
US-10-326-489-6
US-10-423-543-93
US-10-806-018-82
US-10-925-095-513
US-10-029-009-22
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ALIGNMENTS

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Sequence 9, Application US/10484063
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TOLLEN MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: USC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 9: 27
; SEQ ID NO 9: 27
; SEQ ID NO 9: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 9; Conservative
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US-09-367-309A-1 US-10-000-903-4

Sequence 2 Sequence 1,

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Sequence 44, Application US/10476570
Sequence 44, Application No. U220040170644A1
GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: BOUNGALLE-WARATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Dapillomavirus proteins and uses thereof
FILE REPRENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT PILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
NESULT 2

US-10-938-249-513

Sequence 513. Application US/10938249

Publication No. US20050037969A1

GENERAL INCEMENTION:
APPLICANT: Lu. Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schwatzer, Johanna D.
APPLICANT: Achor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE DO INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION NUMBER: US/10/938,249
CURRENT PELICATION NUMBER: US/10/938,249
CURRENT PELICATION NUMBER: US/10/938,249
CURRENT PELICATION NUMBER: US/10/938,249
CURRENT PELICATION NUMBER: US/10/938,249
CURRENT PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
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PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/162,498
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1999-10-21
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PRIOR APPLICATION NUMBER: US 60/196,267
PRIOR PILING DATE: 2000-01-14
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 513
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: HPV16 E6 C-terminal
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ORGANISM: Artificial Sequence
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US-10-476-570-44
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158 US-10-476-570-44
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| Sequence 20, Application US/10484063 |
| Sequence 20, Application US/1048467A1 |
| Sequence 20, Application No. US2005048467A1 |
| GENERAL INFORMATION: |
| APPLICANT: SASTRY, K. JACANNADHA |
| APPLICANT: TOWTOLERO-LUNA, GUILLERMO |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED |
| TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED |
| TITLE OF INVENTION: METHODS AND CONFEROUS GROWTHS, INCLUDING CIN |
| FILE REPERBENCE: UTSC:560US |
| CURRENT APPLICATION NUMBER: PCT/0802/23198 |
| PRIOR APPLICATION NUMBER: PCT/0802/23198 |
| PRIOR PILING DATE: 2002-07-19 |
| PRIOR PILING DATE: 2001-07-20 |
| PRIOR FILING DATE: 2001-07-20 |
| NUMBER OF SEQ ID NOS: 27
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Sequence 6, Application US/1017390

Sequence 6, Application US/1017390

Beneral Information No. US20030143743A1

GENERAL INFORMATION:

APPLICANT: Schuler, Gerold

TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

TITLE OF INVENTION: Polynucleotides by Electroporation

FILE REFERENCE: 021505wo/JH/ml

CURRENT APPLICATION NUMBER: US/10/177,390

CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 57; DB 16; Length 24; Best Local Similarity 100.0%; Pred. No. 0.45; Matches 9; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Human papillomavirus
US-10-484-063-20
                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: artificial sequence
PRIOR FILING DATE: 2001-05-04
                                    NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
LENGTH: 24
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SEQ ID NO 20
LENGTH: 151
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Best Local Similarity 100.
Matches 9; Conservative
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Sequence 2, Application US/10472724;
Sequence 2, Application US/10472724;
Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: ANGER: 2003-09-17
BRIOR APPLICATION NUMBER: BP 01107271.7
PRIOR PILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 2
LENGTH: 171
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                                                                                                                                                                                                                                           APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
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                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
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, OTHER INFORMATION: Synthetic Construct US-10-472-724-2
                                                                                                                                                                         ; Sequence 16, Application US/10367057; Publication No. US20050100554A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 198
SOFTWARE CuraSequist version 0.1
SEQ ID NO 16
LENGTH: 158
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Best'Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-367-057-16
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REPERENCE: UTSC:56003
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR PLILING DATE: 2002-07-19
PRIOR PLILNG DATE: 2001-07-19
PRIOR PLILNG DATE: 2001-07-20
PRIOR PLILNG DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VEY: 2.1
                                                       Gaps
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APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, BSTELLE
APPLICANT: FERRIES, BSTELLE
APPLICANT: PERRIES, BSTELLE
APPLICANT: PERRIESON STATEMENT OF THE BE PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
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       Length 151;
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                                                     0; Indels
                                                       Mismatches
       Score 57;
Pred. No.
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CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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Publication No. US20050033025A1
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
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Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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; ORGANISM: Human Papillomavirus
US-10-858-384-2
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 151
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TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REPERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR FILING DATE: 2004-07-27
PRIOR FILING DATE: 1909-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-24
NUMBER: OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius
OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
OTHER INFORMATION: 16)
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FUBLICATION No. US2002018221A1
SERVEL INFORMATION:
APPLICANT: BLUCK, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10.01
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PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
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US-10-000-903-10
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US-10-899-771-10
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LENGTH: 273
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                                                                                             APPLICANT: MACERRIAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REPERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT APPLICATION NUMBER: 1999-08-11
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR PILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN VOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 57; DB 9; Length 266; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10000903
Publication No. US2002018221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
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Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Gerard, Catherine Marie Ghislaine
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Human papillomavirus type 16
                           Sequence 1, Application US/09167309A Publication No. US20020081329A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-000-903-4
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LENGTH: 266
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
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OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
OTHER INFORMATION: 16)
US-10-899-771-10
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 371
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100.0%; Pred. No. 3.8;
iive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR PLING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR APPLICATION NUMBER: B77262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR PILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
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Publication No. US20020182221A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapien
US-10-000-903-6
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF187869; AAF13399.1; -. InterPro: IPR000148; Papvi_E7. Ffam; PF00527; E7; 1. Pfam; PF00527; E7; 1. NON TER 93 93 SEQÜENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
                    Q81bx1
Q6z489
Q6z489
Q7x669
Q7x669
Q6k796
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Q7x309
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Ponglikitmongkol M., Vaeteewoottacharn K.;

Ponglikitmongkol M., Vaeteewoottacharn K.;

Ponglikitmongkol M., Vaeteewoottacharn K.;

Bubmitad (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF465198; AAO155694.1; -.

InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; F7; 1.

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SEQÜENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
E7 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 protein (Fragment).

Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
100.0%; Score 51; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0.
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Q7XIB4
Q8HX1
Q624S9
Q8LHX2
Q624S9
Q624S8
Q78669
Q67796
Q56947
Q56947
Q56947
Q59955
Q9GP60
WB7 HPV33
Q7V3Q7
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(TrEMBLrel. 23, I
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NCBI_TaxID=10566;
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Listing first 45 summaries
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Lee H.P., Song Y.S., Kim J.W., Rob J.W., Park N.H., Kang S.B.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF187866; AAF13393.1; -.

InterPro; IRR000148; Papvi E7.

Pfam; PF00527; E7; 1.

NON TER 93 93

SEQÜENCE 93 AA; 10452 MW; 83281BBZAE2C8A1F CRC64;
                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 2; Length 93
100.0%; Pred. No. 0.033;
Mismatches 0; Indels
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Viruses, dsDNA viruses, no RNA stage, Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitred (JAN-202) to the EMBL/GenBank/DDBJ databases.
EMBL; AF465197; AA015692.1; -..
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
NON TER
SEQÜENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
                    01-MAY'2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JMD-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment):
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UDM-2003 (TrEMBLrel. 24, Last annotation update)
E7 oncoprotein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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(Rel. 01, Last sequence update)
(Rel. 45, Last annotation update)
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NCBI_TaxID=10581;
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Liee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Liee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1879668, AAR13397.1; -.
InterPro; IPR000148; Papvi_F7.
InterPro; IPR000148; Papvi_F7.
Pfam; PF00527; E7; 1.
NON TER
93
SEQUENCE 93 AA, 10452 MW; 83281BB2AEZC8AIF CRC64;
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B., Submitted (SEP-1999) to the BMBL/GenBank/DDBJ databases.

EMBL, AF187867; AAF13395.1; -.

InterPro, IPR000148; Papvi_E7.
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          Pred. No. 0.033;
; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment)
Human papillomavirus type 16.
Viruses; debna viruses, no RNA stage; Papillomaviridae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2010 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F., "Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
Lee H.-P.,
                                                                                                                                                                                                                                  "Major sequence variants in E7 gene of human papillomavirus type 16 from cervical cancerous and noncancerous lesions of Korean women."; Gynecol. Oncol. 66:275-281(1997).
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
SONG Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
Lee H.P.;
                                                                                                                                                                                                                                                                                                                                                                        Lee H.-P.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U76404; AAC58243.1; -.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                  Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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        05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transforming protein B7.
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                                                                                                              NCBI TaxID=10581;
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                                                                                            Papillomavirus
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SEQUENCE FROM N.A.
MEDLINE-90218027; PubMed=2157796;
MEDLINE-90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
"Expression of the human papillomavirus type 16 genome in SK-v cells,
"Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
J. Gen. Virol. 71:809-817(1990).
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"The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
Cell 53:539-547(1988).
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                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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                                         Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G., "Human papillomavirus type 16 DNA sequence."; Virology 145:181-185(1985).
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C-XX-C motif-2.
9BD612534CD2C9EB CRC64;
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011650;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
SEQUENCE FROM N.A.
MEDLINE=85246220; PubMed=2990099;
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EMBL; AF003020; AAB70737.1; -...
EMBL; AF003024; AAB70741.1; -...
EMBL; AF003025; AAB70741.1; -...
EMBL; AF003025; AAB70741.1; -...
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EMBL; D00735; BAA00633.1; -.
EMBL; U76411; AAB18962.1; -.
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RESULT 8

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MEDLINE=22182962; PubMed=12195358; Chan P.K., Chan P.K., Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.; Cheng A.F.; Cheng J.L.K., Xu L.Y., Cheng A.F.; Cheng J.L.K., Xu L.Y., Cheng A.F.; Cheng A.F.; Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., Cheng J.C., 
                                                                                                                             MEDINE=22182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.H., Xu L.Y., Cheng A.F.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700 (2002). BMBL, FA8486345; AAL96550.1; -.. InterPro; IPR00148; Papvi_E7. E7. Pfam; PF00527; E7; 1. SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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100.0%; Pred. No. 0.035;
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Human papiliomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papiliomavirus.
NCBI_TaxID=10581;
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Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10581;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Jinhu X., Xinxing W., Yun T.;
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Best Local Similarity 100.0
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Papillomavirus.
NCBI_TaxID=10581;
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
Tornerov. 18:2199-2208(1997).
EMBL, AF003021; AAB70738.1;
InterProv. IPF000148; Papvi_E7.
Pfem., PR000148; Papvi_E7.
SEQUENCE 98 AA; 11056 MW, 19DEB8P14CD2C705 CRC64;
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MEDLINE=9743744; PubMed=2292007;
MEDLINE=9743744; PubMed=2292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
T. Sequence variations and viral genomic state of human papillomavirus
T. Gen. Virol. 78:2199-2208(1997).
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Juhu X., Xinxing W., Yun T.;

Submitted (JAN-2020) to the EMBL/GenBank/DDBJ databases.

BMBL; AF003022; AAB7039.1; -.

EMBL; AF47385; AAM03025.1; -.

InterPro; IPR00448; Papvi_E7.

SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ET protein.
Human papillomavirus type 16.
Viruses; delowa viruses, no RNA stage; Papillomaviridae; Papillomavirus.
NCBI_TAXID=10581;
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WEDLINE-20112892; PubMed=10644829;
Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000)
EMBL, AJ388063; CAB45119.1;
InterPro, 1PR000148; Papvi_E7.
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100.0%; Score 51; DB 2; Length 98
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF461264; AAL66736.1; -. Pfam; PF00527; E7; 1. SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;
                                                                                                                                                                                                                                                              E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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98 AA; 10995 MW; 81E53B534CC3281B CRC64;
                        100.0%; Score 51; DB 2; 100.0%; Pred. No. 0.035;
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Best Local Similarity 100.0
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                                                                     1 KCDSTLRLC
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Sequence 1877. A Sequence 1276, Ap Sequence 1273. A Sequence 21. Appl Sequence 21, Appl Sequence 7, Appl Sequence 39, Appl Sequence 25074, A Sequence 25674, A Sequence 25678, A Sequence 25636, A Sequence 26636,
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Sequence 86, Sequence 5, 1 Sequence 5, 1 Sequence 1, 1 Sequence 1, 1

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Length 21;
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Patent No. 5932412
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: DARLICOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
US-09-504-357-12
US-09-252-911A-18776
US-09-198-422A-1276
US-09-252-911A-27237
US-09-356-952-6
US-09-481-593-21
US-09-481-593-21
US-08-900-230-24
PCT-US-66-01720-7
US-08-952-991A-25074
US-09-252-991A-25636
5268290-2
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CORRESPONDENCE ADDRESS:
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWAIER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORIDA
COMPUTER: READABLE FORM:
MEDIUM TYPE: FLORIDA
COMPUTER: MICROSOFT WINDOWS 3.0
SOFTWARE: MICROSOFT WINDOWS 3.0
SOFTWARE: MICROSOFT WARG 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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US-09-627-650B-5
US-09-436-063C-5
US-09-738-884-1
US-10-096-961A-1
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Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                     June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-980-523A-2

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US-08-380-312-12

US-09-389-382-12

US-09-389-380-3

US-09-386-30A-1

US-09-485-885-6

US-09-485-885-6

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US-09-480-016-9721

US-09-949-016-9721

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US-09-9826-509-513

US-09-826-509-513

US-09-270-767-50589

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US-09-674-973A-191

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US-09-674-973A-193

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                - protein search, using sw model
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seq length: 200000000
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57
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Match Length
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Maximum DB (
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Result No.

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not relevant
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Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Sequence 3. Application US/08316239B

Patent No. 5679509

GENERAL INFORMATION:

APPLICANT: Wheeler, Cosette M.

APPLICANT: Wheeler, Cheryl A.

TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Jagtiani & Associates
STREET: Geltery Way Court
CITY: Centreville
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Sequence 2. Application US/09980523A

Patent No. 6783763

GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: COUNTAN, FRANCINE

APPLICANT: COUNTAN, FRANCINE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PRATICULARLY IN VACCINATION

FILE REFERENCE: WOBL AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT APPLICATION NUMBER: E7/FR00/01513

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SONTWARE PATENTING DATE: 1999-06-03
  Gaps
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  Indels
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ZIP: 20120-3400

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  ;
0
0; Mismatches
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
  9; Conservative
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                                                                                    3 TGRCMSCCR 11
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                                        TGRCMSCCR 9
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APPLICANT: Wheeler, Cosette M.

APPLICANT: Wheeler, Cosette M.

APPLICANT: Warmenter, Cheryl A.

TITLE OF INVENTION: Methods and a Diagnostic Aid for

TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi

TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated WITTLE OF INVENTION: Cervical Cancer

TITLE OF INVENTION: Cervical Cancer

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jagtiani & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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ZIP: 20120-3400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jaggianl, Ajay A.
REGISTRATION NUMBER: UNMER: UNMERCE/DOCKET NUMBER: UNMER: UNMERCE/OMMUNICATION NUMBER: UNMERCE/OMMUNICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 57; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
NAME: Jagtiani, Ajay A.
REGISTRATION UNDRER: 35_205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEFROME (703) 817-9453
TELEFRAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08316239B Patent No. 5679509
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TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acid
STRANDENNESS: not relevant
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: EDNARDS, Stirling John
APPLICANT: EDNARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1995-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTING DATE: 1991-12-20
NUMBER OF SEQ ID NOS: 15
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Patent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: EDWARDS, Stirling John

APPLICANT: WEBB, Bilzabeth Ann

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER PEPLICATION NUMBER: PCT/AU95/00868

EARLIER PEPLICATION NUMBER: PCT/AU95/00868

EARLIER PEPLICATION NUMBER: AU PNO157/94

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 2.0
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ORGANISM: Human papillomavirus type 16
                                                                                                                                                           Sequence 10, Application US/08860165A Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match Best Local Similarity 100.
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Best Local Similarity 100.0
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LENGTH: 266
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LENGTH: 266
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: COX, John Cooper
APPLICANT: WBBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPRENCE: 0.1722/70.14
CURRENT APPLICATION NUMBER: US 08/860,165
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 12
LENGTH: 172
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                                                                                                                                                                            Sequence 12, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS. Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEAZER, Ian
ITTLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 57; DB 3; Length 172; 100.0%; Pred. No. 0.56; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                         THE KERNET APPLICATION NUMBER: US/08/860,165A; CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PELCHIN VOR: 15
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09359382 Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
                                                             140 TGRCMSCCR 148
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Sequence 10, Application US/09485885
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US-09-485-885-14
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US-09-485-885-6
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                                                                                                          Sequence 1, Application US/09367309A; Patent No. 642807; Patent No. 6428807; Patent Malitaros, Jim ; Title Of Invention: CHELATING IMMUNOSTIMULATING COMPLEXES; FILE REFERENCE: 017227/0149; CURRENT APPLICATION NUMBER: US/09/367,309A; CURRENT PILING DATE: 1999-08-11; PRIOR PILING DATE: 1998-02-13; PRIOR PILING DATE: 1999-02-13; PRIOR FILING DATE: 1999-02-19; NUMBER OF SEQ ID NOS: 6; NUMBER OF SEQ ID NOS: 6; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 57; DB 3; Length 273; Best Local Similarity 100.0%; Pred. No. 0.82; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 57; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 0.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cerand, Catherine Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/FEP98/05285
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
140 TGRCMSCCR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 TGRCMSCCR 148
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LENGTH: 273
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 266
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Patent No. 6342224;
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
FURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
MUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGAL. 271
Patent No. 634224

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Bruck, Claudine

APPLICANT: Cacan Silva, Teresa

APPLICANT: Gerach, Catherine Marie Ghislaine

APPLICANT: Gerach, Catherine Marie Ghislaine

APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

TITLE OF INVENTION: Vaccine

CURRENT APPLICATION NUMBER: BCT/BE98/05285

FRIOR FILING DATE: 2000-02-18

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-08-22

NUMBER: OF SEQ ID NOS: 23

SOFTWARE: FRASESQ for Windows Version 3.0

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Matches 9; Conservative
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246 TGRCMSCCR 254
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGRCMSCCR 9
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ORGANISM: Homo sapien
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Matches 9; Conserve
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RESULT 11 US-09-485-885-10

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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 80/9949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-09
PRIOR FILING DATE: 2000-00-09
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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Sequence 118, Application US/09663600A

Patent No 6573068

GRNERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumalert, Applicant
APPLICANT: Bouguelert, Lydie
APPLICANT: Bouguelertet, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TILE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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                                                                                                                                                         CURRENT PEDLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FREESEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
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75.0%;
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14
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; ORGANISM: Human
US-09-949-016-9721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-949-016-9721
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LENGTH: 261
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Length 89,
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CURRENT PELLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR PELLING DATE: 1990-11-13
PRIOR FILING DATE: 1998-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-12-17
PRIOR PILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-04-18
PRIOR FILING DATE: 1998-04-18
PRIOR FILING DATE: 1998-04-18
PRIOR FILING DATE: 1998-04-10
PRIOR FILING DATE: 1998-08-10
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: PALENTLENT
LENGTH: 89
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Pred. No. 45;
0; Mismatches
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: -16..-1
US-09-663-600A-118
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Search completed: June 29, 2005, 01:44:22 Job time: 17.9126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec

US-08-170-344-62 51 1 KCDSTLRLC 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	E7 protein - human	E7 protein - human	E7 protein - human	1	growth modulatory	electron transfer	E7 protein - human	probable membrane	growth modulatory	hypothetical profe		~	hypothetical prote			hypothetical prote		DNA-directed RNA p		hypothetical prote		nicotinate-nucleot	conserved hypothet	transrepressor pro	iron-sulfur cluste	site-specific DNA-	cytochrome ba(3) c	hypothetical prote	probable extracell
SUMMARIES	ID	W7WLHS	836574	W7WL35	W7WL31	B46654	F69285	W7WL33	857060	C46654	A69513	T31837	A71288	T20326	E84985	D95998	T34248	D86179	F64324	W7WL58	T00944	E85086	AB1699	AI1072	S41171	Н69393	S01615	A54759	T39773	C82386
	DB	-	~	-	Н	7	~	-	7	N	~	7	7	N	7	7	~	7	7	Н	~	7	0	~	N	N	-	~	7	7
	Length	86	66	66	98	57	247	97	1174	57	8	249	315	349	429	578	798	952	57	86	201	214	281	287	300	363	377	420	428	458
	Query Match	100.0	90.2	86.3	78.4	9.02	9.07	9.89	9.89	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7
	Score	51	46	44	40	36	36	35	32	34	34		34	34	34	34							33					33		33
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RESULT 2
S36574
B7 procein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 08-May.1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S36574

60 KCDSTLRLC 68

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1 KCDSTLRLC

hypothetical prote hypothetical prote	hypothetical prote hypothetical prote E7 protein - human	activin beta A cha trophozoite surfac	hypothetical prote hypothetical prote GTP-binding protei	GTP-binding regula type I restriction hypothetical prote hypothetical prote hypothetical prote
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30 31) W W W 1 W 4 N	36 37 88	3.6 4.0 11.0	4 4 4 4 ሪ 6 4 ሺ

ALIGNMENTS

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Afforced to the type: DNA
A, Residues: 1-98 <SES.
A, Residues: 1-98 <SES.
A, Residues: 1-98 <SES.
A, Residues: 1-98 <SES.
A, Crose-references: UNIPROT: P03129; GB: K02718; NID: g333031; PIDN: AAA46940.1; PID: g33302
B, Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.
EMBO J. 9, 153-160, 1990
A, Title: The region of the HPV E7 oncoprotein homologous to adenovirus Ela and SV40 lax
A, Reference number: $12367; MUID: 90107938; PMID: 2153075
A, Reference number: SI2367
A, Reference number: Brotein
A, Residues: 1-98 <ARR>
B, Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A, Title: A negative element in the human poapillomavirus type 16 genome acts at the le
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C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;S8-94/Region: zinc finger CCCC motif
WYWLHS

B7 protein - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03688; S12367; Til428
R;Secdorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL: K02718; NID: 9333031; PIDN: AAA46940.1; PID: 93333033
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: T10428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <KEN>
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Best Local Similarity
Matches 9; Conserv
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Gaps

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A.Gross-references: UNIPROT:P17387, GB.J04353, NID:9333048, PIDN:AAA46951.1; PID:945991 C; Comment: This protein may be involved in the oncogenic potential of this virus. C; Superfamily: papillomavirus BT protein C; Superfamily: papillomavirus BT protein; C; Keywords: DNA binding; early protein; transcription regulation; zinc finger F; 58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth modulatory factor granulin-2 - common carp
C;Species: Cyprinus carpio (common carp)
C;Species: Cyprinus carpio (common carp)
C;Date: 2-1-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B46654; B40180
R;Belcourt, D.R.; Lazure, C.; Bennett, H.P.
A;Belcourt, Chem. 269, 9237, 1993
A;Title: Isolation and primary structure of the three major forms of granulin-like pept
A;Reference number: A46654; MUID:93252781; PMID:8486624
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Accession: F66285
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
R;Klenk, H.P.; Clayton, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69285
A;Accession: F69285
A;Accession: Kf9285
A;Accession: Kf9285
A;Residues: Dreliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-247 <KLE>
A;Residues: 1-247 <KLE>
A;Residues: 1-247 <KLE>
A;Residues: 1-247 <KLE>
A;Residues: 1-247 <KLE>
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                                                                                                                                                                                                                                                                                                                         Score 40; DB 1; Length 98;
Pred. No. 1.8;
1; Mismatches 1; Indels
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A;Experimental source: spleen and head kidney
A;Note: sequence extracted from NCBI backbone (NCBIP:131315)
C;Keywords: disulfide bond; monomer
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Pred. No. 6.4;
1; Mismatches
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66.7%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 60..
ما و Conservative
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47 RCDSTSTLC 55
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A;Status: preliminary
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R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: 836469
A;Reference number: 836574
A;Molecule type: DNA
A;Residues: 1-99 CBL-
A;Residues: 1-99 CBL-
A;Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g3970
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Er protein - human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapians (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F40824; S36522
C;Accession: F40824; S36522
R;Marich, J.B.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A;Reference number: A40824; MUID:92124753; PMID:1310198
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-99 cMAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
R;Delius, H.; Hofman, B.
Bubmitted to the EMBL Data Library, August 1993
A;Reference number: S36469
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C; Species: human papillomavirus type 31
A; Note: host Home sapiens (man)
A; Note: host Home sapiens (man)
C; Accession: B3244
E7; Acce
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
A; Experimental source: strain 35H
C; Superfamily: papillomavirus E7 protein
C; Keywords: DNA binding; early protein; transcription regulation; zinc finger
F; 59-95/Region: zinc finger CCCC motif
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77.8%; Pred. No. 0.33;
tive 2; Mismatches
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Best Local Similarity 77.8
Matches 7; Conservative
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61 KCEATLRLC 69
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Prochetical protein AF2105 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: A69513
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsc.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Avatures 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Shith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Shith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Shith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Shith, H.O.; Woses, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, T.; Artiach, P.; Kaine, B.P.; Sykes, F. Shith, H.D.; Spriggs, T.; Artiach, T.; Artiach, F. Shith,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
KResidues: 1-89 KLES-
A;Cross-references: UNIPROT:O28175; GB:AE000958; GB:AE000782; NID:g2689281; PIDN:AAB891
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein
F;89/Modified site: 1-thioglycine (Gly) #status predicted
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hypothetical protein T05B4.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 29-ct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31837
R;Bradshaw, H.
R;Bradshaw, H.
A;Description: The sequence of C. elegans cosmid T05B4.
A;Reference number: Z21092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
|||| | | |
878 KCDSALGFC 886
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Best Local Similarity
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R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t A;Reference number: $19906
A;Accession: S23831
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A;Residues: 1-1174 «MAN>
A;Cross-references: UNIPROT:P47108; EMBL:Z49541; NID:g1015692; PID:g1015693; MIPS:YJR041
R;Huang, M.E.: Chuat, J.C.; Galibert, F.
Yeast 11, 775-781, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: EMBL:X64085; NID:g60278; PIDN:CAA45434.1; PID:g60281; EMBL:X64084; C;Superfamily: papillomavirus E7 protein
C;Superfamily: papillomavirus E7 protein; Experion regulation; zinc finger F;S8-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                               A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, A;Reference number: A93020; MUID:86200464; PMID:3009902
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Cross-references: EMBL:L36344; NID:g1197060; PIDN:AAA88743.1; PID:g1197069
Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
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                                                                                             E7 protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun.1987 #sequence_revision 30-Jun.1987 #text_change 09-Jul-2004
C;Accession: A03689; S23831; $23827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable membrane protein YJR041c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein J1622
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul.1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57060; S63765
R;Huang, M.E.; Chundt, J.C.; Galibert, P.
Rshuang, M.E.; Chundt, J.C.; Galibert, P.
A;Reference number: S57052
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A;Map position: 10R
A;Note: YJR041c
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJR041c
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A;Accession: S63765
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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Pred. No. 1.3e+02;
0; Mismatches 3;
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66.7%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                        R;Cole, S.T.; Streeck, R.E. J. Virol. 58, 991-995, 1986
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61 CNTTVRLC 68
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A;Molecule type: mRNA
A;Residues: 1-97 <SNI>
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Pred. No. 71;
1; Mismatches
                                        66.78;
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Matches 6; Conservative
                                                                                6; Conservative
                                                                                                                                                                                                          248 KCYKTLQLC 256
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                                    Best Local Similarity
Matches 6; Conserv
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McDo
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F;5-288/Domain: methylenetetrahydrofolate dehydrogenase (NAD+) homology <MTFD>
                                                                                                                                                 A;Cross-references: UNIPROT:O16420; EMBL:AF016445; PIDN:AAC69060.1; GSPDB:GN00023; CESP. A;Experimental source: strain Bristol N2; clone T05B4 C;Genetics: A;Genet CBSP:T05B4.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        α F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable methylenetetrahydrofolate dehydrogenase (folD) - syphilis spirochete (Species: Treponema pallidum subsp. pallidum (syphilis spirochete) (Species: Treponema pallidum subsp. pallidum (syphilis spirochete) (Species: 4-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 (Spacession: A71288 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004 (Spacession: A71288 F;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R. spin, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998 #title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A;Reference number: A71289 #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VILLS #VI
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20326
R;Smye, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19257
A;Accession: T20326
A;Accession: T20326
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Introns: 34/3; 121/1
C;Superfamily: Caenorhabditis elegans hypothetical protein C49G7.3
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Pred. No. 65;
2; Mismatches 1; Indels
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A;Map position: 5
A;Introns: 10/3; 108/3; 144/3; 160/2; 174/1; 247/3; 308/3
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 55.6%; Pred. No. 53; 5; Conservative 2; Mismatches
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Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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A;Cross-references: UNI
                                                                                     Molecule type: DNA
Residues: 1-249 <BRA>
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DB 2; Length 349;

66.7%; Score 34;

Query Match

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A,Gene: clpX; BU476
C,Superfamily: heat shock protein hslU; FtsH/SEC18/CDC48-type ATP-binding domain homolc
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A;Reference number: A58842; MUID:21396508; PMID:11481431
A;Reference number: A58842; MUID:21396508; PMID:11481431
A;Reference number: A58842; MUID:21396508; PMID:11481431
A;Residues: 1-578 <KUR;
A;Residues: 1-578 <KUR;
A;Residues: 1-578 <KUR;
A;Residues: 1-578 <KUR;
A;Residues: 1-578 <KUR;
A;Residues: 1-578 <KUR;
A;Reference Sinorhizobium meliloti C; Italauri C; Itala
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C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Accession: B84985
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Mature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MuID:20445173; PMID:10993077
A;Reference number: A84930; MuID:20445173; PMID:10993077
A;Residues: DNA
A;Residues: 1-429 <STO>
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66.7%; Score 34; DB 2; Length 429;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 1; Mismatches 2; Indels
       Indels
       2;
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Search completed: June 29, 2005, 01:38:36 Job time: 13.2747 secs

gade Blank (nsbto)

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Gaps
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APPLICANT: Fisher, Christopher
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICANION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 20
                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
RADDRESSES: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Papillomavirus sylvilagi
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ZIP: 20007-5108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ublication actions
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09728466
Patent No. US20010029022A1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 98
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Matches 9; Conserv
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APPLICANT: Jochmus, John
TITLE OF INVENTION: Cytotoxic T-cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
CURRENT APPLICATION WIMBER: US/10/890,526
CURRENT APPLICATION OF THE TRANSMERS: 2004-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kaufman, Andreas
APPLICANT: Kather, Angela
APPLICANT: Kather, Angela
APPLICANT: Schinz, Manuela
APPLICANT: Schinz, Manuela
APPLICANT: Schinz, Manuela
APPLICANT: Manuela
APPLICANTION: T-C-11 Epitopes of the Papillomavirus L1
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE REPERENCE: 50125/0770N
FILE REPERENCE: 50125/0770N
FILE OF INVENTION NUMBER: US/10/432,465
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 0.047;
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                                                                                                                                                                                                                                                                                                                                                                   0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                         TYPE: PRT
ORGANISM: Human papillomavirus type 16
PRIOR APPLICATION NUMBER: US 60/041,726
PRIOR FILING DATE: 1997-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/09/980,177
PRIOR FILING DATE: 2002-05-02
                                                                                                                                                                                                                  ) NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV 16 E7 PEPTIDE
US-10-668-400-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/10432465
Publication No. US20040091479A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 74, Application US/10890526 Publication No. US20040258708A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human papillomavirus
                                             NUMBER OF SEQ ID NOS: 25
SOFWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 19
                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 20
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COMPUTER READABLE FORM:
MUEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: BEACH PC COMPATIBLE
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: O'No. US20030021806A1-2001
CLASSIFICATION SATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAMM: SANGEROCCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 51; DB 10; Length 98; Best Local Similarity 100.0%; Pred. No. 0.21; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                   Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
                                                                                                                               0; Indels
                                                                                       100.0%; Score 51; DB 9;
100.0%; Pred. No. 0.21;
                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
) MOLECULE TYPE: protein
) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10267311; Publication No. US20030050463A1 GENERAL INFORMATION: APPLICANT: Siegel, Marvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEFAX: (202) 672-5399
                                                                                                                                 0
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SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                   Conservative
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                                                                                       Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
                                                                                                                                                                           1 KCDSTLRLC
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                                                                                                                                                                                                                                                                                    RESULT 12
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ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUW TYPE: FILDAPY disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: BA PC COMPATIBLE

COMPUTER: PATORILIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-APL-2001

CLASSIFICATION NUMBER: 09/026,896

FILING DATE: 1998-02-200

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 9; Length 98; 100.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HALLEK, Michael
TITLE OF INVENTION: PARLILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                         NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REGISTRATION INFORMER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; ; MOLECULE TYPE: protein; seQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-820-765-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09824017
Publication No. US20020197668A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KCDSTLRLC 9
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Best Local Similarity
Matches 9, Conserval
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Publication No. US20030143743A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Schuler, Gerold.
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REPERENCE: 021505w0/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: TBA
CURRENT APPLICATION NUMBER: US/10/201,764
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/566,420
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OTHER INFORMATION: Description of Artificial Sequence: fragment of
OTHER INFORMATION: human papilloma virus type 16 B7 gene
US-10-177-390-8
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Lee A. INDUCTION OF A THI-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 14; Length 98; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 14; Length 98; 100.0%; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
          TITLE OF INVENTION: INDUCTION OF A TH1-LIKE PLIE REFERENCE: 12071/002001
CURRENT APPLICATION UNDRER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: fusion sequence US-10-267-311-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-10-201-764-19
; Sequence 19, Application US/10201764
; Publication No. US20030166140A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KCDSTLRLC 9
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US-10-177-390-8
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12, Appl 20, Appl 20, Appl 20, Appl 9, Appl 10, Appl 10, Appl 11, Appl 25, Appl 12, Appl 33, Appl

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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APPLICANT: TINDE, ROBERT
APPLICANT: FERNANDO, GERWAIN
APPLICANT: FERNANDO, GERWAIN
APPLICANT: FRAZER, 1AN
APPLICANT: FRAZER, 1AN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS.& NADEL, P.C.
STREET: PHILADDLEHIA
CITY: PHILADDLEHIA
STATE: PENNSYLVANIA
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CUNTATI USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLLASSIFFCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INPORMATION:
                                         US-09-485-885-8

US-09-485-885-12

US-08-845-885-12

US-08-889-666-20

US-08-465-078-20

US-08-776-20

US-08-117-083-9

US-08-86-015-10

US-09-367-309A-1

US-09-501-097A-25

US-09-501-097A-25

US-09-613-303-33

US-09-613-303-25
                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 38, Application US/08075541D Patent No. 6183745
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REPRENCE/DOCKET UMBER: 875
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                          US-08-075-541D-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
 Query Match
 53, Appli
3, Appli
42, Appli
1, Appli
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19, Appli
19, Appli
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                                                                                             June 28, 2005, 23:37:59; Search time 16.8626 Seconds (without alignments) 39.842 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3,
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Sequence 1
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(cgn2_6/ptodata/1/iaa/SA_COMB.pep:*

// cgn2_6/ptodata/1/iaa/SB_COMB.pep:*

// cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

// cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

// cgn2_6/ptodata/1/iaa/RD_CTUS_COMB.pep:*

// cgn2_6/ptodata/1/iaa/RD_CTUS_COMB.pep:*

// cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-000-003A-8

US-09-080-177A-74

US-08-9380-177A-74

US-08-934-915-52

US-08-934-915-53

US-08-948-394-3

US-08-948-394-3

US-08-948-394-3

US-08-948-394-3

US-08-948-394-3

US-08-948-34-1

US-08-948-1

US-09-98-1

US-09-98-1

US-09-128-466-1

US-09-128-466-1

US-09-128-466-1

US-09-128-466-1

US-09-128-466-1

US-09-107-4

US-09-107-4

US-09-107-4

US-09-107-4

US-09-107-11-8

US-09-107-11-8

US-09-107-11-8

US-09-107-11-8

US-09-107-11-12

US-09-107-11-12

US-09-107-11-12

US-09-11-12

US-09-11-11-12

US-09-11-11-12
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                       US-08-170-344-62
51
1 KCDSTLRLC 9
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                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                Searched:
                                                                                                  Run on:
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Result No.

DB 3; Length 19;

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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 19
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Matches
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                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09000003A
Patent No. 6652850
GENERAL INFORMATION: Philip, Ramila
APPLICANT: Philip, Ramila
TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
THERR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
SPECIFIC IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Alexis Barron, Esq.
STREET: Suite 2600 Aramark Tower, 1101 Market Street
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 4; Length 19; 100.0%; Pred. No. 0.011; Artive 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
ZIP: 19107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/000,003A
FILING DATE: 15-Jun-1998
CLASSIFICATION: <unhalber of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-000-003A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 923-4466
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-09-000-003A-8
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; Sequence 9, Application US/09405986A

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APPLICANT: Occhmus, Ingrid
APPLICANT: Nieland, John
TITLE OF INVENTION: Cyrctoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
TITLE REPERBENCE: 50125/036001
CURRENT APPLICATION NUMBER: 2001-11-29
FRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: DCT/EP00/05006
PRIOR FILING DATE: 1999-06-01
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bay, Sylvie
APPLICANT: Canteacuzene, Daniele
APPLICANT: Leclerc, Claude
APPLICANT: Leclerc, Claude
TITLE OF INVENTION: WULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
TITLE OF INVENTION: WACCINE COMPRISING THE SAME AND USE THEREOF
TITLE OF INVENTION: WACCINE COMPRISING THE SAME AND USE THEREOF
TITLE OF INVENTION: WACCINE COMPRISING THE SAME AND USE THEREOF
TITLE OF INVENTION WINGER: US/09/405,986A
CURRENT APPLICATION NUMBER: US/09/049,847
PRIOR APPLICATION NUMBER: US 09/049,847
PRIOR PILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1997-03-27
SPRIOR FILING DATE: 1997-03-27
SOFTWARE: PARCHIN VERSION 3.1
SEQ ID NOS: 25
SOFTWARE: PATCHIN VERSION 3.1
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100.0%; Score 51; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human papillomavirus type 16
US-09-980-177A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV 16 E7 PEPTIDE
US-09-405-986A-9
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; Sequence 53, Application US/08934915
; Patent No. 2923412
; GENERAL INFORMATION:
   APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: DADILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: LUCKIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,915
FILING DATE: 22-SEP-1997
CLASSIPICATION A135
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                               22-SEP-1997
21-SEP-1997
21: 435
                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC COMPATIBLE
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCH
REGISTRATION NUMBER: 37,133
REGISTRATION NUMBER: 37,133
REGISTRATION NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 813-538-3820
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-934-915-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KCDSTLRLC 9
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Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTRE: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: AC pc/au91/00575
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: DC/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY AGENT INFORMATION:
NUMBE: NADEL, ALAN S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LEMING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLCMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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Best Local Similarity 100.0%; Pred. No. Matches 9; Conservative 0; Mismatch
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US-08-934-915-52
; Sequence 52, Application US/08934915
; Patent No. 5928412
; Patent No. 5928412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 87:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide US-08-075-541D-47
                                                                                                                                                                                                                                      PHILADELPHIA
PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 KCDSTLRLC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KCDSTLRLC 9
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                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: C
STATE:
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REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
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                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 02929-001
CURRENT FILING DATE: 2000-06-20
RICH APPLICATION NUMBER: US/09/486,394
PRIOR PILING DATE: 1998-07-30
PRIOR PILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 51; DB 4; Length 30; Best Local Similarity 100.0%; Pred. No. 0.017; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 51; DB 2; Length 30; Best Local Similarity 100.0%; Pred. No. 0.017; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer STREET: 200 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08406248 Patent No. 5736318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/09486394
; Patent No. 6478749
REFERENCE/DOCKET NUMBER: 1:
TELECOMMUNICATION INCRNATION
TELEPHONE: 813-538-3800
TELEPRX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-934-915-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 KCDSTLRLC 28
                                                                                                                                                                                                                                                                                                                                                                                            3 KCDSTLRLC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KCDSTLRLC 9
                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
US-08-406-248-6
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US-09-486-394-3
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100.0%; Score 51; DB 3; Length 98; 100.0%; Pred. No. 0.054;
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Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09820764 Patent No. 6352696 GENERAL INFORMATION:
                                                                    Williams Jr., Joseph A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672-5399
                                                                                        REGISTRATION NUMBER: 38,659
REPERBNCE/DOCKET UNMBER: 270
TELECOMUNICATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-6448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 98 amino acids
                                                                                            38,659
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                        CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                  98 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 KCDSTLRLC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KCDSTLRLC 9
                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                 US-08-944-368A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 51; DB 3; Length 98; Best Local Similarity 100.0%; Pred. No. 0.054; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Warnia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08944368A
Patent No. 6228368
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
TITLE OF INVENTION: Pormulations and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Darun
STREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTEY: United States of America
ZIP: 60606-6402
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,368A
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09382616A Patent No. 6200746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.0
                                                                    98 amino acids
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                 60 KCDSTLRLC 68
                                                                                                                                                                                                                                                                                                           1 KCDSTLRLC 9
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SOFTWARE: Patentin Ve
SEQ ID NO 1
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicago
                                                                                                                                                                            US-08-075-541D-42
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US-09-382-616A-1
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US-08-944-368A-4
                                                                    LENGTH:
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CINI: ...
STATE: D.C.
COUNTRY: U.S.A.
CONPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.30
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOWERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,764
FILING DATE: 30-Mar-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sandercock, Colin G. REGISTRATION NUMBER: 31,298
                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
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Job time : 17.9126 secs
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Sequence 19, Application US/09566420

Sequence 10, E506641

GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNE RESPONSE
TITLE OF INVENTION: IMMUNER: US/09/566,420

CURRENT APPLICATION NUMBER: US/09/566,420

CURRENT PILING DATE: 1999-05-06

PRIOR APPLICATION NUMBER: 60/132,752

PRIOR APPLICATION NUMBER: 60/132,750

PRIOR PILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 19

SOFTWARE: Patentin Ver. 2.0

LENGTH: 98
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Sequence 8, Application US/09613303
Fatent No. 6495347
GENERAL INFORMATION
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT PELING DATE: 2000-07-08
FILE REPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: 1999-07-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 55
SOFTWARE: PREFERENCE: 1000-07-08
TYPE: PRI
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US-09-566-420-19
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; OTHER INFORMATION: fusion sequence
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9; Conservative
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Search completed: June 29, 2005, 01:44:21

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P17387
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         1612378 seqs, 512079187 residues
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Match Length DB
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43 76.8 109 1 VE7_HPV70 P50785 human papil 42 75.0 93 1 VE7_HPV15 P36820 human papil 42 75.0 266 2 Q7XL73 Q74751 Apple 41 73.2 92 1 VE7_HPV1A Q13751 home sapien 41 73.2 98 1 VE7_HPV1A P04020 human papil 41 73.2 98 1 VE7_HPV6A P04020 human papil 41 73.2 98 1 VE7_HPV6B P06464 human papil 41 73.2 98 2 Q9MG1 Q94194 human papil 41 73.2 98 2 Q9MG1 Q94194 human papil 41 73.2 98 2 Q9MG1 Q96494 human papil 41 73.2 98 2 Q9MG1 Q86699 cryptospori 41 73.2 98 2 Q6VRG0 Q608699 cryptospori 40 71.4 61 2 Q89846 Q89846 Q89846 Melon necro	PET 1 PS OBBEPS OBBEPS OBBEPS OBBEPS O1-MAR-2003 (TrEMBLrel. 23, Created) O1-MAR-2003 (TrEMBLrel. 24, Last sequence update) O1-JUN-2003 (TrEMBLrel. 24, Last annotation update) E7 protein (FramBlrel. 24, Last annotation update) E7 protein (FramBlrel. 24, Last annotation update) E7 protein (FramBlrel. 24, Last annotation update) E8 protein (FramBlrel. 24, Last annotation update) E9 protein (FramBlrel. 24, Last annotation update) E7 protein (FramBlrel. 24, Last annotation update) E8 paillomavirus NCBI_TaxID=10566; [1] F8 paillomavirus NCBI_TaxID=1056; [1] F8 paillomavirus NCBI_TaxID=1056; [1] F8	ULT 2 QQDDH2 QQDDH2 QQDDH2 QQDDH2 QQDH2
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SEQUENCE FROM N.A.
Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.,
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 2; Length 94; 100.0%; Pred. No. 0.11; cive 0; Mismatches 0; Indels
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitred (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF4649197; AA015692.1;
Interpro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
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01-MAR-2003 (TrEMBLrel. 23, Created)
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INTERPRO, IPRR000148; Papvi_B7.
Pfam; PF00527; E7; 1.
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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DT 21-JU2

DT 21-JU3

DT 25-OC

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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF107868; AAF13397.1;
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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100.0%; Score 56; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruees; deDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment)
Pred. No. 0.11;
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NCBI_TaxID=10581;
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MEDLINE-22182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.; Theng A.F.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China.";
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H., Lee H.-P.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                          "Major sequence variants in E7 gene of human papillomavirus type 16 from cervical cancerous and noncancerous lesions of Korean women."; Gynecol. Oncol. 66:275-281(1997).
                                                                                                                                                        MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
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Submitted (AuG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U76404; AAC58243.1; --
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative transforming protein B7.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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ive 0; Mismatches 0
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012337 PRELIMINARY, C12310-1907 (TTEMBLrel. 04, Last seq
01-JUL-1997 (TTEMBLrel. 04, Last seq
01-DEC-2001 (TTEMBLrel. 19, Last snnc
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                                                                                  Papillomavirus
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                                                                                                                SEQUENCE FROM N.A.
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"Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
J. Gen. Virol. 71:809-817(1990).
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-I- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                    Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P., Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR00148; Papvi_E7.
Efam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Trans-acting factor;
Transcription regulation.
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                                        Suhai S., Rowekamp W.G.;
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9BD612534CD2C9EB CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
                                    Seedorf K., Krammer G., Durst M., Suhai S., R. "Human papillomavirus type 16 DNA sequence."; Virology 145:181-185(1985).
SEQUENCE FROM N.A.
MEDLINE=85246220; PubMed=2990099;
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EMBL, U76413; AAB18964.1; -.
EMBL, AF003020; AAB70737.1; -.
EMBL, AF003023; AAB70740.1; -.
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EMBL; D00735; BAA00633.1; -.
EMBL; U76411; AAB18962.1; -.
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Tornesello M.L., Buonaguro P.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
J. Gen. Virol. 78:2199-2208 (1997).
EMBL; AF003021; AAB70738.1; -.
EMBL; AF003021; AAB70738.1; -.
PinterPro; IPR000448; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;
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MEDLINE=9743474; PubMed=9292007;
MEDLINE=97437474; Bubmed=9292007;
Tornesello M.L. Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF003025; ABAB703931; -.
EMBL; AF477385; AAM03025.1; -.
InterPro; IPR000148; Papvi_E7.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
07-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=22182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheung A.F.; Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002). EMBL, FA4864545, AAL96650.1; -.. Interpro; IPR00148; Papvi_E7. Figen; PF00527; E7: 1. SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
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01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
B7 protein.
Human papillomavirus type 16.
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MEDININE-20112892; PubMed=10644829;
van Duin M., Snijders P.J., Voseen M.T., Klaassen E., Voorhorst F.,
van Duin M., Snijders P.J., Voseen M.T., Klaassen E., Voorhorst F.,
van Duin M., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
EMBL, AJ388062; CAB45117.1;
InterPro; IRR000148; Papvi_E7.
Pfem.; PF00527; E7; 1.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; PR461264; AAL66736.1; -. Pfan; PF00527; E7; 10997 MW; 9BD610814CCEA59B CRC64; SEQUENCE 98 AA; 10997 MW; 9BD610814CCEA59B CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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SEQUENCE
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 23:32:21; Search time 11.2747 Seconds (without alignments) 76.805 Million cell updates/sec Run on:

US-08-170-344-61 56

1 CCKCDSTLR 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
3: pir2:*
1: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	E7 protein - human	E7 protein - human	E7 protein - human	E7 protein - human	kalinin B1 - mouse	E7 protein - human	E7 protein - human	hypothetical prote	laminin B1k chain	E7 protein - human	1	E7 protein - human	ᆸ	E7 protein - human	E7 protein - human	probable membrane	E7 protein - human	hypothetical prote		lectin heavy chain	galactose binding	probable membrane	hypothetical prote		E7 protein - human	E7 protein - human	hypothetical prote	E	hypothetical prote
SUMMARIES	ΙD	W7WLHS	W7WL35	S15622	W7WL31	I56985	W7WL39	S36474	T22384	A53612	S15615	W7WL11	W7WL6	T34472	S36574	836562	S64041	W7WLPR	T45305	870663	S70664	T09229	869297	AG2214	S36498	W7WL18	S36528	T26584	E97032	T27255
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Typrotein - human papillomavirus type 35 C;Species: human papillomavirus type 35 A;Note: host Homo sapiens (man) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

58 CCKCDSTLR 66

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RESULT 2 W7WL35

protein F17F8.27 [probable ABC-type	hypothetical prote	E7 protein - human	hypothetical prote	E7 protein - human	probable membrane	neutrophil activat	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	G protein-coupled	hypothetical prote	probable membrane	hypothetical prote
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Cross-references: UNIPROT: P03129; GB: K02718; NID: g333031; PIDN: AAA46940.1; PID: g333033 R; Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H. EMBO. J. 9; 153-160, 1990 A; Fithe: The region of the HPV E7 oncoprotein homologous to adenovirus Ela and SV40 large A; Reference number: S12367; MUID: 90107938; PMID: 21533075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-98 -BAR>
R;Kesidues: 1.04; Haddow, J.K.; Clements, J.B.
A;Virol. 65, 2033-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A;Reference number: Z17014; MUID:91162763; PMID:1848319
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C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;S8-94/Region: zinc finger CCCC motif
E7 protein - human papillomavirus type 16
E7 Species: human papillomavirus type 16
C5 Species: human papillomavirus type 16
C5 Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C5 Accession: A03688; S12367; T10428
E7 Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A; Title: Human papillomavirus type 16 DNA sequence.
A; Reference number: A22355; MUID:85246220; PMID:2990099
A; Accession: A03688
A; Molecule type: DNA
A; Residues: 1-98 cSEE>
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <KEN>
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A;Status: translation not shown
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C;Accession: F40824; S35522
N:Marich, J.E.; Ponteler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillc
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Residus: 1-99 cMARA
A;Acsidus: L-99 cMARA
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A;Accession: Biblibata Library, August 1993
A;Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Accession: S3552
A;Accession: S3552
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A;Residues: 1-99 cDELA
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R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
A;Title: Nucleoride sequence of human papillomavirus type 31: a cervical neoplasia-associative in the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the complex of the
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S.Superfamily: papillomavirus ET protein.
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif
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515622
By protein - human papillomavirus type 57
By protein - human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Datte: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: 515622
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Fille: A comparative sequence analysis of two human papillomavirus (HPV) types 2a A;Reference number: S15614; MUID:91188699; PMID:1964523
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C, Superfamily: papillomavirus B7 protein
C, Keywords: DNA binding; early protein; transcription regulation; zinc finger
F, 59-95/Region: zinc finger CCCC motif
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C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
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Matches 7; Conservative
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CCKCEATLR 67
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A; Residues: 1-92 <HIR>
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A;Molecule type: DNA
A;Residues: 1-109 <VOL>
A;Cross-references: UNIPROT:P24837; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47051.1,
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
A,Molecule type: DNA
A,Residues: 1-98 acOlb.
A,Residues: 1-98 acOlb.
A,Cross-references: UNIPROT: P17387; GB:U04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C,Comment: This protein may be involved in the oncogenic potential of this virus.
C,Superfamily: papillomavirus B7 protein
C,Superfamily: papillomavirus B7 protein;
C,Reywords: DNA binding; early protein; transcription regulation; zinc finger
F,58-94/Region: zinc finger CCCC motif
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C;Abate: 25-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 15-Mar-2004
C;Accession: 156985
R;Utani, A.; Kopp, J.B.; Kozak, C.A.; Matsuki, Y.; Amizuka, N.; Sugiyama, S.; Yamada, Y.
Lab. Invest: 72, 300-310, 1995
A;Title: Mouse kalinin B1 (laminin beta 3 chain): cloning and tissue distribution.
A;Reference number: 156985; MUID:95205823; PMID:7898049
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R;Volpers, C.; Streeck, R.E.
R;Vology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
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C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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Pred. No. 18;
0; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Reddues: 1-1160 <RES.
A;Cosstatus: pretrances: GB:S75486; NID:g912768; PID:g912769
F;376-425/Domain: laminin-type EGF-like homology <LEG>F;478-475/Domain: laminin-type EGF-like homology <LEG1:F;478-528/Domain: laminin-type EGF-like homology <LEG1:F;478-528/Domain: laminin-type EGF-like homology <LEG1:F;578-578/Domain: laminin-type EGF-like homology <LEG1:F;778-578/Domain: laminin-type EGF-like homology <LEG1:F;778-578/Domain: laminin-type EGF-like homology <LEG1:F;778-578/Domain: laminin-type EGF-like homology <LEG1:F;778-578/Domain: laminin-type EGF-like homology <LEG1:F;778-778/Domain: laminin-type EGF-like homology <LEG1:F;778-778/Domain: laminin-type EGF-like homology <LEG1:F;778/Domain: laminin-type EGF-like homol
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authors translated the codon CGA for residue 124 as Gln, GAG for residue 439 as 7

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E7 protein - human papillomavirus type 2a
C;Species: human papillomavirus type 2a
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Similarity 66.7%;
6; Conservative
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Best Local Similarity
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Best Local Similarity
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A; Residues: 1-92 <HIR>
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A; Residues: 1-98 < DAR>
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     F; 18-1170/Product:
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A,Rebidues: 1-93 ADEL.
A,Krebidues: 1-93 ADEL.
A,Cross-references: UNIPROT:P36820; EMBL:X74468; NID:g396924; PIDN:CAA52507.1; PID:g3969
C,Superfamily: papillomavirus E7 protein
C,Keywords: DNA binding; early protein; transcription regulation
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NyAlternate names: kalinin Bl chain, nicein Bl chain
CiSpecies Man sapiens (man)
CiDate: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 09-Jul-2004
CiAccession: A53612
RiGerceck, D.R.; wagman, D.W.; Champliaud, M.F.; Burgeson, R.E.
J. Biol. Chem. 269, 11073-11080, 1994
A;Title: The complete primary structure for a novel laminin chain, the laminin Blk chain
A;Title: The complete primary structure for pwell laminin chain, the laminin Blk chain
A;Title: The complete primary structure for pwell laminin chain, the laminin Blk chain
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A;Experimental source: clone F48F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: UNIPROT:Q13751; GB:L25541; NID:g510702; PIDN:AAA61834.1; PID:g510703
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$36474
By protein - human papillomavirus type 15
CyBoeises: human papillomavirus type 15
CyBoeises: human papillomavirus type 15
CyBoeises: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
CyAccession: $36474
By Delius, H.; Hofman,
By Bubmitted to the EMBL Data Library, August 1993
AyBostription: Primer-directed sequencing of human papillomavirus types.
A;Reference number: $36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F48F5.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22384
R;Lloyd, C.
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2; Length 93;
Pred. No. 9.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19558
A;Accession: T22384
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: CESP:F48F5.4
A;Map position: 5
A;Introns: 17/1; 91/2; 123/3; 170/3; 263/3; 290/1
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Best Local Similarity 77.8
Matches 7; Conservative
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A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1170 <GER>
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Matches 6; Conserv
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R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 131, 124-130, 1986
A;Title: The nucleotide sequence and genome organization of human papilloma virus type 11
A;Reference number: A94338; MUID:86181601; PMID:3008427
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C, Suberfamily: papillomavirus B7 protein
C, Keywords: DNA binding; early protein; transcription regulation; zinc finger
F, 58-94/Region: zinc finger CCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A;Reference number: S15614; MUID:91188699; PMID:1964523
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C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
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C;Species: human papillomavirus type 11
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                        75.0%; Score 42; DB 2; Length 1170; 100.0%; Pred. No. 52; cive 0; Mismatches 0; Indels
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Pred. No. 14;
1; Mismatches 2; Indels
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                                                                                                      F;250-312/Domain: laminin-type EGF-like homology <LEG1>F;738-427/Domain: laminin-type EGF-like homology <LEG>F;430-476/Domain: laminin-type EGF-like homology <EG1>F;532-576/Domain: laminin-type EGF-like homology <LEG2>
                                   cted <SIG>
predicted
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Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches
                                          #status predicted
                                                                         chain #status
Keywords: glycoprotein
;1-17/Domain: signal sequence
;18-1170/Product: laminin Blk
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Search completed: June 29, 2005, 01:38:34 Job time: 13.2747 sec8
Query Match
Best Local Similarity 77.8,
Then 7; Conservative
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                                           First protein - human papillomavirus type 6b
C;Species: human papillomavirus type 6b
C;Species: human papillomavirus type 6b
C;Species: human papillomavirus type 6b
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: D20558
R;Schwarz, B.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfsperger, E.; Su EMBO J. 2, 2341-2348, 1983
A;Title: DNA sequence and genome organization of genital human papillomavirus type 6b.
A;Reference number: A90975; MUID:84131949; PMID:6321162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-623 <MIL>
A;Ccoss-references: UNIPROT:Q23141; EMEL:U58753; PIDN:AAC24437.1; GSPDB:GN00022; CESP:WG
A;Experimental source: strain Bristol N2; clone W03B1
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C,Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P06464; GB:X00203; NID:g60955; PIDN:CAA25019.1; PID:g60957 C,Superfamily: papillomavirus B7 protein C,Keywords: DNA binding: early protein; transcription regulation; zinc finger F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T34472
R;Miller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
submitted to the RMBL Data Library, June 1998
A;Description: The sequence of C. elegans cosmid W03B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
S36574
E7 protein - human papillomavirus type 52
E7 proteis: human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S36574
R;Deblius, H; Hofmann, B.
R;Deblius, H; Hofmann, B.
R;Deblius, H; Hofmann, B.
R;Deplius, Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 85.7
Matches 6; Conservative
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les 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-99 <DEL>
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A; Residues: 1-98 <SCH>
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A,Gene: CESP:W03B1.2
A,Map position: 4
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        Query Match
        69.6%; Score 39; DB 2; Length 99;

        Best Local Similarity
        77.8%; Pred. No. 28;

        Matches
        7; Conservative
        0; Mismatches
        2; Indels
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Sequence 5, Appli Sequence 8, Appli Sequence 17, Appli Sequence 7, Appli Sequence 4, Appli Sequence 12, Appli Sequence 12, Appli

35, Appl 35, Appl 1, Appli 8, Appli 11, Appli 8, Appli

Sequence 35, Sequence 1, A Sequence 8, A

Sequence 35,

Sequence 1, Al Sequence 8, Al Sequence 12, i Sequence 12, i

Sequence Sequence

Sequence 1, Appli Sequence 5, Appl Sequence 33, App Sequence 33, App

US-10-267-311-33 US-10-679-956-33 US-10-267-311-25

ALIGNMENTS

Appli Appli Appli Appli Appli Appli

Sequence 3, A Sequence 5, A Sequence 4, A Sequence 1, A Sequence 1, A Sequence 12,

Sequence 26,

US-09-986-118A-4
US-10-27-311-8
US-10-201-764-19
US-10-201-764-19
US-10-201-764-19
US-10-654-13-29
US-10-681-410-19
US-10-681-410-19
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US-10-681-410-19
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Sequence 19, A Sequence 29, A Sequence 4, Ap

Sequence 8

Sequence 19,

Sequence 3 Sequence 5

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Similarity 100.0%; Score 56; DB 9; Length 9; Similarity 100.0%; Pred. No. 1.6e+06; 9; Conservative 0; Mismatches 0; Indels
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; Sequence 16, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin R.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT:
; TITLE OF INVENTION: HUMAN PAPILLOMA
; TITLE OF INVENTION: HUMAN PAPILLOMA
; FILE REFERENCE: 12071-003001
; CURRENT FILING DATE: 2001-10-19
; PRIOR PLING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PastSEQ for Windows Version 4.0
; FEMALE OF SEQ ID NOS: 140
; FEMALE OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-16
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Best Local Similarity
Matches 9; Conserv
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   LENGTH: 9
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Sequence 16, Appl
Sequence 16, Appl
Sequence 30, Appl
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Sequence 74, Appl
Sequence 74, Appl
Sequence 1, Appli
Sequence 4, Appli
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Sequence 30, Appl
Sequence 30, Appl
                                                                                                       June 29, 2005, 05:18:25; Search time 53.8517 Seconds (without alignments) 64.268 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. (cgn2_6)ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
1. (cgn2_6)ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
2. (cgn2_6)ptodata/1/pubpaa/US06_NEW_PUB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
3. (cgn2_6)ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
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4. (cgn2_6)ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
5. (cgn2_6)ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US00_PUBCOMB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
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6. (cgn2_6)ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US10_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US10_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
6. (cgn2_6)ptodata/1/pubpaa/US10_NEW_PUB.ppp:*
                                                                                                                                                                                                                                                                                                                  1717557
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-10-365-908-30

5 US-10-811-138-30

5 US-10-306-541-96

5 US-10-432-465-49

US-10-890-526-74
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-365-908-16
US-10-871-138-16
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US-09-820-765-4
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Maximum Match 100%
Listing first 45 summaries
                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                               US-08-170-344-61
56
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Match
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               APPLICANT: Neefe, John R.
APPLICANT: Boux, Lealie J.
APPLICANT: Boux, Lealie J.
APPLICANT: Winnett, Mark T.
APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marvinghen B.
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT:
FILE REPERENCE: 12071-003011
CURRENT APPLICATION NUMBER: US/09/891,823
CURRENT FILING DATE: 2001-10-19
FRIOR APPLICATION NUMBER: US 60/214,202
FRIOR APPLICATION NUMBER: US 60/214,202
FRIOR APPLICATION NUMBER: US 60/214,202
FRIOR APPLICATION NUMBER: US 60/214,202
FRIOR APPLICATION NUMBER: US 60/214,202
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FRIOR APPLICATION NUMBER: US 60/214,202
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Publication No. US20030170268A1
GENERAL INFORMATION:
APPLICANT: Neefe, John R.,
APPLICANT: Boux, Leslie J.
APPLICANT: Glascone, Stephen E.,
APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT;
FILE REPERENCE: 12071-003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/365,908
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/891,823
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 10
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Publication No. US20040235741A1
GRNERAL INFORMATION:
APPLICANT: Neefe, John R.
APPLICANT: Boux, Lealie J.
APPLICANT: Winnett, Mark T.
APPLICANT: Winnett, Mark T.
APPLICANT: Goldstone, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-30
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US-10-365-908-30
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US-10-871-138-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
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Sequence 16, Application US/10871138

Publication No. US20040235741A1

GENERAL INFORMATION:
APPLICANT: Neefe, John R.
APPLICANT: Boux, Leslie J.
APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marvin B.
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
FILE REFERENCE: 12071-003001
CURRENT FILING DATE: 2004-06-18
FRICH RELIGNED NUMBER: US/09/891,823
FRIOR APPLICATION NUMBER: US/09/891,823
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PREASER IN NOS: 140
SEQ ID NO 16
                                                                                                       APPLICANT: Noefe, John R.
APPLICANT: Boux, Leslie J.
APPLICANT: Winnet, Mark T.
APPLICANT: Winnet, Mark T.
APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
FILE REFERENCE: 12071-003001
CURRENT APPLICATION NUMBER: US/10/365,908
CURRENT APPLICATION NUMBER: US/09/091,823
PRIOR APPLICATION NUMBER: US 60/214,202
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-0-19
PRIOR FILING DATE: 2001-0-6-26
NUMBER OF SEC ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-365-908-16
, Sequence 16, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human papilloma virus
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Best Local Similarity
Matches 9; Conserv
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US-09-891-823-30
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US-09-728-466-1
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APPLICANT: Kather, Angela
APPLICANT: Kather, Angela
APPLICANT: Schinz, Manuela
TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
TITLE OF INVENTION: Therapy
FILE REPERENCE: 50125/077001
CURRENT APPLICATION NUMBER: US/10/432,465
CURRENT FILING DATE: 2003-12-10
PRIOR PELING DATE: 2001-11-30
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APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mittelman, Abraham
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 96
LENGTH: 15
                                 FILE REPERENCE: 12071-003001
CURRENT APPLICATION NUMBER: US/10/871,138
CURRENT FILING DATE: 2004-06-18
FRIOR APPLICATION NUMBER: US/09/891,823
PRIOR FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 96, Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/10432465; Publication No. US20040091479A1; GENERAL INFORMATION: APPLICANT: Nieland, John APPLICANT: Kaufmann, Andreas
                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: human papillomavirus
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-306-541-96
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Sequence 74, Application US/10890526;

Bublication No. US20040258708A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/03601
CURRENT APPLICATION NUMBER: US/10/890,526
CURRENT FILING DATE: 2004-07-13
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 2000-05-31
FRIOR PLING DATE: 1999-06-01
FRIOR FILING DATE: 1999-06-01
FRIOR FILING DATE: 1999-06-01
SRIOR FILING DATE: 1999-06-01
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; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher. Christopher
; APPLICANT: He, Wanxia
; TITLE OF INNENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT APPLICATION NUMBER: 09/382,616
; PRIOR APPLICATION NUMBER: 09/382,616
; RIGHT APPLICATION NUMBER: 09/382,616
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 15; Length 20; Pred. No. 0.16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
PRIOR APPLICATION NUMBER: DE 10059631.2
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 20
TYPE: PRT
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ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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US-10-432-465-49
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CITY: Wab..

STATE: D.C.

CUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPFRATING SYSTEM: PC-DOS/MS-DOS

SOFFWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

PRIOR APPLICATION NUMBER: 09/026,896

FILING DATE: 1998-02-20

ATTORNEY/AGENT INFORMATION:

MAPPLICATION NUMBER: 31,298

REGISTRATION NUMBER: 31,298

REGISTRATION NUMBER: 31,298

REGISTRATION NUMBER: 31,298

TELEPHONE: (202) 672-5309

TELEPHONE: (202) 672-5309

TELEPHONE: (202) 672-5309

TELEPHONE: SEQUENCES: "TELEPHONE: SEQUENCES: "TELEPHONE: SECUENCES: SEC
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| Sequence 4, Aprication US/09986118A
| Sequence 4, DS20030021806A1
| GENERAL INFORMATION:
| APPLICANT: BURGER, Alexander
| TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
| FORMULATIONS AND METHODS OF USE
   TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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COMPUTER: IBM PC COMPATIBLE
COMPANIO SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: PO. US20030021806A1-2001
CLASSIFICATION: CUNKNOWN>
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0
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                        ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Street, N.W CITY: Washington
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COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                  NUMBER OF SEQUENCES: 28
                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 9; Conservative
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COUNTRY: U.S.A.
ZIP: 2000-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: <UNKNOWN>
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                                                                                              100.0%; Score 56; DB 9; Length 98; 100.0%; Pred. No. 0.59;
                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCII
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K Street, N.W CITY: Washington
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(202) 672-5399
, ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09820765; Publication No. US20020039584A1; GENERAL INFORMATION: APPLICANT: BURGER, Alexander; HALLEK, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09824017; Publication No. US20020197668A1; GENERAL INFORMATION:
APPLICANT: BURGER, Alexander; HALLEK, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 98 amino acide
TYPE: amino acid
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                                                                                                                           Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                   58 CCKCDSTLR 66
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US-09-824-017-4
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US-09-820-765-4
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Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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| Publication No. US20030050469A1
| Publication No. US20030050469A1
| GENERAL INFORMATION:
| APPLICANT: Siegel, Marvin | APPLICANT: Mizzen, Lee A. |
| TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO | FILE REFERENCE: 12071/002001 | CURRENT FILING DATE: 2002-10-9 | PRIOR APPLICATION NUMBER: US/09/613,303 | PRIOR FILING DATE: 2000-07-10 | PRIOR PELICATION NUMBER: US 60/143,757 | PRIOR FILING DATE: 1999-07-08 | NUMBER OF SEQ ID NOS: 55 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 8 | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEG ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF SEQ ID NOS | LEGITHE OF 
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                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8
                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-177-390-8
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CURRENT APPLICATION NUMBER: US/10/177,390

CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn Ver. 2.1

CORGANISM: Artificial Sequence

CORGANI
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Slank (nspto)

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CURRENT APPLICATION NUMBER: US/10/365,908
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/891,823
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Sequence
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-075-541D-38

US-08-934-915-48

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US-08-934-915-53

US-09-486-394-3

US-09-501-097A-6

US-09-501-097A-6

US-08-94-36A-1

US-08-94-36A-4

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Maximum Match 100%
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                      Sequence 16, Application US/10365908
| Patent No. 6797491
| GENERAL INFORMATION:
| APPLICANT: Neefe, John R.
| APPLICANT: Boux, Lealie J.
| APPLICANT: Winnet, Marx T.
| APPLICANT: Siegel, Marxin Boux, TITLE OF INVENTION: HUMAN PAPLILOMA VIRUS TREATMENT:
| APPLICANT: Siegel, Marvin Boux, Lealie J.
| TITLE OF INVENTION: HUMAN PAPLILOMA VIRUS TREATMENT:
| FILE REFERENCE: 12071-003001
| CURRENT APPLICATION HUMBER: US/10/365,908
| CURRENT APPLICATION NUMBER: US/09/891,823
| PRIOR FILING DATE: 2001-10-19
| PRIOR FILING DATE: 2000-06-26
| NUMBER OF SEQ ID NOS: 140
| SEQ ID NO 16
| SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 30, Application US/10365908
Patent No. 6797491
GENERAL INFORMATION:
APPLICANT: Boux, Leslie J.
APPLICANT: Boux, Leslie J.
APPLICANT: Goldstone, Stephen E.
APPLICANT: Siegel, Marvin TITLE OF INVENTION: HUMAN PAPILLOMA
FILE REFERENCE: 12071-003001
          US-08-860-165-14
US-09-359-382-12
US-09-613-303-35
US-09-613-303-35
US-09-485-885-1
US-09-485-885-12
US-09-485-885-12
US-09-485-885-12
US-08-459-818-20
US-08-459-666-20
US-08-465-078-20
US-08-455-078-20
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-09-359-382-10
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                                                                                                                                                     -08-117-083-9
                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCKCDSTLR
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STRET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIPICATION NUMBER: 07/949,836
FILING DATE:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. FOULCH
REGISTRATION NUMBER: 37,133
REGISTRATION NUMBER: 1946.6
TELEPHONE: 813-58-3800
                                                                                                                                                         Sequence 48, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
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                                CCKCDSTLR 13
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                                                                                                                                                                                                                                                    100.0%; Score 56; DB 4; Length 10; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: W B 3876
FILING DATE: 12-DEC-1990
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCt/augl/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 8795-4
TELECOMMUNICATION NUMBER: 8795-4
TELECOMMUNICATION NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEFRAION SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                 0; Mismatches
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/214,202
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
TENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-075-541D-38
; Sequence 38, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                , ORGANISM: Human papilloma virus
US-10-365-908-30
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....hes 9; Conservative
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Best Local Similarity luv...
Lac 9; Conservative
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TOPOLOGY: linear
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### Sequence 7.4 Application US/09980177A

| Sequence 74. Application US/09980177A
| Sequence 74. Application US/09980177A
| Patent No. 6338084
| GENERAL INFORMATION:
| APPLICANT: JOCHUMUS, Ingrid
| TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the 1TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and 1TILE OF INVENTION: Therapy
| TITLE OF INVENTION: Therapy
| FILE REFERENCE: 50125/036001
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                                                                                Gaps
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Query Match
100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.044;

100.08;

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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                   DB 4; Length 20;
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APPLICANT: FERNAND, GERVAIN
APPLICANT: FRAZER, IAN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOWA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUUNTRY: USA

ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UN-1993
CLASSIFICATION NUMBER: AU PK 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: Dct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 27,363
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REFERENCE/DOCKET NUMBER: 27,363
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1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                 100.0%; Score 56; DB 4; 100.0%; Pred. No. 0.036;
    CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR FILING DATE: 2000-05-31
PRIOR APLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
LENGTH: 20
CURRENT APPLICATION NUMBER: US/09/980,177A
                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-117A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47, Application US/08075541D Patent No. 6183745
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PENNSYLVANIA
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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100.0%; Score 56; DB 3; Length 25;

Query Match

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   0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CHENC,
TITLE OF INVENTION: SYNTHELLCUMAVIRUS 1, 2, C.
TITLE OF INVENTION: PAPILLCMAVIRUS 1, 3, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: MASON & ASSOCIATES, P.A.
CORRESPONDENCE ADDRESSE:
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   0; Mismatches
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FILING DATE: 22-SEP-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAMME: LOUISE A. FOULCH
REGISTRATION NUMBER: 37,133
                                                                                                                                                                                                                                                                                                                            Sequence 52, Application US/08934915
Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible SYSTEM: Windows 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Word 6. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHENG, HWEE-MING
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DILLNER, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-934-915-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. COMPUTER READABLE FORM:
                                                                                                                      15 CCKCDSTLR 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCKCDSTLR 9
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                           1 CCKCDSTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-934-915-53
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Gaps

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

MUGEV, Karl

TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING

TITLE OF INVENTION: TRANSFORMED CELLS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer

STREET: 200 State Street

CITY: Boston

STATE: MA

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100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                       100.0%; Score 56; DB 4; Length 30; 100.0%; Pred. No. 0.051;
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MEDIUM TYPE: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: T2Y-Choou Wu
APPLICANT: T2Y-Choou Wu
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICATION VUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 38
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09501097A
Patent No. 6734173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
CLASSIFICATION: 10FORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: HAZ-CTELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: human papillomavirus
                                                                                                                                                                9; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                    18 CCKCDSTLR 26
                                                                                                                                                                                                                                     1 CCKCDSTLR 9
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                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-501-097A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-501-097A-6
                         US-09-486-394-3
                                                                                                                                                                Matches
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is Sequence 3, Application US/09486394

is Sequence 3, Application US/09486394

is Patent No. 647849;

general information:

in Applicant: Hopfl, Reinhard

in TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

in TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

in TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

in FILE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

in FILE OF INVENTION: Diagnostic Kit for Skin Tests, and Method

in CURRENT FILING DATE: 1030-06-20

in FRIOR FILING DATE: 1998-07-30

in FRIOR FILING DATE: 1997-08-27

in NUMBER OF SEQ ID NOS: 6

in SEQ ID NO 3

in LENGTH: 30

in LENGTH: 30
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TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8, TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56, TITLE OF INVENTION: USEPUL IN IMMUNOASSAY FOR TITLE OF INVENTION: DIAGNOSTIC PURPOSES NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS: ADDRESSE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARMATER
                         SYNTHETIC PEPTIDES OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                     STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER: ELORDY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FLING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION A 435
PRIOR APPLICATION NUMBER: 07/949,836
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 31,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEPAK: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37,133
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LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
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SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-934-915-53
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TOPOLOGY:
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US-08-075-541D-42

Sequence 42, Application US/08075541D

Sequence 42, Application US/08075541D

SETURAL INFORMATION:

APPLICANT: TINDLE,

APPLICANT: FRAZER, IAN

TITLE OF INVENTION: SUBINIT PAPILLOMA VIRUS VACCINE AND

TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 56; DB 1; Length 98; Best Local Similarity 100.0%; Pred. No. 0.14; Matches 9; Conservative 0; Mismatches 0; Indels
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ZIP: 19103-2398
COUNTER READABLE FOR
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: AU PK 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCt/au91/00575
FILING DATE: 12-DEC-1991
ATCHING DATE: 12-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PHINADELPHIA STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
9; Conservative
                                                                                                                                                   ; MOLECULE TYPE: protein US-08-406-248-6
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STRANDEDNESS: single
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STREET: 160
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                                                                                                               TOPOLOGY:
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US-US-382-516A-1.

Sequence 1, Application US/09382616A
Fatent No. 6200746

GENERAL INFORMATION:
APPLICANT: Fisher Christopher
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: 09/99/382,616
FRIOR PRING DATE: 1999-08-25
FRIOR PRING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
ENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 56; DB 3; Length 98; 100.0%; Pred. No. 0.14;
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Patent No. 6228368
GENERAL INFORMATION:
APPLICANT: Gissman, et al.
TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
TITLE OF INVENTION: Formulations and Methods of Use
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 233 South Wacker Drive, 6300 Sears Tower CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1:0, Version #1:30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,368A
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; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1
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REFERENCE/DOCKET NUMBER: 27013
TELECOMMUNICATION:
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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GY: linear
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                                        Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSE: FOLKY & LARDNER
ADDRESSE: FOLKY & LARDNER
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER: IEB PC Compatible
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COMPUTER: IEB PC COMPATIBLE
SOFTWARE: PATCATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
FILING DATE: 20-FEB-1998
FILING DATE: 20-FEB-1998
FILING DATE: 20-FEB-1998
FREDERINGE/DOCKET NUMBER: 37067/102
FEB-PRINCE/DOCKET NUMBER: 37067/102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPLICOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09820764; Patent No. 6352696; GENERAL INFORMATION:
                                                                                                                                                                     58 CCKCDSTLR 66
                                                                                                                 1 CCKCDSTLR 9
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US-09-820-764-4
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Search completed: June 29, 2005, 01:44:20 Job time : 16.9126 secs

58 CCKCDSTLR 66

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1 CCKCDSTLR 9

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77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;
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NCBI_TaxID=10566;
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SEQUENCE
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Q8B5P5
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Q8B563
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                                                                                   June 28, 2005, 21:24:19; Search time 55.1 Seconds (without alignments) 83.643 Million cell updates/sec
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Q9qdh2
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Q6xgy1
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Q95mg6
Q788b5
Q6f4i9
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          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                   1612378 seqs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length
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100.0
100.0
92.7
92.7
85.5
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Maximum DB
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             Q6u104
Q7zzp0
Q800v9
Q9de63
Q8dyh5
Q8dyh5
P25485
P25485
P22160
Q9ihw9
Q7qtc1
Q7355
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF540023, AAO16640.1, -.
InterPro; IPR000148; Papvi_B7.
Pfam; PF00527; B7; 1.
NON TER 65
SEQÜENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;
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Ponglikitmongkol M., Vaeteewoottacharn K.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databages.

EMBL; AF469198; AAO15694.1;

Interior: IRF8000148; Papvi_E7.

Pfam; PP00527; E7; 1.

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JMV-2003 (TrEMBLrel. 24, Last annotation update)
E7 protein (Fragment).
Human papillomavirus
Viruees; debNA viruses, no RNA stage; Papillomaviridae;
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Papillomavirus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UND-2003 (TrEMBLrel. 24, Last annotation update)
E7 protein (Fragment).
Human papillomavirus.
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07S3B5
LY6G_MOUSE
            Q6U104
Q7ZZPO
Q7ZZPO
Q800V9
Q9DE3
Q8R155
Q8R155
Q8DYH3
V8T HPV2A
V8T HPV2A
Q8THW957
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Best Local Similarity 100.
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Length 77;

DB 2;

100.0%; Score 55;

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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187867; AAF13395.1; -.
InterPro; IPR00148; Papvi_E7.
Pfam; PF00527; E7; I.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                          01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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NON TER 93 93

SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
E7 oncoprotein (Fragment).
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Best Local Similarity 100.
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52 YNIVTFCCK 60
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SEQUENCE FROM N.A.
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100.0%; Score 55; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ET procein (Fragment)
Human papillomavirus type 16.
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93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
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52 YNIVTFCCK 60
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NCBI_TaxID=10581;
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SEQUENCE
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Q9QDH4
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Phelps W.C., Yee C.L., Munger K., Howley P.M.;
"The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A.";
Cell 53:539-547(1988).
-!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G., "Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia."; J. Gen. Virol. 71:809-817(1990).
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Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                 100.0%; Score 55; DB 2; Length 94; 100.0%; Pred. No. 0.055;
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469197, AA015692.1; -.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                        94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
87 protein.
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MEDLINE=90218027; PubMed=2157796;
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                                                                                                            Best Local Similarity 100.
Matches 9; Conservative
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YNIVTFCCK 60
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MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplassa in southern China.";
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MEDLINE=97407827; PubMed=9264576; DOI=10.1006/97no.1997.4756;
                                                                                                                                                                    PIR; A03688; W7WLHS.

TherePro; IPR00148; Papvi_E7.

Pfam; PF00627; E7; 1.

DNA-binding; Early protein; Oncogene; Trans-acting factor;

Transcription regulation.
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Terai M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databages.
EMBL; U76404; AAC58243.1; -.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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C-XX-C motif-2.
9BD612534CD2C9EB CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last seq
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EMBL; U76413; AAB18964.1; -.
EMBL; AF003020; AAB70737.1; -.
EMBL; AF003024; AAB70741.1; -.
EMBL; AF003024; AAB70742.1; -.
EMBL; AF003026; AAB70742.1; -.
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SEQUENCE FROM N.A. MEDINDE-218295358; MEDINDE-22182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng T.H., Li W.W.H., In Willems J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22182962; PubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:656-700(2002). BMBL, A4866345, AAL96501; -. InterPro; IPR00148; Papvi_E7. Pfam; PP00527; E7; I. SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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                                                                                                                                                                                                                                                                                     Length 98;
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                                                                                             Jinhu X., Xinxing W., Yun T.;
Submitted (JAN-2020) to the EMBL/GenBank/DDBJ databases.
BMBL; AF003022: AAB70739.1;
EMBL; AF477385; AAM03025.1;
EMBL; AF477385; AAM03025.1;
EMBL; AF477385; AAM03025.1;
EMBL; AF477385; AAM03025.1;
EMBL; AF60527; B7;
EMBL; AF60527;
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
  type 16 in penile carcinomas from Ugandan patients."; J. Gen. Virol. 78:2199-2208(1997).
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
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NCBI_TaxID=10581;
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.,
Beth-Giraldo E., Giraldo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL, AF003021; ARB7073811. --
InterPro: IRR00148; Papvi_E7.
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MEDLINE=974374; PubMed=9292007;
Tornesello, M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
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EMBL; AF486333; AAL96638.1; --
EMBL; AF486334; AAL96639.1; --
EMBL; AF486338; AAL96643.1; --
EMBL; AF486338; AAL96643.1; --
EMBL; AF486346; AAL96653.1; --
EMBL; AF486350; AAL96655.1; --
EMBL; AF486350; AAL96656.1; --
EMBL; AF48637; AAQ10404.1; --
INTEXTRO: IPRO00148; Papvi_E7.
Pfam; PPF0027; E7; 1.
Pfam; PPF0027; E7; 1.
Pfam; PPF0027; E7; 1.
Pfam; PPF0027; E7; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;
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52 YNIVTFCCK 60
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Matches 9; Conservative 0; Mismatches 0; Indels
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; FF461264; AAL66736.1;
Pfam; PF00227; E7: 11
SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OTN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses; dabNa viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
EMBL; AF486344; AAL96649.1; -.
Interpro; IPRO00148; Papvi_B7.
Pfam; PF00527; B7; 1.
SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
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52 YNIVTFCCK 60
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Db 52 YNIVTFCCK 60
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Search completed: June 28, 2005, 23:28:15 Job time : 55.1 secs (otosu) Anola ago^{a sidi}

Sequence 73, Appl

Searched:

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Sequence 107, App
Sequence 1, Appli
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ilarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
US-10-890-526-73
US-09-728-6541-107
US-09-728-6541-107
US-09-824-017-4
US-09-86-118A-4
US-09-986-118A-4
US-09-986-118A-4
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US-10-267-311-8
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US-10-392-113-29
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US-10-654-129-4
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US-10-679-971-1
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Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR PELICATION NUMBER: 60/333,249
PRIOR PELING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8:0 for Windows
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; Sequence 108, Application US/10306541
; Publication No. US20040171081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: human papillomavirus
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| Cgn2_6/ptodata1/pubpaa/USO6_PUBCMB.ppp:*
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| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
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               5.1.6
Compugen Ltd.
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Copyright (c) 1993 - 2005
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Maximum DB seq length: 200000000
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Sequence 1, Appli Sequence 8, Appli

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2 3 4 4 7 7 10 10

ReBult No.

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; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-62
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US-10-306-541-64
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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0;
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Sequence 62, Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
TITLE REPERENCE: Darja
TITLE REFERENCE: 123544
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 62
LENGTH: 15
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
FPLICANT: Kanduc, Darja
FILE REFERENCE: 12354/4
CURRENT APPLICATION UNDMER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/333,249
FRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61, Application US/10306541
Publication No. US20040171081A1
GENERAL INPORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                      ORGANISM: human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-61
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US-10-306-541-61
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LENGTH: 15
                                                                                                                                                                                                                                         TYPE: PRT
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Query Match 100.0%; Score 55; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.035; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                        US-10-306-541-63
US-10-306-541-63
US-10-306-541-63
Sequence 63, Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Mittelman, Abraham
APPLICANT: Mittelman, Abraham
CURRENT MAPLICANTON WUMBER: US/10/306,541
CURRENT APPLICATION WUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 63
LENGTH: 15
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 64, Application US/10306541
| Publication No. US20040171081A1
| Publication No. US20040171081A1
| GENERAL INFORMATION:
| APPLICANT: Mittelman, Abraham
| APPLICANT: Kanduc, Darja
| TITLE OF INVENTION: Improved Antigens
| FILE REFERENCE: 12354/4
| CURRENT APPLICATION NUMBER: US/10/306,541
| CURRENT FILING DATE: 2003-11-25
| PRIOR FILING DATE: 2001-11-23
| NUMBER OF SEQ ID NOS: 108
| SOFTWARE: WordPerfect 8:0 for Windows
| SEQ ID NO 64
| LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: human papillomavirus
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Sequence 48, Application US/10432465
; Sequence 48, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kauleman, Andreas
; APPLICANT: Kauleman, Andreas
; APPLICANT: Kauleman, Andreas
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; TILE REPREBENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR PELING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
      Sequence 14, Application US/10484063

Publication No. US2050048467A1

GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: FOLLEN, MICHELE
ITILE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
ITILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERRINCE: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR PLLING DATE: 2002-07-19
PRIOR PLLING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2:1
: SOFTWARE: Patentin Ver: 2:1
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; Publication No. US20040170606A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-14
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; ORGANISM: Human papillomavirus
US-10-432-465-48
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TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
FILE REPERENCE: 109739
CURRENT APPLICATION NUMBER: US/10/654,200
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR PILING DATE: 2002-09-03
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2002-09-03
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN OFFICE SOFTWARE: 10/457,082
PRIOR FILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTING DATE: 2003-06-06
LENGTHRE: PATENTING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTING DATE: 2003-06-06
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NUMBER OF SEQ ID NOS: 106
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NUMBER OF SEQ ID NOS: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment; OTHER INFORMATION: for E7 of HPV US-10-858-384-16
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RESULT 7
US-10-858-384-16
| Sequence 16, Application US/10858384
| Sequence 16, Application US/10858384
| Publication No. US20050033025A1
| GENERAL INFORMATION:
| APPLICANT: CHOPPIN, JEANNINE
| APPLICANT: BOURGAULT VILLADA, ISABELLE
| APPLICANT: GONRAN, FRANCINE
| APPLICANT: GONNAN, FRANCINE
| TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
| TITLE OF INVENTION: PARTICULARLY IN VACCINATION
| TITLE REFERENCE: 0508-1037-1
| CURRENT APPLICATION NUMBER: US/10/858,384
| CURRENT FILING DATE: 2004-06-02
| PRIOR FILING DATE: 1999-06-03
| NUMBER OF SEQ ID NOS: 24
| SOOTWARE: PATCHILIN VET: 3.2
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; ORGANISM: Human Papilloma Virus
US-10-654-200-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity luv.
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US-10-484-063-14
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LENGTH: 17
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Publication No. US20020039584A1
GENERAL INFORMATION:
APPLICANT: BUGGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
             CURRENT APPLICATION NUMBER: US/10/306,541
                                  CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION UNMBER: 60/333,249
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 107
LENGTH: 21
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Papillomavirus sylvilagi
                                                                                                                                                                                                                                                                    TYPE: PRT

// ORGANISM: human papillomavirus

US-10-306-541-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conservê
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US-09-820-765-4
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WS-10-890-556-73

Sequence 73, Application US/10890526

Publication No. US20040258708A1

GENERAL INFORMATION:
APPLICANT: Nieland, John
TITLE OF INVENTION: Cytocoxic T-Cell Epitopes of the
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: 105/10601

FILE REFRENCE: 50125/03601

CURRENT FILING DATE: 2004-07-13

PRIOR APPLICATION NUMBER: US/10/890,526

CURRENT FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 77

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
FILE REPERENCE: N9739
CURRENT APPLICATION NUMBER: US/10/654,200
CURRENT PILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR PLIING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Human papillomavirus type 16
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Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REPERENCE: 12354/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-654-200-57
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 YNIVTECCK 18
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US-10-306-541-107
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LENGTH: 20
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LENGTH: 20
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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: <ur>
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
FREDENCHORY DOCKET NUMBER: 37067/102
FELEPOWNUNICATION INFORMATION:
TELEFRAX: (202) 672-5300
TELEFRAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4
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Search completed: June 29, 2005, 05:18:17 Job time : 116.15 secs

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Gaps

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Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB E Maximum DB E

Database

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Sequence 27, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBMIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PREPTIDES FOR USE THEREIN
WUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 12;
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ZIP: 19103-2398

COMPUTER READBLE FORM:
MEDIUM TYPE: Flogby disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NMS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING APPLICATION: 424
PRIOR APPLICATION UNMER: AU pk 3876
FILING APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
                                                                  US-09-501-097A-7
US-09-613-097A-1
US-09-613-303-12
US-08-613-303-12
US-08-860-165-12
US-08-860-165-14
US-09-359-382-12
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US-09-485-885-8
US-09-485-885-12
                                          -10-201-764-19
-09-637-746-3
                                                                                                                                                                                    -09-613-303-35
                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                              US-08-075-541D-27
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  Query Match
  155, App
10, App
10, App
10, App
20, App
52, App
3, App
7, App
6, App
6, App
11, App
11, App
11, App
11, App
                                                                                          June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
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Sequence (
Sequence 1
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'/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

'cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

'cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

'cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

'cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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S-08-075-541D-29
S-08-075-541D-18
S-08-075-541D-18
S-08-075-541D-3
S-08-075-541D-3
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S-08-075-541D-3
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S-09-980-177A-73
S-08-075-541D-47
S-08-075-541D-20
S-08-486-394-3
S-09-486-394-3
S-09-075-541D-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-075-541D-42
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US-09-986-118A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-406-248-6
                                                                                                                                                                                                                                                       513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                  US-08-170-344-60
55
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Match
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Score

Result

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Sequence 18, Application US/08075541D

Sequence 18, Application US/08075541D

PATENT TINDLE, ROBERT

APPLICANT: TINDLE, ROBERT

APPLICANT: FERNANDO, GERMAIN

APPLICANT: FRAZER, IAN

TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 56

CORRESPONDENCES: 56

CORRESPONDENCES: 66

STREET: 1601 MARKET STREET, 36TH FLOOR

CITY: PHILADELPHIA

STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 55; DB 3; Length 14; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCES ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                   CUDNIKY: 0.298

CUNTIKY: 0.298

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-JUN-1993

CLASSIPICATION: 424

PRIOR APPLICATION DATA: APPLICATION NUMBER: AU pk 3876

FILING DATE: 12-DEC-1990

PRIOR APPLICATION NUMBER: DCC/990

PRIOR APPLICATION NUMBER: DCC/990

PRIOR APPLICATION NUMBER: 27,363

REGISTRATION NUMBER: 27,363

RESTERNICE/DOCKET NUMBER: 27,363

REFERENCE/DOCKET NUMBER: 8795-4

TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
TELECOMMULICATION INPORMATION:
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COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
--worTTER: IBM PC COMpatible
--worTTER: TRM PC COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-30, 210 NO: SEQUENCE CHARACTERISTICS: LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                  CITY: PHILADELPHIA STATE: PENNSYLVANIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 YNIVTFCCK 12
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                                                                                                                                                                                                                                                                                                                                   Sequence 28, Application US/08075541D
Fatent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FERNANDO, GERMAIN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSE:
ADDRESSES:
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          Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 19103-2396
COUNTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UNN-1993
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: DCt/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEFHONE: 215-567-2020
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US-08-075-541D-29
Sequence 29, Application US/08075541D
Sequence 183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 13 amino acida
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                   2 YNIVTFCCK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YNIVTFCCK 11
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                                                                                                            1 YNIVTFCCK 9
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US-08-075-541D-28
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0; Gaps

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HOPPIN, JEANNINE

HOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERAED

APPLICANT: CONNAN, FRANCINE

APPLICANT: CONNAN, FRANCINE

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PRATICULARLY IN VACCINATION

FILE REFERENCE: WOBI AO INS

CURRENT PILLING DATE: 2002-04-29

PRIOR PILLING DATE: 2000-05-31

PRIOR PILLING DATE: 2000-05-31

PRIOR PILLING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 16

LENGTH: 17

TYPE.
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                                                                                                                                                                                                                                                Length 17;
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GENERAL INFORMATION:

APPLICANT: TENDLE, ROBERT

APPLICANT: FRAZER, IAN

TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.

STREET: 1601 MARKET STREET, 36TH FLOOR

CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                    ; Score 55; DB;
; Pred. No. 0.0
0; Mismatches
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  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human Papillomavirus
                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCES: 56
CORRESPONDENCES: ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/augl/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 WARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PENNSYLVANIA
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                    FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 40-1993
PRIOR APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY, AGENT INFORMATION: NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEPHONE: 215-567-2020
TELEPHONE: 215-567-2020
TELEPHONE: 215-567-2020
SEQUENCE CHARACTERISTICS:
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 25, Application US/08075541D Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: NADEL, ALAN S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S YNIVTECCK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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US-08-075-541D-25
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Score 55; DB 3; Length 19;
Pred. No. 0.017;
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TITLE OF INVENTION: SYNTHEDIC PEPTIDES OF HUMAN
TITLE OF INVENTION: SYNTHEDIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
CORRESPONDENCE ADDRESS:
ADDRESSES: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
COMPUTER: FLORIDA
COMPUTER: IBM PC compatible
OCHEMATING SYSTEM: Windows 3.0
SOFTWARE: MICTOSOFT WORD 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ANAME: ADDRESSES
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: pct/aug1/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S.
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2991
JINFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
LENGTH: 10 acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-934-915-48
; Sequence 48, Application US/08934915
; Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFRENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37,133
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Best Local Similarity 100.0%;

Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48:
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APPLICANT: DILLINER, JOAKIM
APPLICANT: DILLINER, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 YNIVTFCCK 17
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-075-541D-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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100.0%; Score 55; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3., Application US/08075541D
Patent NO. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCES ADDRESS:
ADDRESSEE: PAMITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                                                                                                                           CIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING APPLICATION: 424
PRIOR APPLICATION NUMBER: US/08/075,541D
FILING APPLICATION NUMBER: US/08/075,541D
FILING APPLICATION 1424
FRIGHT APPLICATION NUMBER: US/08/075,541D
FILING DATE: 12-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PENNSYLVANIA
                                                                                          ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                          PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YNIVTFCCK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-075-541D-30
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US-08-075-541D-3
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Gaps

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CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-075-541D-10
                                                                                                                                                  STREET:
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                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 55; DB 2; Length 20; 100.0%; Pred. No. 0.018; tive 0; Mismatches 0; Indels
                                                 100.0%; Score 55; DB 2; Length 20; 100.0%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                              SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                              11, 16, 18, 31, 33 AND 56
USEFUL IN IMMUNOASSAY FOR
DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYGTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                             Sequence 155, Application US/08934915
Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08075541D Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37,133
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3820
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids TYPE: amino acid
                                             Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
; MOLECULE TYPE: peptide
US-08-934-915-48
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                             YNIVTFCCK 14
                                                                                                                1 YNIVTFCCK 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                              RESULT 10
US-08-934-915-155
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US-08-075-541D-10
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US-09-980-177A-73

Sequence 73, Application US/09980177A

Fatent No. 6838084

GRAERAL INFORMATION:
APPLICANT: Jochmus, Ingrid
APPLICANT: Jochmus, Ingrid
APPLICANT: Jochmus, Ingrid
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/03601
CURRENT APPLICATION NUMBER: US/09/980,177A
FILE REFERENCE: 2001-11-29
FRIOR APPLICATION NUMBER: DE1925199.1
FRIOR APPLICATION NUMBER: DE 19925199.1
FRIOR APPLICATION NUMBER: DE 1995-06-01

WUMBER OF SEQ ID NOS: 77

SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: TINDLE, ROBERT
APPLICANT: PERNANDO, GRAWAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION NUMBER: WB/08/075,541D
FILING APPLICATION NUMBER: US/08/075,541D
FILING APPLICATION NUMBER: US/08/075,541D
FILING DATE: 12-DEC-1990
PROOF APPLICATION NUMBER: APPLICATION NUMBER: DEC-1991
ATPONEY/AGENT INPORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
                                                                                                                                                                   3: PANITCH SCHWARZE JACOBS & NADEL, P.C. 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                 ZIP: 19103-2398
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
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16 YNIVIFICK 24
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                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                 US-08-075-541D-20
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                                                                                                          Query Match
100.0%; Score 55; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 55; DB 3; Length 25; 100.0%; Pred. No. 0.022; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 47, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM 11FE: F109PY G12A.

COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INCORMATION:
NAME: NADEL, ALLAN S
REGISTRATION NUMBER: 27,3635
REGISTRATION NUMBER: 27,3635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: PANITCH SCHWARZE JACOBS & NADEL, P.C.
1601 MARKET STREET, 36TH FLOOR
                                    ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27,363
3ER: 8795-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 47: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNSYLVANIA
                                                                                                                                                                                                             3 YNIVTFCCK 11
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                                                                                                                                                                                       1 YNIVTFCCK 9
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                                                                                                                                                                                                                                                                                RESULT 13
US-08-075-541D-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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SEQ ID NO 73
LENGTH: 20
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0
Sequence 20, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: FRAZEN:
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: 56
CORRESPONDENCE ADDRESS: ADDRESSE: PANTICH SCHWARZE JACOBS & NADEL, P.C.
STREET: 11601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 3; Length 26; 100.0%; Pred. No. 0.022; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-UN-1993
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 42
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DC-1991
ATION NUMBER: DC-1991
ATION NUMBER: 12-DEC-1991
ATIONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52. Application US/08934915

Patent No. 592412

GENERAL INFORMATION:

APPLICANT: DILLARE, JOAKIM

APPLICANT: DILLARE, LENA

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: DIABLE IN 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2921
TELEFAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: NADEL, ALAN S
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           CITY: PHILADELPHIA STATE: PENNSYLVANIA
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0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                 STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Flory disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/934,915
FILING DATE: 22.5EP-1997
CLASSIFICATION: 435
PRIOR APPLICATION UNMBER: 07/949,836
FILING DATE: ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-52
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Search completed: June 28, 2005, 23:37:55 Job time : 18.05 secs

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SEQUENCE FROM N.A.
MEDLINE=218465229; PubMed=11857370;
MEDLINE=218465229; PubMed=11857370;
MATCH K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404694; AAL01345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                          000000000000
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
    15881151151158
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LOTTIHDII 10
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Shippy R., Siwkowski A., Hampel A.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U59900; AAB03505.1; -.
EMBL; C1900042055, C1host cell nucleus; IEA.
G0; G0:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=21046229; PubMed=11857370;

MEDLINE=21046229; PubMed=11857370;

Matts K.J., Thompson C.H., Cossart V.E., Rose B.R.;

Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16

"Sequence variation and physical state of human papillomavirus type 16

"Sequence variation and physical state of human papillomavirus type 16

"Sequence isolates from Australia and New Caledonia.";

Int. J. Cancer 197.868-874(2002).

EMBL, AF404698; ABL01533.1.

EMBL, AF404698; Chost cell nucleus; IEA.

GO; GO:0004777; F:DNA binding; IEA.

Pfam; PF00518; EG; 1.
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MEDILINE=21846229; PubMed=11857370;
WALTE K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
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                                                                                                                                                                                                        100.0%; Score 45; DB 2; Length 138; 100.0%; Pred. No. 0.35; vative 0; Mismatches 0; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Be protein (Fragment).
Human papillomavirus type 16.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                        SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL, AF404702; AAL01361.1; -.

GO; GO:0042025; C:host cell mucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

PÉAM; PF00518; E6; 1.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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MEDLINE=9743744; Pubmed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.;
Beth-ciraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penlle carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL, AF003015; AAB70732.1;
GO; GO:0042025; C.Hoet cell nucleus; IEA.
GO; GO:0042025; C.Hoet cell nucleus; IEA.
InterPro; IPR001334; E6.
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MEDLINE=9743744; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penlle carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2008(1997).
Gen. Virol. 78:2199-2008(1997).
GO: 0042025; C:host cell nucleus; IEA.
GO: GO:0042025; C:host cell nucleus; IEA.
GO: GO:003677; F:NbM binding; IEA.
FILTE-PRO0118; E6: 1.
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                                                                                  Query Match 100.0%; Score 45; DB 2; Length 143; Best Local Similarity 100.0%; Pred. No. 0.36; Matches 9; Conservative 0; Mismatches 0; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
1
143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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MEDLINE-20112892; PubMed=10644829; MEDLINE-20112892; PubMed=10644829; MEDLINE-20112892; PubMed=10644829; Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 B6 variants in relation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments."; J. Virol. 69:7743-7753(1995).
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
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100.0%; Pred. No. 0.38;
tive 0; Mismatches 0; Indels
                                        Query Match 100.0%; Score 45; DB 2; Length 151; Best Local Similarity 100.0%; Pred. No. 0.38; Matches 9; Conservative 0; Mismatches 0; Indels
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EMBL; U34114; AAA91661.1; -.
EMBL; U34125; AAA91672.1; -.
EMBL; U34131; AAA91677.1; -.
EMBL; U34131; AAA91678.1; -.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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151 AA; 18206 MW; SIC12A8B149C6D8A CRC64;
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SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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Matches 9; Conservative
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SEQUENCE FROM N.A.
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NCBI_TaxID=10566;
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NCBI_TaxID=10581;
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SEQUENCE
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Variable 2012 (2017) (1998) W. T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Variables of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
EMBL; AF469197; AA015691.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:00518; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Ffam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CFIF CRC64;
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p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; Gen. Virol. 81:317-325 (2000).
EMBL; AJ388056; CAB45114.1; ---
EMBL; AJ388061; CAB45114.1; ---
EMBL; AJ388065; CAB45124.1; ---
EMBL; AJ388065; CAB45124.1; ---
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Barly transforming protein E6 variant (Transforming protein E6).
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Pred. No. 0.38;
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100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred; No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
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MEDLINE=20112892; PubMed=10644829;
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Gaps

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Length 151; 0; Indels

100.0%; Score 45; DB 2; 100.0%; Pred. No. 0.38; tive 0; Mismatches 0;

60CD2A34DAF48CB7 CRC64;

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EMBL, AF003018; AAB70735.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                 Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18221 MW;
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Best Local Similarity 100.
Matches 9; Conservative
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[1]
SEQUENCE FROM N.A.
STRAIN-Xinjiang;
Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
"Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopeies in Xinjiang.";
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Martins C.R.F.;
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MEDLINE=97437474; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;

Beth-Giraldo E., Giraldo G.;
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
EMBL, AF003019; AAB70736.1; --
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SEQUENCE FROM N.A.
MEDLINE-20112892; PubMed=10644829;
MEDLINE-20112892; PubMed=10644829;
Verheijen M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
J. Gen. Virol. 81:317-325(2000).
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;

DeFilippis V.R., Ayala F.J., Villarreal L.P.;

"Evidence of diversifying selection in human papillomavirus type 16
but not E7 oncogenes.";

J. Mol. Evol. 55:491-499(2002).
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                                                                                                 Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10581;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
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SEQUENCE FROM N.A.
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the B6, L2, and L1 coding segments.";
J. Virol. 69:7743-7753 (1995).
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34122; AAA91669.1, -.
GO; GO:0004255; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IRR001334; E6.
Pfam; PP00518; E6; 1.
SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                           (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 25, Last annotation update)
151 AA.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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MEDLINE=97437474; PubMed=9292007;
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Matches 9, Conservative
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A van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
A van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmernborst T.J., Meijer C.J., Walboomers J.M.;
Verheijen S. Chuman papillomavirus type 16 E6 variants in relation to
T. P53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
R. EMBL; AF003014; AAB70731.1; -.
R. EMBL; AAP472509; AAB70731.1; -.
R. EMBL; AAP472509; AAB70730.1; -.
R. EMBL; AJ388068; CAB45128.1; -.
R. EMBL; Chost cell nucleus; IEA.
R. GO; GO:00042025; C.host cell nucleus; IEA.
R. GO; GO:00044025; C.host cell nucleus; IEA.
R. InterPro; IPR001334; E6.
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L., Beth-Giraldo E., Giraldo G., "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients."; J. Gen. Virol. 78:2199-2208(1997).
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"Human papiliomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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                                                                                                                                                               Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18221 MW; 60CD2A34DAF48CB7 CRC64;
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SEQUENCE 151 AA; 1.
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SEQUENCE 151 AA; 1
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es 9; Conser
                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                         SEQUENCE FROM N.A.
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NCBI_TaxID=10566;
                                                                                                                                                                                                                                       SEQUENCE
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Matches
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100.0%; Score 45; DB 2; Length 151;

Query Match

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populations characterized by nucleotide sequence analysis of the E6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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J. Virol. 69:7743-7753(1995).
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                                                                          19 LQTTIHDII 27
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SEQUENCE FROM N.A.
1 LQTTIHDII
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 18:23:48; Search time 11.2 Seconds (without alignments) 77.317 Million cell updates/sec Run on:

US-08-170-344-6 45

1 LQTTIHDII 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq.length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein E6 - human	pulmonary surfacta	cysteine proteinas	serine/threonine k	hypothetical prote	hypothetical prote	hemagglutinin hag2	purine nucleoside	E6-II protein - hu	н	E6-I protein - hum	Ω	E6 protein - human	E6 protein - human	DNA-directed RNA p	ю		hypothetical prote		hypothetical prote	ď	otcZ protein - Str	hypothetical prote	probable pyruvate	probable integrase	sodium/solute symp	ถ	hypothetical prote	beta-hexosaminidas
SUMMARIES	ID	M6WLHS	LNDGPS	T12042	A55921	G84274	T49278	B47698	D69614	S19906	S19909	S23825	AE0792	W6WL33	W6WLPR	RNLVA	NMEBST	T23809	AG1858	S44258	S60904	T18418	S18571	T48286	G71527	T36043	A95154	G71543	T15104	139839
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d	Query Match	100.0	82.2	80.0	80.0	77.8	77.8	75.6	75.6	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	71.1	71.1	71.1	71.1	71.1	71.1	71.1	71.1
	Score	45	37	36	36	35	32	34	34	33	33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	35
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probable membrane probable ATP-depen	probable calcium-t	isoprenylated prot	conserved hypothet	hypothetical prote	probable fecB - My	conserved hypothet	dnaJ protein homol	dnaJ protein homol	dnaJ protein homol	DnaJ-like protein	phenylalanyl-trna	hypothetical prote	probable cysteinyl	two-component sens
S67053	T40737	T06391	G90190	T34296	G70860	D89975	T07371	S71199	T49127	T09338	T41560	T31546	D84717	D84044
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776	1258	98	241	335	359	383	419	420	420	423	429	449	563	589
71.1	71.1	68.9	68.9	68.9	68.9	68.8	68.9	68.9	68.8	68.9	68.9	68.8	68.9	68.9
32	32	31	31	31	31	31	31	31	31	31	31	31	31	31
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1
WEWLHS
protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence revision 28-May-1986 #text change 09-Jul-2004
C;Accession: A03682; T10427 _
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A; Reference number: A22355; MUID: 85246220; PMID: 2990099
A;Accession: A03682
A; Molecule type: DNA
A;Residues: 1-158 <see></see>
A; Cross-references: UNIPROT: P03126; GB: K02718; NID: 9333031; PIDN: AAA46939.1; PID: 9333032
R; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A; Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-158 < KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C;Genetics:
A;Gene: E6
C;Superfamily: papillomavirus E6 protein

C, Kefwords: DNA binding; early protein; zinc finger F;37-73/Region: zinc finger CCCC motif F;110-146/Region: zinc finger CCCC motif

Gaps ö Query Match 100.0%; Score 45; DB 1; Length 158; Best Local Similarity 100.0%; Pred. No. 0.093; Matches 9; Conservative 0; Mismatches 0; Indels

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26 LOTTIHDII 34 1 LQTTIHDII 9 셤 ò

RESULT 2

pulmonary surfactant protein A precursor - dog
pulmonary surfactant protein A precursor - dog
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated ;
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Species: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 16-Jul-1999
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 16-Jul-1999
Froc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985
A;Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino acade A;Accession: A25296
A;Accession: A25296
A;Accession: A25296
A;Molecule type: mRNA

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A; Cross-references: FlyBase: FBgn0011300
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93 VDTTIHDIL 101
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6; Conserve
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A;Molecule type: DNA
A;Residues: 1-132 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ripatthy, L.

Nature 325, 490, 1987

A; Reference number: A93388; MUID:87115834; PMID:3808053

A; Reference number: A93388; MUID:87115834; PMID:3808053

A; Contents: annotation; animal lectin domain homology

C; Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers to C; Comment: This protein is a slaidoglycoprotein synthesized by alveolar type II cells. It pendent on the presence of calcium ions.

C; Superfamily: mannose-binding lectin; C-type lectin homology
                                  A, Note: the authors translated the codon TTG for residue 60 as Pro A, Note: part of the sequence, including the amino end of the mature protein, was confirm R, Liau, D.F.; Ryan, S.F. Chem. Chem. Phys. Lipids 59, 29-38, 1991
A, Title: Purification of surfactant protein A from dog lung by reconstitution with surfactence number: A61227; MUID:92163993; PMID:1790579
                                                                                                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 18-32 <LIA>
R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Biochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification of
A;Reference number: A60142; MUID:86159848; PMID:3006781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Risenyuk, V.; Becker, C.; Muentz, K.
submitted to the EMBL Data Library, October 1997
A;Description: Isolation of cDNA clone encoding cysteine proteinase (CP4) from a cotyled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Reywords: alveolar proteinosis; calcium; disulfide bond; gaseous exchange; hydroxyprol
F;1-17Domain: signal sequence #status predicted <SIGD of SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTION SECTIO
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C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;30/Modified site: 4-hydroxyproline (Pro) #status experimental
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A.Cross-references: UNIPROT:024324; EMBL:299955
A.Cross-references: UNIPROT:024324; EMBL:299955
C.Superfamily: papain: cultivar Moldavian; cotyledon; clone cp4
C.Superfamily: papain: proteinase; hydrolase
F.1-21/Domain: signal sequence #status predicted <SIG>F:22-137/Domain: propeptide #status predicted <PRO>F:138-377/Product: cysteine proteinase 4 #status predicted <MAT>F:162,305,332/Active site: Cys, His, Asn #status predicted
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Pred. No. 16;
1; Mismatches 0; Indels
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1
Pred. No. 6.4;
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A;Residues: 24-34;95-101,'X',103-108 <ROS>
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75.0%;
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Best Local Similarity 75.0
... 6; Conservative
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A;Accession: T12042
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Best Local Similarity
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C;Accession: A55921
R;Wrana, J.L.; Tran, H.; Attisano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, h Mol. Cell. Biol. 14, 944-950, 1994
Asi,Title: Two distinct transmembrane serine/threonine kinases from Drosophila melanogaster A;Reference number: A55921; MUID:94119112; PMID:8289834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gispecials: Halobacterium sp. NRC-1
Cispecials: House, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. R; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A,Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liz A,Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
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R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S., submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C;Keywords: ATP F;301-597/Domain: protein kinase homology <KIN> F;303-317/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                       A,Accession: A55921
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-601 <WRA>
A,Cross-references: UNIPROT:Q23975, GB:U04692; NID:g436960; PIDN:AAA18959.1; PID:g436961
C,Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
                                   C,Species: Drosophila melanogaster
C,Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
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serine/threonine kinase Atr-1 - fruit fly (Drosophila melanogaster)
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Pred. No.
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Genetics:

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A;Cross-references: UNIPROT:034925; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13854.1
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cispecies: human papillomavirus type 33 (fragment)
Cispecies: human papillomavirus type 33
Cispecies: human papillomavirus type 33
Cispecies: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
Cistocession: S19906
Rishijders, P.J.F.; van den Brule. A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Mensubmitted to the EMBL Data Library, January 1992
A.Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via tvA.R.R.Eference number: S19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: human papillomavirus type 33
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S;9909
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Messubmitted to the EMBL Data Library, January 1992
submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via tv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNA
A,Residues: 1-32 <SNI>
A,Cross-references: UNIPROT:Q81885; EMBL:X64086; NID:g60282; PIDN:CAA45435.1; PID:g60283
C,Superfamily: papillomarirus E6 protein
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C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
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E6-I protein - human papillomavirus type 33 (fragment)
C;Species: human papillomavirus type 33
C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S23825; S23829
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Pred. No. 4.2;
2; Mismatches 0; Indels
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                                                                                                                          C; Superfamily: purine-nucleoside phosphorylase pnp
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75.0%;
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Similarity 75.0%;
6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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217 QTTFHDMI 224
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C;Keywords: early protein
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A; Residues: 1-35 <SNI>
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Matches
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D69614
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D.; Smmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maueda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, B.; Roche, B.; Rose, M.; Sadade, Y.; Sato, T.; Saron,
A;Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekjuchi, J.; Sekowska, A.; Sato,
A;Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sato,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Vochiyama,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Ritle: The complete genome sequence of the Gram-Dositive bacterium Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hemagglutinin hag2 - Eikenella corrodens
C;Species Eikenella corrodens
C;Species Eikenella corrodens
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B47698; S23848
C;Accession: B47698; S23848
C;Accession: B47698; Proguske-Pox, A.
J. Gen. Microbiol. 139, 639-650, 1993
A;Title: Cloning, characterization and sequencing of two haemagglutinin genes from Eiker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT: P35648; EMBL: Z12610; NID: 941653; PIDN: CAA78254.1; PID: 941655
                                                                                                                                                                                                        A;Map position: 3
A;Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2
                                                                                    A;Cross-references: UNIPROT:Q9M301; EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.90
A;Experimental source: cultivar Columbia; BAC clone T21J18
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A;Note: sequence extracted from NCBI backbone (NCBIN:129988, NCBIP:129990)
C; Superfamily: Eikenella corrodens hemagglutinin hag2
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Pred. No. 22;
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Pred. No. 33;
3; Mismatches
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66.7%; Pred. No. 22,
2; Mismatches
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66.7%;
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Best Local Similarity 66.7,,
6, Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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277 VKTTIHDIM 285
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LOSTIHDAL 169
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                                                        A; Residues: 1-470 <RIE>
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A; Residues: 1-212 <RAO>
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preliminary
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21 LDTTLHDV 28
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Best Local Similarity
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Matches 5; Conserv
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A; Residues: 1-340 <FUK>
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R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
A;Reference number: S19906
                                                                                                                                                                  A;Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; EMBL:X64084; NID:g60273; PIDN:CAA454
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AE0792
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable membrane protein STY2516 [imported] - Salmonella enterica subsp. enterica serov C.Speciese: Salmonella enterica subsp. enterica serova Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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A; Residues: 1-149 <COL>
A; Cross-references: UNIPROT: P06427; CB:M12732; NID:g333049; PIDN: AAA46958.1; PID:g463177
A; Cross-references: UNIPROT: P06427; CB:M12732; NID:g333049; PIDN: AAA46958.1; PID:g463177
C; Superfamily: papillomavirus Es protein;
C; Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
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EG protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequenc_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
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Pred. No. 6.5;
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Pred. No. 9.6;
0; Mismatches
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75.0%;
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77.8%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
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                                                                                                                            A; Residues: 1-47 <SNI>
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Molecule type: DNA
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C;Genetics:
A;Gene: STY2516
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A;Reference number: A38014
A;Contents: annotation; gene organization, sites, features
R;Fukuzawa, H.; Kohchi, T.; Sano, T.; Shirai, H.; Umesono, K.; Inokuchi, H.; Ozeki, H.; C. J. Mol. Biol. 203, 333-351, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-340 <OHY>
A; Cross-references: UNIPROT: P06270
R; Ohyama, K.; Fukuzama, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi)
Nature 322, 572-574, 1986
A; Title: Chloroplast gene organization deduced from complete sequence of liverwort March?
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A,Reference number: S01529; MUID:89068687; PMID:3199436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - liverwort (Marchantia polymorpha)
C;Species: chloroplast Marchantia polymorpha
C;Species: chloroplast Marchantia polymorpha
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A00687; S01565
R;Ohyama, K. Rshar A00150
A;Reference number: A00150
A;Recession: A00687
                                                                   A; Mote: host Homo sapiens (man)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: C40509
R; Reuter, S; Delius, H; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A; Title: Characterization of a novel human papillomavirus DNA in the cervical carc.
A; Reference number: A40509; MUID:91374616; PMID:1716694
A; Accession: C40509
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-158 *REU>
A; Cross-references: UNIPROT:P27962; GB:M73258
C; Superfamily: papillomavirus E6 protein
C; Superfamily: papillomavirus E6 protein
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58;
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C;Superfamily: DNA-directed RNA polymerase alpha chain
C;Keywords: chloroplast; nucleotidyltransferase; transcription
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E6 protein - human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
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Pred. No. 58;
2; Mismatches
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Search completed: June 28, 2005, 19:23:19 Job time: 12.2 secs

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Sequence 102, App
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US-10-133-210-279
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US-10-751-845-56
US-10-48-063-2
US-10-476-570-21
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Maximum Match 1008
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Sequence 20, Appl
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Sequence 263390,
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Sequence 230650,
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Sequence 14, 1
Sequence 10, 1
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Sequence 10,
Sequence 23,
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APPLICANT: Lunsford, Lynn B.
APPLICANT: Putnam, David
APPLICANT: Hedley, Mary Lynn
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
TITLE OF INVENTION: ACID
FILE REFERENCE: 08191/014001
FILE REFERENCE: 08191/014001
FILE REFERENCE: 2011-07-18
PRIOR APPLICATION NUMBER: LOS1-07-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FARELER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FARELER FILING DATE: 1099-05-27
SEQ ID NO 102
                                               Sequence Sequence 3
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6 US-10-476-570-9
6 US-10-476-570-19
7 US-10-476-570-19
7 US-10-484-063-27
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; ORGANISM: Hepatitis B virus
US-09-909-460-102
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1082
1198
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Gaps

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Sequence 2, Application US/10484063
Publication No. US20050048467A1
GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: FOLLEN MICHELE
ITILE OF INVENTION: RET-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
ITILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
CURRENT PAPLICATION NUMBER: US/10/484,063
CURRENT PILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
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Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
ITILE OF INVENTION: NUCLEAR CIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REPERENCE: 08191-013001
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100.0%; Pred. No. 1.6e+06;
Live 0; Mismatches 0;
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CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/164,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER: OF SEQ ID NOS: 163
SEQ ID NO 56
FILE REFERENCE: 08191-012001
CURRENT APPLICATION NUMBER: US/10/758,970
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US/09/715,708A
PRIOR FILING DATE: 2000-11-17
PRIOR PLING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 109
NOFFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 102
                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-102
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; ORGANISM: Human Papilloma virus
US-10-751-845-56
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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| Sequence 279, Application US/20030103964A1
| GENERAL INPORMATION:
| APPLICANT: DeLisi, Charles
| APPLICANT: DeLisi, Charles
| APPLICANT: Gellukota, Xamalakar
| APPLICANT: Gellukota, Kamalakar
| APPLICANT: Weng, Zhiping
| APPLICANT: Weng, Zhiping
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Publication No. US20050037086A1
GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Hedley, Waich-educk
APPLICANT: Hey, Yung-Yueh
APPLICANT: Tyo, Michael
TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                   APPLICANT: MCKGEVE, Una
APPLICANT: MCKGEVE, Una
APPLICANT: Hedley, Mary Lynne
TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REPERENCE: 08191-018001
CURRENT APPLICATION NUMBER: US 60/208,836
CURRENT FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-06-02
NUMBER: OF SEQ ID NOS: 120
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102
LENGTH: 9
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
      Sequence 102, Application US/09872836
Publication No. US20040142475A1
GENERAL INFORMATION:
APPLICANT: Barman, Shikha P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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CORGANISM: Homo sapiens
US-09-872-836-102
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US-10-758-970-102
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CURRENT APPLICATION NUMBER: US/10/476,570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRERAL INCOMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MALLIERE, BERTAAT
APPLICANT: MALLIERE, BERTAAT
APPLICANT: MALLIERE, BERTAAT
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6
TITLE OF INVENTION: Mixture of peptides derived from E6
TITLE OF INVENTION: Mixture of peptides derived uses thereof
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR PLICATION NUMBER: FR 01 05980
PRIOR PLICATION DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 21
LENGTH: 15
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MALLERER, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BUURGAUT-VILLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: PADALILING PADALILIMENTION: PADALILIME SEPERENCE: 45616-5071-US
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                                                                                                                                                                                                                                                                                                     100.0%; Score 45; DB 17; Length 10; 100.0%; Pred. No. 0.053;
                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
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                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-2
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Best Local Similarity 100...
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US-10-476-570-22
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FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE BETNACH
APPLICANT: MOUNGLIE-MORATILIE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENITON: Mâxture of peptides derived from E6 and/or E7
TITLE OF INVENITON: papillomavirus proteins and uses thereof
TITLE OF INVENITON: papillomavirus proteins and uses thereof
TITLE OF INVENITON WUMBER: E031-04
PRIOR FILING DATE: 2003-11-04
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MATLLERER, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
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CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR PILING DATE: 2002-05-03
PRIOR PPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
LENGTH: 15
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                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 32
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Matches
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APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: US 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VOY: 3.2
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APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7;
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7;
TITLE OF INVENTION: Papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/PR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 53
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 30;
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 9; Conservative
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12 LOTTIHDII 20
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US-10-858-384-4
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LENGTH: 30
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Maxuire of peptides derived from B6 and/or E7
TITLE OF INVENTION: Maxuire of peptides derived from 6 and/or E7
TITLE OF INVENTION: Maxuire of peptides derived from 86 and/or E7
TITLE OF INVENTION: MAINER: U5/1-U5
CURRENT APPLICATION NUMBER: U5/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NOS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION NO. US. COUGAINTON:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: MAILLERE BETTANT MAILLERE
BETTANT: MAILLERE BETTANT
APPLICANT: MAILLERE BETTANT
APPLICANT: BOURGAULT-VILLADA, ISABElle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
TITLE OF INVENTION WUBBER: U5/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATCHTIN VEY. 2.1
SEQ ID NOS: 63
SEQ ID NOS: 63
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; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Sequence 9, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:

RESULT 12 US-10-476-570-9

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Publication No. US20050048467A1

GENERAL INPORMATION:
APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: FOLLEN, MICHELE

TITLE OF INVENTION: METHOLES

TITLE OF INVENTION: METHOLES

TITLE OF INVENTION: METHOLES

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT APPLICATION NUMBER: DCT/US02/23198

PRIOR APPLICATION NUMBER: PCT/US02/23198

PRIOR APPLICATION NUMBER: E0/4-01-16

PRIOR APPLICATION NUMBER: E0/306,809

PRIOR PILING DATE: 2002-07-19

PRIOR PILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 20

LENGTH: LS1

TYPE: PRT

CORGANISM: Human papillomavirus

US-10-484-063-20
Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION.
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polymuclectides by Electroporation
; TITLE OF INVENTION: Polymuclectides by Electroporation
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 202-06-20
; NUMBER OF SEQ ID NOS: 34
; SEG ID NOS: 34
; SEQ ID NO 6
; LENGTH: 151
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                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Human papillomavirus type 16
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-484-063-20
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Search completed: June 29, 2005, 03:24:06 Job time: 57.55 secs

(Oldsu) Right (Uspto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 18:27:48; Search time 17.15 Seconds (without alignments) 39.174 Million cell updates/sec

US-08-170-344-6 45 Title: Perfect score:

1 LQTTIHDII 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de				
Result No.	Score	Query Match	Length	DB	QI	Description
7	45	100.0	6	7	US-08-787-547-102	Sequence 102, App
7	45	100.0	Q	ო	US-08-159-339A-248	248,
٣	45	100.0	14	٦	US-07-909-122-3	3, A
4	45	100.0	30	Н	US-08-363-586-4	4
S	45	100.0	30	4	US-09-980-523A-4	4
9	45	100.0	158	4	US-09-980-523A-2	7
7	45	100.0	162	Н	08-316-2	m
œ	45	100.0	162	Н	US-08-316-239B-4	4
σ	45	100.0	172	ო	US-08-860-165-14	14,
10	45	100.0	172	ო	US-09-359-382-14	14,
11	45	100.0	182	٦	US-08-117-083-10	Sequence 10, Appl
12	45	100.0	266	٣	US-08-860-165-10	10,
13	45	100.0	266	m	US-09-359-382-10	10,
14	45	100.0	266	4	US-09-367-309A-1	1, A
15	45	100.0	273	٣	US-09-485-885-4	4,
16	45	100.0	292	m	US-09-485-885-10	10,
11	45	100.0	371	m	US-09-485-885-6	. 9
18	45	100.0	390	٣	US-09-485-885-14	14,
19	40	88.9	20	~	US-08-934-915-159	159,
20	40	88.9	317	m	US-08-913-159-14	14, 7
21	33	73.3	166	4	US-09-270-767-33046	3304
22	33	73.3	166	4	US-09-270-767-48263	
23	33	73.3	297	٣	US-08-706-281A-8	æ
24	33	73.3	297	٣	US-09-097-231-8	8
25	33	73.3	297	4	US-09-353-099-8	8
56	33	73.3	200	4	US-09-354-123-6	Sequence 6, Appli
27	32	71.1	168	4	US-09-270-767-32894	328

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Gaps

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Length 9;

Query Match 100.0%; Score 45; DB 1; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels

	Sequence 11304, A Sequence 4, Appli
US-09-489-019A-14156 US-09-252-991A-30492 US-09-243-681A-6825 US-09-248-796A-19137 US-08-197-484-72 US-08-107-72 US-08-95-12121-72 US-08-95-12121-72 US-08-95-12121-72 US-08-95-12121-72 US-08-95-12121-72 US-08-95-12121-72 US-08-95-1216-72 US-08-95-1216-72 US-08-95-1216-72 US-08-95-1216-72 US-08-785-795-1 US-09-603-208A-62 US-09-603-208A-62	US-09-949-016-11304 US-09-227-725A-4
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77777777777777777777777777777777777777	68.9
	31
22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	44 45

ALIGNMENTS

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APPLICANT: Heddley, Mary Lynne
APPLICANT: Curley, Joanne M.
APPLICANT: Curley, Joanne M.
APPLICANT: Curley, Joanne M.
TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
TITLE OF INVENTION: OF NUCLEIC ACID
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,547
FILING DATE: 22-JNN-1997
CLASSIFTCATION: 514
PRIOR APPLICATION DATA:
APPLICATION INFORMATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REPERENCE/DOCKET NUMBER: 08191/003001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 617-542-8906
                    Sequence 102, Application US/08787547 Patent No. 5783567 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                   CCUNTRIA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
COUNTRY: US
US-08-787-547-102
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   DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 45; DB 1; Length 14; 100.0%; Pred. No. 0.032; tive 0; Mismatches 0; Indels
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GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Dutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 28,052
REGISTRATION NUMBER: 28,000-20105.01
TELEPHONE: (415) 813-5600
TELEPKX: (415) 813-5600
TELEPKX: (415) 494-0792
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APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
TITLE OF INVENTION: DIAGNOSTIC PEP
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08363586
Patent No. 5629161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LOTTINDII 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LQTTIHDII 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-07-909-122-3
                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
TELEX: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-363-586-4
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                                                                                                                                                                                                                              Sequence 248, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Bateban
TITLE OF INVENTION: Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          red. No. 4.1e+05;
Mismatches 0;
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MEDIUM TYPE: Diskette
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: DISKET
COMPUTER: DISKET
CO
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Patent No. 5415995;
GENERAL INFORMATION:
GENERAL SCHOOLNIK, GARY K.;
APPLICANT: PALEFSKY, JOEL M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 248: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: peptide
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                                                                                                                                                                      RESULT 2
US-08-159-339A-248
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Gaps

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Sequence 3, Application US/08316239B Patent No. 5679509
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; ORGANISM: Human Papillomavirus
US-09-980-523A-2
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not relevant
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TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LQTTIHDII 9
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STRANDEDNESS: not
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Sequence 4, Application US/09980523A

Patent No. 6783763

GENERAL INFORMATION:
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GHOPPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, PRANCINE
APPLICANT: CONNAN, PRANCINE
APPLICANT: CONNAN, PRANCINE
APPLICANT: PRERIES, ESTELLE
TITLE OF INVENTION: PROTEING OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILLS OF INVENTION: PRATICULARLY IN VACCINATION
FILLS OF INVENTION NUMBER: US/09/980,523A
CURRENT APPLICATION NUMBER: PST/FR00/01513
FRIOR PILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-06-03
FRIOR FILING DATE: 1990-06-03
FRIOR FILING DATE: 1990-06-03
FRIOR PILING DATE: 1990-06-03
FRIOR FILING DATE: 1990-06-03
FRIOR PAPELICATION NUMBER: PST/FROWNER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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0.071;
hes 0; Indels
FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02481-1195-00000
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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GENERAL INCORMATION:
APPLICANT: CHOPPIN, JEANNINE APPLICANT: GUILLET, JEAN-GERARD APPLICANT: GUILLET, JEAN-GERARD APPLICANT: CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4
                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
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Best Local Similarity 100.00
The 9; Conservative
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Best Local Similarity 100.00
Thes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-363-586-4
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                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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TITLE OF INVENTION: PROFERING OF HOWELD READERS OF THE SE AND ET TITLE OF INVENTION: PROFESSION FROM THE PRODUCTION AND THEIR USE TITLE OF INVENTION: PROFESSION OF HOW THEIR REPRESENCE WOLD AD IN SECURITY IN VACCINATION

FILES REFERENCE: WOLD AD IN SECURITY IN VACCINATION

FILES REFERENCE: WOLD AD IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECURITY IN SECU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09359382

| Sequence 14, Application US/09359382
| Patent No. 6306397
| GENERAL INFORMATION:
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: EDWARDS, Stirling John
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: WEBB, Elizabeth Ann
| APPLICANT: PRAZER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANT: PRAZER, Ian
| APPLICANT: 1999-01-23
| CURRENT FILING DATE: 1999-07-23
| EARLIER PILING DATE: 1999-09-22
| FARLIER APPLICATION NUMBER: PCT/AU95/00868
| SARLIER APPLICATION NUMBER: AU PNO157/94
| SARLIER PILING DATE: 1994-12-20
| NUMBER OF SEQ ID NOS: 27
| NUMBER OF SEQ ID NOS: 27
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APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
NUMBER OF SEQUENCES: 70
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          FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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US-09-359-382-14
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                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 14
LENGTH: 172
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conser
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APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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US-08-860-165-14
US-08-860-165-14
; Sequence 14, "Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
                                  100.0%; Score 45; DB 1; Length 162; 100.0%; Pred. No. 0.42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 162;
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ZIP: 20120-3400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSTRICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JGGTIANI, AJAY A.
REGISTRATION NUMBER: 35,205
REGISTRATION NUMBER: 35,205
REGISTRATION NUMBER: 35,205
REGISTRATION NUMBER: UNMER:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 45; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches
                                                                                                   0; Mismatches
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STREET: 6126 Rocky Way Court
CITY: Centreville
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.vv
9; Conservative
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amino acid
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26 LOTTIHDII 34
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                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS. Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                          100.0%; Score 45; DB 3; Length 266; 100.0%; Pred. No. 0.7;
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APPLICANT: MACFARLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT PAPLICATION NUMBER: PCT/AU98/00080

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO.: 2.66
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                                                                           0; Indels
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CURRENT FILING DATE: 1990-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER PPLICATION NUMBER: AU PN0157/94
EARLIER PPLING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VEY: 2.0
SSOFTWARE: PATENTIN VEY: 2.0
LENGTH: 266
                                                                           Mismatches
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
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, ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
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Patent No. 6428807
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                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conserva
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Best Local Similarity
Matches 9; Conserv
                                                                                                                             1 LOTTINDII
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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
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GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBS, Dilabeth Ann
APPLICANT: FRAZER, Ian
TITE OF INVENITON: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFRENCE: 1722/130
CURRENT TILING DATE: 1997-09-22
CURRENT TILING DATE: 1995-12-20
ERALIER APPLICATION NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
MUMBER OF SEQ ID NOS: 1955-12-20
SAFLIER FILING DATE: 1994-12-20
NUMBER: PATENTON NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
SOFTWARE: PATENTON NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
SOFTWARE: PATENTON NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
SOFTWARE: PATENTON NUMBER: AU PNO157
EARLIER FILING DATE: 1995-12-20
SEQ ID NO 10
SEQ ID NO 10
SEQ ID NO 10
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the open reading frame."
                                                                                                                          COUNTRY: USAN
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REPRENCE/DOCKET NUMBER: A-58783
TELEPHONE: 415-781-1989
TELEFRAX: 415-781-1989
TELEFRAX: 415-781-1989
TELEFRAX: 415-781-1989
TELEFRAX: 415-781-1989
TELEFRAX: 415-781-1989
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
'ENCTH: 182 amino acids
             SEB: Walter H. Dreger
: 4 Embarcadero Center, Suite 3400
San Francisco
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US-08-860-165-10
'Sequence 10, Application US/08860165A
'Patent No. 6004557
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
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USA
                                                                                                STATE: C. COUNTRY:
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                                                                                                   RESULT 15
US-09-485-885-4

i Sequence 4, Application US/09485885

i Patent No. 6342224

i GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Delisse, Anne-Marie Eva Fernande

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Gerard, Catherine Marie Ghislaine

TITLE OF INVENTION: Vaccine

TITLE REFERENCE: B45107

CURRENT APPLICATION NUMBER: US/09/485,885

CURRENT FILING DATE: 2000-02-18

PRIOR PILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 273

TYPE: RFT

CORGANISM: Homo sapien

US-09-485-885-4
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132 LQTTIHDII 140
1 LQTTIHDII 9
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26 LQTTIHDII 34
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Search completed: June 28, 2005, 19:29:10 Job time: 25.15 secs

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Query Match
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                                                               June 28, 2005, 21:24:19; Search time 55.1 Seconds (without alignments) 83.643 Million cell updates/sec
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GenCore version 5.1.6
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NCBI_TaxID=10581;
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Lee H.P., Song Y.S., tim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF187869; AAF13399.1; -.
InterPro; IPR000148; Papvi_E7.
Pfam, PF00527; E7; 1.
NON_TER 93
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Liee H.D., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Liee H.D., Song Y.S., tim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187868; AAF13397.1; -.
InterPro; IPR000148; Papvi_F7.
Pfan; PF00527; E7; 1.
NON_TER 93
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Pred. No. 0.01;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Matches 9; Conservative
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NCBI_TaxID=10581;
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EMBL; AF187867; AAF13395.1; -.
InterPro; IPR000148; Papvi E7.
Pfam; PF00577; E7; 1)
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Lue H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1878866, AAF13393.1; -.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
NON TER
SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (Fragmmath)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
O9QDH6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E7 procein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 0.012;
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SEQUENCE FROM N.A

93 AA.

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MEDLINE=90218027; PubMed=2157796;
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
"Expression of the human papillomavirus type 16 genome in SK-v cells, a line derived from a vulvar intraepithelial neoplasia.";
J. Gen. Virol. 71:809-817(1990).
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Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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MEDLINE-85246220; PubMed=2990099;
MEDLINE-85246220; PubMed=2990099;
Sedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
"Human papillomavirus type 16 DNA sequence.";
Virology 145:181-185(1985).
                                                                                                                                                                                                                                                       100.0%; Score 58; DB 2; Length 94; 100.0%; Pred. No. 0.012;
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF463197; AAO15692.1; -.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; B7; 1.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=22182962; PubMed=12195358;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
Thuman papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
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Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
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                                                  EMBL, AF003023, AAB70737.1; -.
EMBL, AF003023, AAB70740.1; -.
EMBL, AF003024, AAB70741.1; -.
EMBL, AF003025, AAB70742.1; -.
EMBL, AF003025, AAB70742.1; -.
EMBL, AF003025, AAB70743.1; -.
PIR, A03688, WWLHS.
InterPro. IPR000148; Papvi_E7.
Pfam, PF00527, E7. 1.
DNA-binding, Early protein; Oncogene; Trans-acting factor;
Transcription regulation.
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; U76404; ARC58243.1; -.
EMBL; AF472209; AAUS6511.1; -.
EMBL; AF48326; AAL96631.1; -.
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Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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C-XX-C motif-2.
9BD612534CD2C9EB CRC64;
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100.0%; Pred. No. 0.013;
Live 0; Mismatches 0
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", U76412; AAB18963.1; -..., U76413; AAB18964.1; -..., AF00320; AAB10737.1; -..., AF003023; AAB70740.1; -..., AF003025; AAB70742.1; -..., AF003026; AAB70743.1; -..., AF003026; AAB70743.1; -..., AF003026; AAB70743.1; -...
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NCBI_TaxID=10581;
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MEDLINE=2182962; DubMed=12195358; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.; Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002). EMBL, PAR864345, AAL96650.1; -. InterProf. IPR001048; Papvi_E7.

Fami, PR00527; B7: 1.

SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;
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                                                                                                                                                                                        100.0%; Score 58; DB 2; Length 98; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
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                                                            Jinhu X., Xinxing W., Yun T.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/AF003022; AAB70739-1; --
EMBL, AF477385; AAM03025-1; --
EMBL, AF477385; AAM03025-1; --
EMBL, AF477385; AAM03025-1; --
Pfam; PF00527; B7; 1 10999 WW; 9BD612534CCEA59B CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
   type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78;2199-2208(1997).
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Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Glatalo G.,
Gitalo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virtol. 78:2199-2208(1997).
EMBL, AF003021; ABB70738.1; -.
LINTERPRO; IPR000148; Papvi_E7.
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EMBL; AF486333; AAL96638.1; -.

REMBL; AF486334; AAL96641.1; -.

REMBL; AF486336; AAL96643.1; -.

REMBL; AF486336; AAL96651.1; -.

REMBL; AF486350; AAL96651.1; -.

REMBL; AF486350; AAL96655.1; -.

REMBL; AF486351; AAL96655.1; -.

REMBL; AF534061; AAQ10404.1; -.

REMBL; AF534061; AAQ10404.1; -.

REMBL; AF534061; AAQ10404.1; -.

REMBL; AF5340625; E7; 1.

REMBL; AF5340625; E7; 1.

REMBL; AF534061; AAQ10404.1; -.

REMBL; AF5340625; E7; 1.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dapiNA viruses, no RNA stage; Papillomaviridae;
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NCBI_TaxID=10581;
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SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E7 protein.
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MEDLINE=22182962; PubMed=12195358;

MEDLINE=22182962; PubMed=12195358;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M., Cheung J.L.K., Xu L.Y., Cheng A.F.;

Cheung J.L.K., Xu L.Y., Cheng A.F.;

Human papillomavirus type 16 intratypic variant infection and risk for cervical neoplasia in southern China.";

J. Infect. Dis. 186:696-700(2002).

EMBL; AF486329; AB6634-1; -.

InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; 1.

SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
E7 protein.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:656-700(2002).
EMBL; AF486344; AAL96649.1; -.
PITERPRO; IPRO00148; Papvi_E7.
PITER; PRO0527; E7; 1.
SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Oy 1 HYNIVTFCC 9

Db 51 HYNIVTFCC 59
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Search completed: June 28, 2005, 23:28:15 Job time : 57.1 secs Colosu) Anola appla sidi

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec Run on:

US-08-170-344-59 58 Title: Perfect score:

1 HYNIVTFCC 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* **Database**:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

Result	Ċ	Query	:		SUMMARIES	
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1	58	100.0	98	٦	W7WLHS	E7 protein - human
7	51	87.9	98	-	W7WL31	1
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9	41	70.7	322	~	F88987	otein C50H1
7	40	69.0	98	Н	W7WL6	E7 protein - human
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11	38	65.5	184	~	A81561	hypothetical prote
12		65.5	184	7	C72110	_
13	38	65.5	184	~	D86513	
14	37	63.8	71	~	T09312	н
15	37	•	346	~	T21398	hypothetical prote
16	37		350	(7	T25172	_
17	37	•	354	7	T22967	
18	37		628	7	S44629	u
13	37	63.8	619	7	T25895	hypothetical prote
20	37	63.8	737	~	F85092	
21	37	63.8	737	~	T51620	DNA mismatch repai
22	36	62.1	271	~	E89950	hemA concentration
23	36	62.1	279	N	857139	probable membrane
24	36	62.1	403	~	H64861	hypothetical prote
25	36	62.1	445	~	S65734	•~
56	36	62.1	1092	N	H96619	protein T30E16.17
27	35.5	61.2	98	Н	W7WLC1	E7 protein - pygmy
28	35	60.3	92	Н	S15615	protein -
53	35	60.3	92	-	S15622	protein -

E7 protein - human probable membrane	probable integral G protein-coupled	hypothetical prote	٠.,	neterodisulfide re probable formate a	hypothetical prote iodopsin homolog -	flagellar biosynth hypothetical prote	beta-amylase (EC 3	probable membrane hypothetical prote
S36498 S51974	T35521 JN0621	E84730	T18460	F69421 AH0602	S57062 A46191	C84958 T27222	\$36094	S45413 T34544
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30 31	. e. e.	1 & G	36	38	3.9 4.0	41	43	44 45

ALIGNMENTS

E7 protein - human papillomavirus type 16 C;Species: human papillomavirus type 16 C;Species: human papillomavirus type 16 C;Bate: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004 C;Accession: A03688; Si237; Til428 R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G. N;rology 145, 181-185, 1985 A;Title: Human papillomavirus type 16 DNA sequence. A;Reference number: A22355; MUID:85246220; PMID:2990099

A; Molecule type: DNA A; Residues: 1-98 <SEE>

A;Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033 R;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H. EMBO J. 9, 153-160, 1990 A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large A;Reference number: S12367; MUID:90107938; PMID:2153075

A;Status: preliminary
A;Molecule type: protein
A;Rolecule type: protein
A;Residues: 1-98 <BAR>
B;Residues: 1-98 <BAR>
J. Wixol. 6.5, 2093-2097, 1991
A;Ticlle: A negative element in the human poapillomavirus type 16 genome acts at the level
A;Reference number: Z17014; MUID:91162763; PMID:1848319

A,ACCEBBION: T10428
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-98 <KEN>
A,Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

A.Gene: E7 C.Superfamily: papillomavirus E7 protein C.Keywords: DNA binding, early protein; transcription regulation; zinc finger F;58-94/Region: zinc finger CCCC motif

Gaps 100.0%; Score 58; DB 1; Length 98; ilarity 100.0%; Pred. No. 0.0067; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 9; Conserv

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RESULT 2
W7WL31
E7 protein - human papillomavirus type 31
E7 Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

N

0; Indels

0.1;

87.9%; 88.9%;

Ouery Match Best Local Similarity 85.. 8. Conservative

SI NYNIVTFCC 59 1 HYNIVTFCC 9

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A;Status: translation not shown

A; Accession: B32444

Molecule type: DNA Residues: 1-98 <GOL>

1; Mismatches

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E7 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Auge 1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Auge 1986 #sequence_revision 18.4 Auge 1986 #text_change 09-Jul-2004
C;Auge 1980 # A. Dataman, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A;Fitle: The nucleotide sequence and genome organization of human papilloma virus type 11
A;Reference number: A94338; MUID:86181601; PMID:3008427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein C50H11.16 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: F88987
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Rote: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/,Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: F88987
A;Accession: F88987
A;Accession: Preliminary
A;Molecule type: DNA
A;Residuss: 1-322 <STO>
A;Cross-references: GB:chr_V; PIDN:AAB65980.1; PID:g2315479; GSPDB:GN00023; CESP:C50H11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A03690
A,Molocule type: DNA
A,Molocule type: DNA
A,Cross-references: UNIPROT:P04020, GB:M14119; NID:g333026; FIDN:AAA46928.1; PID:g496194
A,Cross-references: UNIPROT:P04020, GB:M14119; NID:g333026; FIDN:AAA46928.1; PID:g496194
C,Superfamily: papillomavirus E7 procein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;S8-94/Region: zinc finger CCCC motif
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             A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999 A;Experimental source: strain 35H C;Superfamily: papillomavirue E7 protein C;Superfamily: papillomavirue E7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc finger P;59-95/Region: zinc finger CCCC motif
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C;Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12
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                                                                                                                                                                                                               Score 43; DB 1; Length 99;
Pred. No. 2.3;
1; Mismatches 1; Indels
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66.7%; Pred. No. 4.9;
live 1; Mismatches 2; Indels
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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52 NYNIVTSCC 60
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A, Residues: 1-99 < DEL>
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C;Species: human papillomavirus type 35
A;Note: human papillomavirus type 35
A;Note: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F40824; S36522
C;Accession: F40824; S36522
A;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
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R;Maillou, J.; Dreiseikelmann, B.
R;Maillou, J.; Dreiseikelmann, B.
R;Maillou, J.; Dreiseikelmann, B.
R;Maillou, J.; Dreiseikelmann, B.
R;Ticle: The sim gene of Escherichia coli phage P1: nucleotide sequence and purification A;Reference number: A46337; MUID:90223995; PMID:2327075
                       R'Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Vicology, 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assod A;Reference number: A94398; MUID:89299478; PMID:2545036
                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917 C; Comment: This protein may be involved in the oncogenic potential of this virus. C; Superfamily: papillomavirus BT protein C; Superfamily: papillomavirus BT protein C; Keywords: DNA binding; early protein; transcription regulation; zinc finger R;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
*Residues: 1-239 «MAL»
A;Cross-references: UNIPROT:Q38410; GB:M34382; NID:g215661; PIDN:AAA32426.1; PID:g215663
C;Superfamily: phage P1 sim region ORF2 protein
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C;Species: phage Pl
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
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62.5%; Pred. No. 3.2;
tive 3; Mismatches 0; Indels
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Pred. No. 0.1;
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Best Local Similarity 62.9 Matches 5, Conservative

Query Match

Status: preliminary

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Gaps

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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Socosion: G75027
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002217; GB:AE002161; NID:g7189493; PIDN:AAF38406.1; PID:g7189501
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: UNIPROT: Q9UXV2; GB: AJ248288; GB: AL096836; NID: 95458960; PIDN: CAB50661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CP0588 [imported] - Chlamydophila pneumoniae (strain AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Janar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: A81561
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nalson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                          alanyl-tRNA synthetase related protein PAB1190 - Pyrococcus abyssi (strain Orsay)
                  A,Gene: CESP:Y73C8C.6
A,Map postition: 5
A;Introns: 163/2; 313/1
C,Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12
                                                                                                                                              67.2%; Score 39; DB 2; Length 337;
55.6%; Pred. No. 28;
tive 2; Mismatches 2; Indels
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26;
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Pred. No. 32;
1; Mismatches
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Pred. No. 26;
2; Mismatches
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C,Genetics:
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62.5%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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307 HYNVVTF 313
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Matches 5; Conserv
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A;Molecule type: DNA
A;Residues: 1-405 <KAW>
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <REA>
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HYSVFTFC
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C;Genetics:
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                                                                                                                                                                    Rischwarz, E.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfsperger, E.; Su Babo J. 2, 2341-2348, 1983
A;Title: DNA sequence and genome organization of genital human papillomavirus type 6b. A;Reference number: A90975; MUID:84131949; PMID:6321162
A;Accession: D20558
A;Molecule type: DNA
A;Residues: 1-98 <SCH>
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A;Cross-references: UNIPROT:Q9TXW3; EMBL:AF101318; PIDN:AAC69346.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone Y73C8C
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                                                                                                                                                                                                                                                                                                                                                      A, Cross-references: UNIPROT: P06464; GB: X00203; NID: g60955; PIDN: CAA25019.1; PID: g60957 C, Superfamily: papillomavirus B7 protein
C; Keywords: DNA binding; early protein; transcription regulation; zinc finger
F; 58-94/Region: zinc finger CCCC motif
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                                                                   E7 protein - human papillomavirus type 6b
C;Species: human papillomavirus type 6b
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: D20558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Accession: T26919
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Cibate: 29-Oct.1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
CiAccession: T33793
RiBemis, G.; Courtney, L.; Wohldmann, P.
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A;Map position: 4
A;Introns: 217/3; 292/1; 451/3; 556/2; 637/3; 755/3; 823/2; 946/1; 1078/3
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Pred. No. 47;
1; Mismatches 2; Indels
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R, Bemis, G.; Courtney, L.; Wohldmann, P.
submitted to the EMBL Data Library, October 1998
A, Description: The sequence of C. elegans cosmid Y73C8C.
A, Reference number: Z21412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y73C8C.6 - Caenorhabditis elegans
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Pred. No. 7.3;
1; Mismatches
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, January 1998
A;Reference number: 220286
A;Accession: T26919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: 1-1101 <WIL>
A,Cross-references: UNIPROT:062471; EA,Experimental source: clone Y45F10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.0%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
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886 HENVTCCC 894
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Best Local Similarity
Matches 6; Conserv
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Search completed: June 28, 2005, 23:32:14
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209 HYSIIIFC 216
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-184 <STO>
A;Cross-references: UNIPROT;Q92904; GB:BA000008; NID:g8978553; PIDN:BAA98390.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q92904; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD1833
A;Experimental source: strain CWL029
C;Genetics:
A;Gene: CPn0180
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C,Genetics:
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C;Species: human herpesvirus 6
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09312
R;Micholas, J; Martin, M.
J; Wirol. 68, 597-610, 1994
A;Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of PA;Reference number: Z16644; MUID:94118404; PMID:8289364
C;Species: Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: C72110
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, i. Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUD:99206606; PMID:10192388
A;Status: preliminary
A;Wolecule type: DNA
A;Residues: 1-184 <ARN>
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Pred. No. 26;
2; Mismatches 1; Indels
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Pred. No. 26;
2; Mismatches 1; Indels
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A;Molecule type: DNA
A;Residues: 1-71 <NIC>
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62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
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51 HYSVFTFC 58
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51 HYSVFTFC 58
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Best Local Similarity
Matches 5; Conserv
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Nypotherical protein F26D2.1 - Caemorhabditis elegans
C;Species: Caemorhabditis elegans
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C;Species: Caemorhabditis elegans
C;Species: Caemorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21398
A;Accession: T21398
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A;Accession: T21398
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5; Conservative 2; Mismatches 1; Indels
Score 37; DB 2; Length 71;
Pred. No. 18;
                                                                                                                               3; Indels
                                                                                                                               1; Mismatches
      63.8%;
                                                                                                                               5; Conservative
      Query Match
Best Local Similarity
Matches 5; Conserv
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Sequence 57, Appl Sequence 73, Appl Sequence 107, Appl Sequence 107, Appl Sequence 4, Appli Sequence 4, Appli

sequence 4, Appli Sequence 8, Appli Sequence 19, Appli Sequence 29, Appl Sequence 29, Appli Sequence 19, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli

Sequence 12, Appl Sequence 26, Appl Sequence 5, Appli Sequence 8, Appli

Sequence 17, Appl Sequence 7, Appli Sequence 4, Appli

Sequence 12, Appl Sequence 13, Appl Sequence 35, Appl Sequence 1, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli

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Length 9; 0; Indels

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Sequence 9, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.;
; APPLICANT: Mark T.
; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Stephen E.;
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; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Stephen E.;
; APPLICANT: Goldstone, Barring
; CURRENT FILING DATE: 2001-10-19
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; COFTWARE: FASELEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 58; DB 9; I Similarity 100.0%; Pred. No. 1.6e+06; 9; Conservative 0; Mismatches 0;
US-10-432-465-48
US-10-654-200-57
US-10-306-54-107
US-09-306-54-107
US-09-306-54-107
US-09-306-54-107
US-09-306-118A-4
US-09-306-118A-4
US-10-177-310-8
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US-10-654-139-1
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US-10-654-139-1
US-10-657-311-12
US-10-657-311-13-13-1
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ORGANISM: Human papilloma virus
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 9
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                                                                                                 June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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'(gnz 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-871-138-9
US-10-871-138-9
US-10-306-541-62
US-10-306-541-64
US-10-306-541-64
US-10-858-384-16
US-10-654-200-56
US-10-6484-063-14
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                                                                                                                                                                                                                                                             1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                       US-08-170-344-59
58
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Match Length
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                                                                                                   Run on:
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ALIGNMENTS

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APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/333,249
PRIOR APPLICATION NUMBER: 60/333,249
PRIOR PILING DATE: 2001-11-23
NUMBER OF SEC ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEC ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
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US-10-365-908-9

Sequence 9, Application US/10365908

Publication No. US20030170268A1

GENERAL INFORMATION:

APPLICANT: Neefe, John R.

APPLICANT: Biegel, Mark T.

APPLICANT: Siegel, Mark T.

APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Neefe, John R.
APPLICANT: Boux, Leslie J.
APPLICANT: Winnett, Mark T.
APPLICANT: Goldstone, Stephen B.
APPLICANT: Siegel, Marvin
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
FILE REFERENCE: 12071-003001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 58; DB 16;
ilarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US/09/891,823
PRIOR FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,202
PRIOR FILING DATE: 2000-06-26
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENCTH: 9
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; Sequence 9, Application US/10871138
: Publication No. US20040235741A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human papilloma virus
US-10-365-908-9
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US-10-871-138-9
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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Sequence 61, Application US/10306541 Publication No. US20040171081A1

US-10-306-541-61

RESULT 4

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100.0%; Score 58; DB 16; Length 15; 100.0%; Pred. No. 0.0096;
                                            Indels
                                               0; Mismatches
                                                                                                                                                                                                                                                 Sequence 5.1 Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITIE OF INVENTON: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 62
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-306-541-63
Sequence 63, Application US/10306541
Sequence 63, Application US/10306541
Sequence 63, Application US/10306541
SEQUENCE INFORMATION:
APPLICANT: Mittelman, Abraham
TITLE OF INVENTION: Improved Antigens
TITLE OF INVENTION: Improved Antigens
FILE REFRENCE: 12354/4
CURRENT FILING DATE: 2003-11-25
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 63
LENGTH: 15
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), OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment; OTHER INFORMATION: for E7 of HPV US-10-858-384-16
                                                                                                                    APPLICANT: BOURGAULT ULLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: COUNTAIN, FRANCINE
APPLICANT: COUNTAIN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: F8 997012
PRIOR APPLICATION NUMBER: F8 997012
PRIOR APPLICATION NUMBER: F8 997012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALEGALIN Ver: 3.2
SEQ ID NO 16
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 58; DB 17; Length 17; Best Local Similarity 100.0%; Pred. No. 0.011; Matches 9; Conservative 0; Mismatches 0; Indels
                                   Sequence 16, Application US/10858384
Publication No. US20050033025A1
GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 56, Application US/10654200
; Publication No. US20040170606A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-654-200-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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RESULT 9
US-10-858-384-16
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0
                                                                                   Length 15;
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                                                                                                                         0; Indels
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100.0%; Pred. No. 0.0096;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 58; DB 16;
100.0%; Pred. No. 0.0096;
tive 0; Mismatches 0;
                                                                            100.0%; Score 58; DB 16;
100.0%; Pred. No. 0.0096;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                      US-10-306-541-64

Sequence 64, Application US/10306541

Sequence 64, Application US/10306541

Publication No. US20040171081A1

GENERAL INFORMATION:

APPLICANT: Mittelman, Abraham

APPLICANT: Kanduc, Darja

TITLE OF INVENION: Improved Antigens

TILE REFERENCE: 12354/4

CURRENT APPLICATION NUMBER: 105/10/306,541

CURRENT APPLICATION NUMBER: 60/333,249

PRIOR APPLICATION NUMBER: 60/333,249

PRIOR APPLICATION NUMBER: 60/333,249

NUMBER OF SEQ ID NOS: 108

SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 74, Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REPERENCE: 12354/4
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/333,249
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 74
               ; ORGANISM: human papillomavirus US-10-306-541-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-64
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ORGANISM: human papillomavirus
                                                                            Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-10-306-541-74
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TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS FILE REFERENCE: N9739
FILE REFERENCE: N9739
CURRENT APPLICATION NUMBER: US/10/654,200
CURRENT FILING DATE: 2003-09-03
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 56
SEQ ID NO 56
SEQ ID NO 56
SEQ ID NO 56
SEQ ID NO 56
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US-10-484-063-14

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APPLICANT: Jochmus, Ingrid
APPLICANT: Nieland, John
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus il-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
TITLE OF INVENTION: Therapy
FILE REPERENCE: 50125/03601
CURRENT APPLICATION NUMBER: US/10/990,177
FRIOR APPLICATION NUMBER: US/10/900,177
FRIOR APPLICATION NUMBER: DE 19925199.1
FRIOR APPLICATION NUMBER: DE 19925199.1
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-01
WUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
  APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
FILE REFERENCE: N9739
CURRENT APPLICATION NUMBER: US/10/654,200
CURRENT FILING DATE: 2003-09-03
PRIOR PAPLICATION NUMBER: 60/407,795
PRIOR APPLICATION NUMBER: 60/407,795
PRIOR PILING DATE: 2002-09-03
PRIOR APPLICATION NUMBER: 10/457,082
PRIOR APPLICATION NUMBER: 10/457,082
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
PRIOR PILING DATE: 2003-06-06
SOFTWARE: PATENTIN Version 3.2
SEQ ID NOS: 106
SOFTWARE: PATENTIN VERSION 3.2
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100.0%; Score 58; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels
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ORGANISM: Human papillomavirus type 16
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Publication No. US20040171081A1
GENERAL INFORMATION:
APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12334/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-890-526-73
; Sequence 73, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human Papilloma Virus
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Best Local Similarity 100.
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US-10-306-541-107
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US-10-432-465-48

i Sequence 48, Application US/10432465

j Sequence 48, Application US/10432465

j Publication No. US20040091479A1

j GENERAL INFORMATION:
    APPLICANT: Raufmann, Andreas
    APPLICANT: Kather, Angela
    APPLICANT: Kather, Angela
    APPLICANT: Kather, Angela
    APPLICANT: Kather, Angela
    APPLICANT: Father, Angela
    APPLICANT: Father, Angela
    APPLICANT: State of Invention: T-cell Epitopes of the Papillomavirus L1
    TITLE OF INVENTION: Therapy
    TITLE OF INVENTION: Therapy
    TITLE OF INVENTION: Therapy
    FILE REFERENCE: 50125/077001

    CURRENT APPLICATION NUMBER: US/10/432,465
    CURRENT PLING DATE: 2001-11-30
    RELOR APPLICATION NUMBER: D: 10059631.2
    RELOR PILING DATE: 2000-12-01
    NUMBER OF SEQ ID NOS: 116
    NUMBER OF SEQ ID NOS: 116
    NUMBER FE FEARLESEQ for Windows Version 4.0
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Sequence 14, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REPERENCE: UTSC:65002
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR PILING DATE: 2001-07-19
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver: 2.1
; SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human papillomavirus
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US-10-654-200-57
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; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR PILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 107
; LENGTH: 21
; TYPE PRT
; ORCANISM: human papillomavirus
US-10-306-541-107

Query Match
Best Local Similarity 100.0%; Score 58; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: June 29, 2005, 05:18:17 Job time: 117.15 secs

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Run on:

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Sequence 27, Application US/08075541D
Patent No. 6183745
GENERAL: INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERWAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEBE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-9
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Best Local Similarity 100.
Matches 9; Conservative
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US-08-075-541D-27
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                               513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/10365908
| Patent No. 6797491
| GENERAL INFORMATION:
| APPLICANT: Neefe, John R. |
| APPLICANT: Boux, Leslie J. |
| APPLICANT: Winnett, Mark T. |
| APPLICANT: Winnett, Mark T. |
| APPLICANT: Siegel, Marvin PAPLILOMA VIRUS TREATMENT |
| TITLE OF INVENTION: HUMAN PAPLILOMA VIRUS TREATMENT |
| FILE REFERENCE: 12071-003001 |
| CURRENT APPLICATION NUMBER: US/10/365,908 |
| CURRENT APPLICATION NUMBER: US/09/891,823 |
| PRIOR PELLING DATE: 2001-10-19 |
| PRIOR FILING DATE: 2000-06-26 |
| NUMBER OF SEQ ID NOS: 140 |
| SEQ ID NO 9 |
| LENGTH: 9
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100.0%; Pred. No. 4.1e+05
tive 0; Mismatches 0
                                       US-09-637-746-3
US-09-501-097A-7
US-09-900-52A-12
US-09-613-303-12
US-10-267-311-12
US-08-660-165-14
US-09-359-382-12
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US-10-267-311-35
US-09-485-885-1
US-09-485-885-8
            US-10-267-311-8
US-10-201-764-19
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APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBDNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSEE: ADD
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STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
SCHATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN 1993
CLASSIFICATION NUMBER: US/08/075,541D
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/aug1/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
                                                                                                                           US-08-075-541D-29; Sequence 29, Application US/08075541D; Patent No. 6183745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 HYNIVTECC 10
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TINDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-075-541D-28
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GENERAL INFORMATION:
GENERAL
APPLICANT: TINDLE, ROBERT
APPLICANT: FERRANDO, GERMAIN
APPLICANT: FERRANDO, GERMAIN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSES: ADMITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 WARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STREET: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 58; DB 3; Length 12; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DC/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY AGENT INFORMATION:
NAME: NADEL, ALAN S
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTEY FIGURE AND COUNTEY FURNING TO COUNTEY FURNING TO COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UNN-1993
CLASSIFICATION 1424
PRIOR APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
                                                            ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
       PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HYNIVTFCC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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US-08-075-541D-28
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Gaps

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Sequence 25, Application US/08075541D
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STREET: 16
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                                                                                100.0%; Score 58; DB 3; Length 14; 100.0%; Pred. No. 0.0036;
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                                                                                                                                                                                                                                                                                   Sequence 18. Application US/08075541D

Patent No. 6183745

GENERAL INFORMATION:

APPLICANT: TINDLE, ROBERT

APPLICANT: FERNANDO, GERMAIN

APPLICANT: FEAZER, IAN

TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

TITLE OF INVENTION: PERTIDES FOR USE THEREIN

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PENNSYLVANIA
                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 27,363
REPERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 18:
                                                                            Query Match
Best Local Similarity 100.
Matches 9, Conservative
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-29
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Best Local Similarity
Matches 9; Conserva
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US-08-075-541D-18
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APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REPERENCE; WOBL
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APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     STATE: PERMINSTLVANIA
CUUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UN-1993
CLASSITCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BY 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                            E: PANITCH SCHWARZE JACOBS & NADEL, P.C. 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/980,523A CURRENT FILING DATE: 2002-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/FR00/01513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INPORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 17 amin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide
US-08-075-541D-25
                                                                                                                                                                                                                                              CITY: PHILADELPHIA STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HYNIVTFCC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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US-08-075-541D-25

RESULT 6

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SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27,363
BER: 8795-4
                                                                                                                                                      Sequence 3, Application US/08075541D Patent No. 6183745 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-934-915-48
; Sequence 48, Application US/08934915
; Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HMEE-MING
TITLE OF INVENTION: SYNTHEFIC
TITLE OF INVENTION: PAPILLOMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 HYNIVTFCC 16
                                            7 HYNIVTFCC 15
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                                                                                                                                                                                                                                           100.0%; Score 58; DB 4; Length 17;
100.0%; Pred. No. 0.0043;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 58; DB 3; Length 18; Best Local Similarity 100.0%; Pred. No. 0.0045; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAM
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: rc-bos/ms-bos
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UNN-1993
CLASSIETCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/augl/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,365
REGISTRATION NUMBER: 27,365
REGISTRATION NUMBER: 27,365
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION WHEER: FR 99/07012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-075-541D-30
Sequence 30, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 87
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHILADELPHIA
PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                         1 HYNIVTFCC 9
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APPLICANT: TINDE, ROBERT
APPLICANT: FERAZER, IAR
APPLICANT: FERAZER, IAR
APPLICANT: FRAZER, IAR
APPLICANT: FRAZER, IAR
APPLICANT: FRAZER, IAR
APPLICANT: FRAZER, IAR
AUTILE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PETTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANTICH SCHWARZE JACOBŞ & NADEL, P.C.
STREET: PHILADDLEHIA
CITY: PHILADDLEHIA
STREET: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
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Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      STATE: PERNISTLYANIA

STATE: DENISTRYANIA

ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTRANE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27.0503
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Parent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE:
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILABLEPHIA STATE: PHILABLEPHIA STATE: PENNSYLVANIA
                         US/08/934,915
                                                                                                 PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOLICA
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3820
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 155: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27,363
                                                  22-SEP-1997
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REGISTRATION NUMBER: 27,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide US-08-934-915-155
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HYNIVTFCC 9
                                                  FILING DATE: 22 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-075-541D-10
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APPLICANT: DILLINER, JOAKIM
APPLICANT: DILLINER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56, TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR NUMBER OF SEQUENCES: 193 CORRESPONDENCE ADDRESS: ADDRESSER: MASON & ASSOCIATES, P.A. STREET: 1775 V.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: FLORIDA COMPUTER: IBM PC COMPATIONS SOFTWARE: IBM PC COMPATIONS SOFTWARE: MICROSOFT WORD 6.0 CURRENT APPLICATION DATE: 22-SEP-1997 CLASSIPICATION NUMBER: US/08/934,915 FILING DATE: 22-SEP-1997 CLASSIPICATION NUMBER: 07/949,836 FILING DATE: APPLICATION NUMBER: 07/949,836 FILING DATE: ATTORNAY AGENT INFORMATION: NAME: LOUISE A. FOULCH REGISTRATION NUMBER: 37,133, CONTINUED ATE: MADDING MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER: MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER: MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER: MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER: MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER: MAMER: MATER APPLICATION NUMBER: 37,133, CONTINUED ATE: MAMER APPLICATION NUMBER: 37,133, CONTINUED ATE: MATER APPLICATION NUMBER: 37,133, MATER APPLICATION NUMBER: 37,133, MATER APPLICATION NUMBER: 37,133, MATER APPLICATION NU
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ADDRESSER: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 58; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 9; Conservative 0; Mismatches
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US-08-934-915-155
; Sequence 155, Application US/08934915
; Patent No. 592412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: peptide US-08-934-915-48
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COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYNIVTECC 13
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: TIDLE, ROBERT
APPLICANT: FRENANDO, GERMAIN
APPLICANT: FRAZER, IAN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan Proceeding 1.25
CURRANE: PatentIn Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATPONEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27.363
REGISTRATION NUMBER: 27.363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
           APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION NUMBER: US/08/075,541D
PRIOR APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REGISTRATION NUMBER: 27,363
REFERENCE/POCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2991
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27,363
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
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US-08-075-541D-20
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US-09-980-177A-73

Sequence 73, Application US/09980177A

Patent No. 6838084

GENERAL INFORMATION:

APPLICANT: JOCHMUS, Ingrid

APPLICANT: Meland, John

TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and

TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and

TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and

TITLE OF INVENTION: Papilloma Virus LI-Protein and Use Thereof in Diagnosis and

TITLE OF ILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: DE 19925199.1

PRIOR APPLICATION NUMBER: PE 1992-199.1

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 77

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 20

TENGTH: 20
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| Patent No. 6183745
| GENERAL INFORMATION:
| APPLICANT: FINDLE, ROBERT
| APPLICANT: FEAZER, IAN
| TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
| TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
| NUMBER OF SEQUENCES: 56
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
| STREET: 1601 MARKET STREET, 36TH FLOOR
| CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 58; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                       100.0%; Score 58; DB 3; Length 20; 100.0%; Pred. No. 0.005;
                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy Disk
COMPUTER: PB PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
20 amino acids
                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                       single
                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HYNIVTECC 9
                                                          linear
                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                           US-08-075-541D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-075-541D-47
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Matches 9; Conservative 0; Mismatches 0; Indels
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INPORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: peptide
WOLECULE TYPE: peptide
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Search completed: June 28, 2005, 23:37:54 Job time: 17.05 secs

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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404701; AAL01359-1.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
MEDLINE=21846229; PubMed=11857370;
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Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404700; AAL01357.1; ---
GO, GO:0042025; C:host cell nucleus; IEA.
GO, GO:0003677; F:DNA binding; IEA.
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruees; deDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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EMBL, AF404703; AAL01363.1; -0.00 GO: GO:0042025; C:host cell nucleus; IEA GO; GO:0003677; F:DNA binding; IEA. Pfam; PF00518; E6; 1.
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SEQUENCE FROM N.A.
MEDLINE=21846229; PubMed=11857370;
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Matches 9; Conservative
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EMBL; AF404699; AAL01355.1;
GO; GO:0003677; F:DNA binding; IEA.
PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL, AF404696; AAL01349-1. -
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein (Fragment).
Human papillomavirus type 16.
Virusee; deDNA viruses, no RNA stage; Papillomaviridae;
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130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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(TrEMBLrel. 25, Last annotation update)
                                                                            100.0%; Score 51; DB 2; 100.0%; Pred. No. 0.38;
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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Conservative 0
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Conservative 0
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002)
EMBL; AF404702; AAL01361.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (Fragment).
Es protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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100.0%; Pred. No. 0.41;
iive 0; Mismatches 0.
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   0; Mismatches
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MEDLINE=21846229; PubMed=11857370;
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Matches 9; Conservative
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Matches 9; Conservative
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).

EMBL, FAF04694; AL01145.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.
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                          DB 2; Length 130;
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                                                                                      0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
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Pred. No. 0.4;
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GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNA binding; IEA.
Pfam; PP00518; BG; 1.
                              100.0%; Score 51; 100.0%; Pred. No.
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MEDLINE=21846229; PubMed=11857370;
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                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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NCBI_TaxID=10581;
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0; Gaps

Length 143; 0; Indels

ö Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(202).
EMBL; AF404698; AAL01353.1;
GO; GO:00042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA. Gaps ö 100.0%; Score 51; DB 2; Length 143; 100.0%; Pred. No. 0.41; 0; Indels 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; Papillomavirus. 143 AA; 17274 MW; SFBOF7E1EC6DBA82 CRC64; PRT; 143 AA. 0; Mismatches

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Jenison S.A.;
"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
J. virol. 69:7743-7753(1995).
                                                                                                                                                                                                                                                                                                         MEDLINE-96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51, DB 2; Length 151; 100.0%; Pred. No. 0.43; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farmer A.D.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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05-JUL-2004 (TEMBLrel. 27, Last annotation update)
Es protein.
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APÉM, PF00518; B6; 1.
SEOUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
                                                                                                       076TSO;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
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NCBI_TaxID=10566;
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MEDLINE-9747474; PubMed=9292007;

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Beth-Giraldo E., Giraldo G.,

"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.",

Gen. Virol. 78:2199-2208(1997).

EMBL, AF003015; AAB70732.1; -.

GO, GO:0003677; F.DAst cell nucleus, IEA.

InterPro; IPR001334; E6.
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SEQUENCE FROM N.A.

MEDILIS-97437474; PubMed=9292007;

Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

Beth-Giraldo E., Giraldo G.;

"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";

Gen. virol. 78:2199-2208(1997).

EMBL. AROBOJOG, ABAD7733.1;

GO; GO:0003076; F:DNA binding; IEA.

InterPro; IPR001334; E6.
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                                                                                                                                                                                              E6 protein.
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6DBA CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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139 CCRSSRTRR 147
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MEDLINE-20112892; PubMed=10644829;
A MEDLINE-20112892; PubMed=10644829;
A van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
van Duin M., Snijders P.J., Wessen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
T. Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).

R. EMBL; AF465197; AAO15691.1;
GO, GO:0042025; CAB45118.1;
R. GO; GO:0003677; F.DNA binding; IEA.
R. GO; GO:0003677; F.DNA binding; IEA.
R. InterPro; IPR001334; E6.
R. PFam; PR00318; E6: 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 oncoprotein (E6 protein).
Human papillomavirus type 16.
Viruses; dsNNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 21:28:02; Search time 11.05 Seconds Run on:

(without alignments)
78.367 Million cell updates/sec

Title: Perfect score:

US-08-170-344-58 51 1 CCRSSRTRR 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 3 2 ::

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		de			SUMMARIES	-
Result No.	Score	Query Match	Length	DB		Description
	51	100.0	158	-	Wewles	protein E6 - human
7	38	74.5	86	~	154366	D4 r
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φ	36	70.6	214	~	D84899	hypothetical prote
7	35		114	N	D72600	
œ	38	68.6	152	~	T34649	hypothetical prote
6	35	9.89	229	~	S60454	>
	35	9.89	303	7	AE3504	tryptophan synthas
I	35	9.89	371	7	G97530	probable zinc-bind
12	35	9.89	414	~	T45639	hypothetical prote
13	35	9.89	640	7	T08179	
14	35	9.89	826	~	C96694	hypothetical prote
15	34	66.7	48	7	S29973	- 1
16	34	66.7	141	~	C70575	PPE
17	34	66.7	222	~	T26209	cal
18	34	66.7	321	~	A58458	isopenicillin N sy
19		66.7	409	N	C97527	hypothetical prote
20	34	66.7	438	~	T12494	hypothetical prote
21	34	66.7	811	~	E97040	v
22	34	66.7	1548	~	S34583	serine proteinase
23	33.5	65.7	49	7	800228	protamine - horse
24	33.5	65.7	49	~	S02007	protamine I - rabb
25	m.	'n.	51	7	HSMSS1	protamine - mouse
56	۳.	65.7	51	N	S03997	- 1
27	۳.	65.7	206	~	T01788	aminoglycoside 6'-
28	33.5	65.7	451	N	H84479	probable PttA-like
53	33	64.7	105	7	T27719	hypothetical prote

dopamine D4 receptor - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Accession: I54366

R;Nothen, M.M.; Cichon, S.; Hemmer, S.; Hebebrand, J.; Remschmidt, H.; Lehmkuhl, G.; Pour Hum. Mol. Genet. 3, 2207-2212, 1994

A;Fitle: Human dopamine D4 receptor gene: frequent occurrence of a null allele and observaleties: D4. Speciession: I54366; MUID:95187162; PMID:7881421

A;Stetus: preliminary; translated from GB/EMBL/DDBJ

A;Nolecule type: mRNA

En/Spm-like transp	En/Spm transposon	hypothetical prote	hypothetical prote	En/Spm transposon	hypothetical prote	O-sialoglycoprotei	glutamyl-tRNA redu	lysine-tRNA ligase	mucin-like peptide	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	serum albumin - se	transcription regu
C84502	F84502	T48319	T27660	H84492	T24054	H69056	T10186	S14834	A42112	T25338	T04571	T23229	T21891	S27941	AD3622
127 2	307 2	335 2	337 2	400 2	433 2	534 2	552 2	576 2	837 2	870 2	889 2	905 2	1059 2	1423 1	95 2
64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	63.7
33	33	33	33	33	33	33	33	33	33	33	33	33	33	33	32.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-188 «SEE»
A; Residues: 1-189 «SEE»
A; Residues: 1-180 «SEE»
A; Residues: 1-180 «SEE»
A; Residues: 1-180 «SEE»
A; Residues: 1-180 «SEE»
A; Remnedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A megative element in the human poapillomavirus type 16 genome acts at the level
A; Reference number: Z17014; MUID:91162763; PMID:1848319
A; Recession: T10427
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protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
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A,Molecule type: DNA
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C,Genetics: C,Genetics: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
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                                                                                                              R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G. Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; WUID:85246220; PMID:2990099
A;Accession: A03682
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C,Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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Wypothetical protein At2946160 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: O2-Reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (C;Accession: D84899 (C;Accession: D84899 (C;Accession: D84899 (C;Accession: D7: Fulin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Nature 402, 761-768, 1999 (Cronin, L.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Reference number: A84420; MUID:20083487; PMID:10617197 (A;Abidopsis thaliana. A;Accession: D84899 (A;Atatus: preliminary A;Anolecule type: DMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: UNIPROT:082353; GB: AE002093; NID: 93702333; PIDN: AAC62890.1; GSPDB:GNK
       S-receptor kinase (EC 2.7.1.-) T26M18.110 precursor - Arabidopsis thaliana
N.Alternate names: KI domain interacting kinase 1-11ke protein; protein T26M18.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T09349
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, A;Reference number: Z16650
A;Accession: T09349
A;Molecule type: DNA.
                                                                                                                                                                                                                                                      A;Residues: 1-849 <BEV>
A;Cross-references: UNIPROT:Q9T058; EMBL:AL078606; ATSP:T26M18.110; GSPDB:GN00062
A;Experimental source: cultivar Columbia; BAC clone T26M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.5%; Score 37; DB 1; Length 849; 77.8%; Pred. No. 1e+02; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.6%; Score 36; DB 2; Length 214; 75.0%; Pred. No. 63; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-214 <STO>
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A;Map position: 2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F2A19.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20.Apr-2000 #sequence_revision 20.Apr-2000 #text_change 09-Jul-2004
C;Accession: T47947
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet submitted to the Protein Sequence Database, January 2000
A;Reference number: 224480
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-212 dDEH>
A;Residues: 1-212 dDEH>
A;Residues: 1-212 dDEH>
A;Experimental source: cultivar Columbia; BAC clone F2A19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted to the EMBL Data Library, April 1995
A;Reference number: Z19702
A;Accession: T23167
A;Accession: T23167
A;Statues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-389 <WIL>
A;Residues: 1-389 <WIL>
A;Cross-references: UNIPROT:Q21081; EMBL:Z49068; PIDN:CAA88855.1; GSPDB:GN00020; CBSP:KG
C;Genetics:
A,Residues: 1-98 <RES>
A;Cross-references: UNIPRROT:Q16303, GB:S76942, NID:g913280; PIDN:AAB33728.1; PID:g913281
A;Cross-family: vertebrate rhodopsin
C;Keywords: neurotransmitter receptor
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23167
R;Sims, M.
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Pred. No. 44;
1; Mismatches 1; Indels
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66.7%; Pred. No. 63;
tive 2; Mismatches 1; Indels
                                                                                                                    Length 98;
                                                                                                                                                                  2; Indels
                                                                                                                      2;
                                                                                                                 Score 38; DB 2; Pred. No. 19; 0; Mismatches
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F;132-183/Domain: RING finger homology <RRN>
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A;Map position: 2
A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3
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77.8%;
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                     7; Conservative
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Best Local Similarity
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Best Local Similarity
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A, Map position: 3
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RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. SGI. UG.S.A. 99, 443-448, 2002
A.J. Acad. SGI. UG.S.A. 99, A13-448, 2002
A.J. The genome sequence of the facultative intracellular pathogen Brucella melitensi A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable zinc-binding alcohol dehydrogenase [imported] - Agrobacterium tumefaciens (straj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A,Reference number: A97359, MUID:21608551, PMID:11743194
A,Accession: G97530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: I
C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase
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C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: 697530
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
                                                                                                                                                                                                         tryptophan synthase (EC 4.2.1.20) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002 C;Accession: AE3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: AGR C 2601
A;Map position: circular chromosome
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE008917; PIDN: AAL53200.1; PID: g17984074; GSPDB: GN00190
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 85.7%; Pred. No. 1.1e+02; 6; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain 16M
                                                    60 CCRASRSAK 68
            1 CCRSSRTRR 9
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Matches 6, Conserv
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A; Molecule type: DNA
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hypothetical protein APE1268 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72600
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; NA; Fes. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
A;Molecule type: DNA
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C;Species: Zea mays (maize)
C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 860454; 849585
R;Chevalier, C; Bourgeois, E.; Pradet, A.; Raymond, P.
R;Chevalier, C; Bourgeois, B.; Pradet, A.; Raymond, P.
A;Title: Molecular cloning and characterization of six cDNAs expressed during glucose st A;Reference number: 860453; MUID:95359405; PMID:7632917
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9YC19; DDBJ:AP000061; NID:g5104821; PIDN:BAA80258.1; PID:d1
A;Experimental source: strain K1
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R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1999
A;Reference number: 221551
A;Accession: T34649
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A;Cross-references: UNIPROT:Q41855; EMBL:X82617; NID:g575425; PIDN:CAA57939.1; PID:g5754
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Experimental source: strain A3(2)
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Pred. No. 63;
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Best Local Similarity 55.6%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 75;
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Best Local Similarity 85.
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Best Local Similarity 75.0
Matches 6; Conservative
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C;Genetics:
A;Gene: SCOEDB:SC1A11.02c
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A, Gene: APE1268
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Length 826;

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Rioliva, R. Submitted to the EMBL Data Library, December 1991
A;Reference number: 829972
A;Accession: 829973
A;Accession: 829973
A;Accession: 829972
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A;Residues: 1-48 < OLH>
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C;Species: Cavia porcellue (guinea pig)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S29973; S29972
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C,Genetics:
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C;Superfamily: sperm histone
C;Keywords: chromosomal protein; DNA binding; DNA condensation;
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55.6%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity
Matches 5; Conserv
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            A; Gene: F1019.10
A; Map position: 1
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Crosi-references: UNIPROT:Q9FZH7; GB:AE005173; NID:g9755453; PIDN:AAF98214.1; GSPDB:GN
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C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08179
R;Gloeckner, G.; Beck, C.F.
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R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; submitted to the Protein Sequence Database, November 1999
A;Reference number: 223010
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A; Residues: 1-640 <GLO>
A; Cross-references: UNIPROT: Q96397; EMBL: U73817; NID: g1644369; PID: g1644370
C; Genetics:
A; Gene: LRG5
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A;Note: F13112.80
C;Superfamily: Arabidopsis thaliana hypothetical protein At2g23160
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66.7%; Pred. No. 1.8e+02;
tive 0; Mismatches 3; Indels
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Pred. No. 1.4e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                     A; Accession: T45639
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-414 <CHO>
A; Cross-references: UNIPROT: Q9SD70; EMBL: AL133292
A; Experimental source: cultivar Columbia; BAC clone F13112
C; Genetics:
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Best Local Similarity 71.4%;
Matches 5; Conservative
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CCKSSKT 155
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nucleosome core; spermatc

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Gaps

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3; Indels

Score 34; DB 2; Length 48; Pred. No. 54; 0; Mismatches 3; Indels

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APPLICANT: INFORMATION:
APPLICANT: Babinowitz, Joshua D.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Schweizer, Johannes
APPLICANT: Arbor Vita Corporation
ITILE OF INVENTION: Cells
FILE OF INVENTION: Cells
FILE OF INVENTION: Cells
FILE REFERENCE: 020054-0011308
CURRENT FILING DATE: 2004-09-10
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 2000-11-28
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
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PRIOR PILING DATE: 1999-10-21
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PRIOR PILING DATE: 1999-12-13
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APPLICATION NUMBER: US 60/182,296
FILING DATE: 2000-02-14
APPLICATION NUMBER: US 60/196,267
FILING DATE: 2000-04-11
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Sequence 27, Appl
Sequence 2, Appli
Sequence 16, Appli
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Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
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                                                                                                                                                                                                                             June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:+
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.ppp:+
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:+
| Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:+
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:+
| Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:+
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:+
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-899-771-4
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 44, Application US/10476570

Sequence 44, Application No. US20040170644A1

Sequence 47, Application No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLERE, Bernard

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: BOURGAULT-VILLADA, Isabelle

APPLICANT: GUILLET, Jean-Gerah

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

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TITLE OF INVENTION: Mixture of Peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of Peptides derived from E7

TITLE OF INVENTION: Mixture of Peptides derived from E6 and/or E7

TITLE OF INVENTION: Mixture of Peptides derived from E7

TITLE OF INVENTION: Mixture of Peptides derived from E7

TITLE OF INVENTION:
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Publication No. US20030143743A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear
TITLE OF INVENTION: Polynuclecides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 543
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 513
LENGTH: 20
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                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: HPV16 E6 C-terminal
US-10-938-249-513
                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: artificial sequence
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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LENGTH: 24
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Sequence 20.45

Fublication No. US20050048467A1

GENERAL INFORMATION:

APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORTOLERO-LUNA, GUILLERMO

APPLICANT: FOLLEN, MICHELE

TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT PAPLICATION NUMBER: PCT/US02/23198

PRIOR APPLICATION NUMBER: PCT/US02/23198

PRIOR FILING DATE: 2004-01-16

PRIOR FILING DATE: 2002-07-19

PRIOR FILING DATE: 2001-07-20

NUMBER: OF SEQ ID NOS: 27

SEQ ID NO 20

LENGTH: 151

SEQ ID NO 20

LENGTH: 151
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; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT PILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
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                                                                                                                                  Query Match
100.0%; Score 51; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
LENGTH: 151
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-177-390-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
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SEQ ID NO 27
LENGTH: 151
                                                                                                                                                                                                                                                                                                       139 CCRSSRTRR 147
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146 CCRSSRTRR 154
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET JEAN-GERARD
APPLICANT: GUILLET JEAN-GERARD
APPLICANT: GUILLET JEAN-GERARD
APPLICANT: GONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REPERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 1099-06-03
PRIOR FILING DATE: 1999-06-03
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                            Length 151;
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; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Lewin, David A.;
; APPLICANT: Lewin, David A.;
; APPLICANT: Lewin, David A.;
; APPLICANT: Cooplexes and Methods of Using Same;
; TITLE OF INVENTON: Complexes and Methods of Using Same;
; TITLE OF INVENTON: Complexes and Methods of Using Same;
; TITLE OF INVENTON: Complexes and Methods of Using Same;
; TITLE OF INVENTON: Complexes and Methods of Using Same;
; TITLE OF INVENTON: Complexes and Methods of Using Same;
; PILE REFERENCE: 21402-559
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LEMOTH: 158
                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10858384; Publication No. US20050033025A1; GENERAL INFORMATION: APPLICANT: CHOPPIN, JEANNINE
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                         Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 2
LENGTH: 158
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Best Local Similarity 100.
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1 CCRSSRTRR 9

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US-10-472-724-2
US-10-472-724-2
Sequence 2, Application US/10472724
PUBlication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
TITLE OF INVENTION: WOMBER: US/10/472,724
CURRENT APPLICATION UNMER: US/10/472,724
CURRENT FILING DATE: 2003-03-12
PRIOR PEPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MACFALLAN, RODERICK I.
APPLICANT: MACFALLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
TITLE OF INVENTION NUMBER: U$/09/367,309A
CURRENT PILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN OF SEQ ID NOS: 6
SOFTWARE: PALENTIN OF SEQ ID NOS: 6
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
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US-10-000-903-4
; Sequence 4, Application US/10000903
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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271 CCRSSRTRR 279
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ORGANISM: Homo sapien
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Sequence 4, Application US/10899711

Sequence 4, Application No. US20050031638A1

GENERAL INFORMATION:

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Gerard, Catherine Marie Ghislaine

TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

TITLE OF INVENTION: And Fusion Proteins Adjuvanted with a CpG Oligonucleotide

CURRENT APPLICATION NUMBER: US/09/581,976

PRIOR FILING DATE: 2000-6-20

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 28

SOCTHWARE: FRREEE FRREEE FRREEE FRREEE FRREEE FRIEND VALIDANCE FRIEND VALIDANCE FROM THE PRIOR FILING DATE: 1999-12-34
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100.0%; Score 51; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 9; Conservative 0; Mismatches 0; Indels (
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Londardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: US/10/000,903
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PLING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PLING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PastSEQ for Windows Version 3.0
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 273
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US-10-899-771-4
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APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Dalemans, Wilfried L.J.

TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide

FILE REFERENCE: B45124

CURRENT APPLICATION NUMBER: US/09/581,976

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR APPLICATION NUMBER: DCT/EP98/08563

PRIOR PILING DATE: 1998-12-18

PRIOR PILING DATE: 1999-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastsEQ for Windows Version 3.0

SEQ ID NOS: 28
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OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
OTHER INFORMATION: 16)
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                                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT PILING DATE: 2001-10-01
FRIOR APPLICATION NUMBER: PT/REP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
Sequence 10, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 10, Application US/10899771; Publication No. US20050031638A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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RESULT 14

RESULT 12 US-10-000-903-10

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Sequence 6, Application US/10899771
; Sequence 6, Application US/10899771
; Sequence 6, Application VIS20050031638A1
; GENERAL INFORMATION:
    APPLICANT: Dalemanns Wilfried L.J.
    APPLICANT: Gerard, Catherine Marie Ghislaine
    TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
    TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
    TITLE OF INVENTION WINDER: US/10/899,771
    TITLE OF INVENTION NUMBER: US/09/581,976
; PRIOR APPLICATION NUMBER: PCIVEP98/08563
; PRIOR FILING DATE: 2000-06-20
; PRIOR FILING DATE: 1998-12-18
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FRSESEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
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100.0%; Pred. No. 7.5;
vative 0; Mismatches 0; Indels (
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JOSTIC GOOD STATE OF THE PARTICAL OF SEQUENCE 6, APPLICANT: BUILD SEQUENCE 6, APPLICANT: BUILD SEQUENCE OF STATE OF SEQUENCE OF STATE OF SEQUENCE OF STATE OF SEQUENCE OF STATE OF SEQUENCE OF STATE OF SEQUENCE OF STATE OF SEQUENCE OF S
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapien
US-10-000-903-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCRSSRTRR 9
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252 CCRSSRTRR 260

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Search completed: June 29, 2005, 05:18:16 Job time : 116.15 secs

Lipis bade Blank (nebto)

Wed Jun

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ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGIGTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 813-538-3820
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; MOLECULE TYPE: peptide
US-08-934-915-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-934-915-167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Applisaciones 12, Applisaciones 12, Applisaciones 10, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8615, Ap
Sequence 30052, A
Sequence 25071, A
Sequence 35, Appl
Sequence 29444, A
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Sequence 30039, A
Sequence 36971, A
Sequence 52188, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Appl
Sequence 381, App
Sequence 33122, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 29076,
Sequence 21156,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12930,
                                                                                                                                                                      June 28, 2005, 21:33:36 ; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
version 5.1.6
- 2005 Compugen Ltd.
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US-08-316-238B-3

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US-08-860-165-12

US-09-359-382-12

US-09-359-382-12

US-09-359-382-10

US-09-359-382-10

US-09-485-885-10

US-09-485-885-10

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US-09-252-991A-33122

US-09-252-991A-33122

US-09-252-991A-33039

US-09-252-991A-30039

US-09-270-76-52188

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US-09-252-991A-30039

US-09-252-991A-30059
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US-09-252-991A-2944
US-09-252-991A-29076
US-09-252-991A-21156
US-09-489-039A-12930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
   GenCore
Copyright (c) 1993
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Maximum DB seq length: 2000000000
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51
1 CCRSSRTRR 9
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Match Length
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No.
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Length 21;

Score 51; DB 2; Pred. No. 0.22;

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27914, A
26229, A
72, Appl
73, Appl
26200, A
24413, A
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24140,
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Sequence
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APPLICANT: DILLARE, LENA
APPLICANT: DILLARE, LENA
APPLICANT: DILLARE, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARMATER
STATE: FLORIDA
CONDUTRY: US.A.
COMPUTER: TAN PC COMPATIALDIA
COMPUTER: TAN PC COMPATIALDIA
OPERATING SYSTEM: WINGOWS 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 2-SEP-1997
CLASSIFICATION NUMBER: 07/949,836
FILING DATE: PRODUCT OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF THE STANDARD OF
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US-10-141-645-73
US-10-141-645-73
US-10-141-645-73
US-09-222-991A-26200
US-09-222-991A-2413
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US-09-252-991A-2162
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Patent No. 5932412
GENERAL INFORMATION:
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that is Associated with an
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                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 1; Length 162; 100.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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ZIP: 20120-3400

CONFUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REPERENCE/DOCKET NUMBER: UNME-0001
TELECHOME: (703) 817-9453
TELEPHONE: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrent No. 56/2000.
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Permenter A.
APPLICANT: Preveloping
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Wethods and a Diagno TITLE OF INVENTION: Distinguishing a Sub TITLE OF INVENTION: Increased Risk of De TITLE OF INVENTION: Cervical Cancer NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: Jagtiani & Associates
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPHONE: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Jagtiani & Associates
6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/08316239B
; Patent No. 5679509
                                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                        LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserva
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STATE:
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Sequence 3, Application US/08316239B

Barent No. 5679509

GENERAL INFORMATION:
APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOUNGAULT VILLADA, ISABELLE
APPLICANT: BOUNGAULT VILLADA, ISABELLE
APPLICANT: GONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
APPLICANT: FERRIES, ESTELLE
APPLICANT: FRENCE: WOBLAO INS
TITLE OF INVENTION: PROTEINS OF HVY, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REPERENCE: WOBLAO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
FRIOR FILING DATE: 2000-05-31
FRIOR FILING DATE: 1999-06-03
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       Gaps
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    Indels
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ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
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  Mismatches
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30-SEP-1994
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STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                         Sequence 2, Application US/09980523A
Patent No. 6783763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human Papillomavirus
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
  9; Conservative
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                                                                                             CCRSSRTRR 17
                                                 CCRSSRTRR 9
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                                                                                                                                                                                        US-09-980-523A-2
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  Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
                                                                                                                                                                                                                                                                                     APPLICANT: FRAZEK, IAA

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130

CURRENT APPLICATION NUMBER: US/08/860,165A

CURRENT FILING DATE: 1997-09-22

EARLIER PELLING DATE: 1997-09-22

EARLIER FILING DATE: 1995-12-20

EARLIER PELLING DATE: 1994-12-20

MUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

SEQ ID NO 10

LINGTH: 266
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Glizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 01722/1018
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
FEARLIER PELING DATE: 1999-07-23
FEARLIER PILING DATE: 1999-102-20
FEARLIER PILING DATE: 1999-12-20
FEARLIER APPLICATION NUMBER: AU PNO157/94
FEARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 10
SEQ ID NO 10
FEARLIER PLENG DATE: 2.0
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                                                                                                                                                        Sequence 10, Application US/08860165A Patent No. 6004557
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Patent No. 6306397
GENERAL INFORMATION:
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: EDMARDS, SLITLING JOHN
APPLICANT: COX, JOHN COOPER
APPLICANT: WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                            Sequence 12, Application US/08860165A

Fatent No. 6004557

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: PRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 17227/130

CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER PILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12

LENGTH: 172

TYDE: DOT
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Sequence 12, Application US/09359382

Patent No. 6306397

GENERAL INFORMATION

APPLICANT: EDWARDS, Stirling John

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: WEBB, Elizabeth Ann

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REPERENCE: 01722/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT APPLICATION NUMBER: US/09/359,382

EARLIER FILING DATE: 1999-07-23

EARLIER PILING DATE: 1999-07-23

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-09-12-20

EARLIER FILING DATE: 1997-09-12-20

EARLIER PILING DATE: 1997-09-12-20

EARLIER FILING DATE: 1997-01-12-20
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100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 100.
Matches 9; Conservative
                                           146 CCRSSRTRR 154
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                                                                                                                             RESULT 5
US-08-860-165-12
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LENGTH: 172
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100.0%; Score 51; DB 3; Length 371; 100.0%; Pred. No. 2.3;
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                                                       GENERAL INFORMATION:

APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCTEP98/05285
PRIOR APPLICATION NUMBER: PCTEP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR STILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENUREAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFRENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
FRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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Application US/09485885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09485885
Patent No. 6342224
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Matches 9: Conservative
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Matches 9; Conservative
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
                                                  GENERAL INFORMATION:
     Sequence 10, Appl:
Patent No. 634222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-485-885-10
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US-09-485-885-6
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APPLICANT: MACFARLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 51; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 51; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE RFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
FRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
NUMBER: OF SEQ ID NOS: 23
SOFTWARE: FRASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 266

TYPE: PRT

CONTROL PRT

CONTROL Human papillomavirus type 16

MS-09-367-309A-1
                                                                                                 RESULT 9
18-08-367-309A-1
Sequence 1, Application US/09367309A
Patent No. 6428807
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146 CCRSSRTRR 154
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LENGTH: 273
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US-09-485-885-10
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US-09-485-885-4
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Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN.1
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR TITLE OF INVENTION: DIGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 3; Length 390; illarity 100.0%; Pred. No. 2.3; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
              APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5.
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
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ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium leprae
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INFORMATION FOR SEQ ID NO: 381:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 171 amino acids
TYPE: amino acid
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STATE: MASSACHUSETTS
COUNTRY: USA
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US-09-485-885-14
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Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196,136
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ERNGTH: 230
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Pred. No. 43;
0; Mismatches 1; Indels
                   DB 4; Length 171;
                 Score 44; DB 4
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                            Sequence 33122, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 28, 2005, 23:37:54
Job time : 17.05 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33122
               86.3%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
Query Match
Best Local Similarity 88.9.
....nes 8; Conservative
                                                                                                                                          4 CCRSSYTRR 12
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US-09-252-991A-33122
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Q9wmp3 Q9wmp4 Q9wmp5 P03126

09w931

29wmp2

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SEQUENCE FROM N.A.
Alvarez-Salas L.M., Wilczynski S.P., Burger R.A., Monk B.J.,
DiPaolo J.A.;
Polymorphism of the HPV-16 E6 gene of cervical carcinoma.";
Int. J. Oncol. 7:261-266(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 50; DB 2; Length 20; 100.0%; Pred. No. 0.099;
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Alvarez-Salas L.M., DiPaolo J.A.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 036978;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
Mutant early transforming protein E6 (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein (Fragment).

Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

NCBI_TaxID=10581;
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20 AA; 2357 MW; 23DA169D44DF4932 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA
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NCBI_TaxID=10581;
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Matches
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404692; AAL01342.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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WEDLINE-2108-6229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
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E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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(TrEMBLrel. 19, Last sequence update)
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EMBL, AF404703, AAL01363.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

Pfam; PF00518; E6; 1.

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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-874[2002].
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Watts K.J. Thompson C.H., Cossart Y.B., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404700; AAL01357.1; ---
GO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404701; AAL01359.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                            June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-359-382-12
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US-09-359-382-10
US-09-367-309A-1
US-09-485-885-14
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US-09-485-885-14
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US-09-252-991A-25612
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50313, A 29249, A 9099, Ap 532, App 532, App	Sequence Sequence Sequence Sequence Sequence	US-09-270-767-50313 US-09-252-991A-2249 US-09-949-016-9099 US-09-439-313-532 US-09-636-215-532	44464	245 248 287 292 292		4444444	######################################	ਧਾਧਾਧਾਧਾ
641, App 31933, A 35096, A	Sequence Sequence Sequence	US-09-198-452A-641 US-09-252-991A-31933 US-09-270-767-35096	444	210 218 245	ش هن هن		38 39 35 35 35 35	m m 4*
32518, A	Sequence	US-09-252-991A-32518	4	197	ω.		, m) m
32502, A	Sequence	US-09-252-991A-32502	4 4	168	ω α	6 4 4	35 35	cu c
20715, A	Sequence	US-09-252-991A-20715	4	167	89.		e	e
54087, A 17724, A	Sequence	US-09-270-767-54087 US-09-252-991A-17724	4 4	44 147	œ. œ.	64 64	mm	m m
38870, A	Sequence	US-09-270-767-38870	4	44	8		31 35	m
	Sequence	US-09-252-991A-30039	4	953	7	66.7	36 36	m
18070, A	Sequence	US-09-252-991A-18070	4	329	7		36	~
1276, Ap	Sequence	US-09-198-452A-1276	4	84	۲.	99	28 36	7

ALIGNMENTS

Length 21;

100.0%; Score 54; DB 2; 100.0%; Pred. No. 0.38;

Gaps

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S-08-316-239B-4
Sequence 4, Application US/08316239B
Sequence 5. Application US/08316239B
Sequence 7. Application US/08316239B
Sequence 7. Sef03508
GENERAL INFORMATION:
APPLICANT: Wheeler, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Litimation a Subset of HPV that is Associated with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Parmenter, Cheryl A. TITLE OF INVENTION: Methods and a Diagnostic Aid for TITLE OF INVENTION: Methods and a Diagnostic Aid for TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
ZIP: 20120-3400
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35.205
REFERENCE/DOCKET NUMBER: UNWE-0001
TELECOMMUNICATION INFORMATION:
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STREET: 6126 Rocky Way Court
CITY: Centreville
                                                     TELEFAX: (703) 817-9453
TELEFAX: (703) 803-9387
INPORMATION FOR ESQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY
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NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                        TOPOLOGY: not relevar
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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STRANDEDNESS: no
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APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
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APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUNGAULT VILLADA, ISABELLE
APPLICANT: GUNGAU, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPTTOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR OF INVENTION: PRICAL TO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-03
Gaps
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Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
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Mismatches
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30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Jagtiani & Associates
6126 Rocky Way Court
                                                                                                                                                                                        US-09-980-523A-2
, Sequence 2, Application US/09980523A
, Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/08316239B
; Patent No. 5679509
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ATTORNEY/AGENT INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 158
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Best Local Similarity 100.
Matches 9; Conservative
9; Conservative
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                                                                                              CMSCCRSSR 14
                                              1 CMSCCRSSR 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-316-239B-3
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MEDLINE=21846229; PubMed=11857370; MEDLINE=21846229; PubMed=11857370; MEDLINE=21846229; PubMed=11857370; MEDLINE=21846229; PubMed=11857370; Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868=874(2002). Cancer 97:868=874(2002). Go:0042025; C:host cell nucleus; IEA. Go:0003677; F:DNA binding; IEA. Pfont BE: Cell Control Co
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
                        Q9wmp3
Q9wmp4
Q9wmp5
Q9mmp5
Q8dm0
Q8dh0
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Q8drd5
Q8drd6
Q8drd6
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0919B4;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
01-Oct-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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100.0%; Pred. No. 0.81;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AA
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                     G9WMP3
G9WMP4
G9WMP4
G9WMP3
VB6_HPV16
G8GNFV0
G8GHP0
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G8GRD5
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Conservative 0
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NCBI_TaxID=10581;
Papillomavirus
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Q919D6;
01-DEC-2001
01-DEC-2001
  Query Match
Best Local S
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Q919D6
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                                                                                                                                                                         June 28, 2005, 21:24:19; Search time 55.1 Seconds (without alignments) 83.643 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404696, AAL01349.1;
GO; GO:0003677; F:DNA total nucleus; IEA.

Fram, PRO0518; E6; 1.
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EMBL, AF404699; AAL01355.1; "Cossart S.C., Cossart S
                                                                                  100.0%; Score 54; DB 2; Length 130; 100.0%; Pred. No. 0.98;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OFC-2003 (TrEMBLrel. 25, Last annotation update)
01-OFC-2003 (Fragment)
Human papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
                                         130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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    Pfam; PF00518; E6; 1.
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NCBI_TaxID=10581;
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SEQUENCE
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404701; AAL01359.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GG; GO:0003677; F:DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404700; AAL01357.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNB binding; IEA.
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EMBL; AF404703; AAL01363.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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SEQÜENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
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01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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Best Local Similarity 100.00
Local 9; Conservative
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Matches 9; Conservative
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MEDLINE=21846229; PubMed=11857370; MEDLINE=21846229; PubMed=11857370; Matte K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:866-874 [2002]. EMBL; AF404694; AAL01345.1; GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:003677; F:DNA binding; IEA. Pfam; PP00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF444702; AAL01361.1;
GO; GO:0042025; C:host cell nucleus; IEA.

PF0003677; F:DNA binding; IEA.
                                                              Query Match 100.0%; Score 50; DB 2; Length 130; Best Local Similarity 100.0%; Pred. No. 0.57; Matches 9; Conservative 0; Mismatches 0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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Matches 9; Conservative
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NCBI_TaxID=10581;
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MEDLINE=21046229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL, AF404656; AAL01149-1; ---
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0043677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
EMBL, AF404695; AAL01347.1;
CO, GO:0042025; C:host cell nucleus; IEA.
GO; GO:000317; F:DNA binding; IEA.
PFMB, PF00518; E6; 1.
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01-OFT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
PFam; PF00518; E6; 1.
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SEQÜENCE 130 AA; 15779 MW; 26D0147D39
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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MEDINE=9743744; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
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Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL, AR03016; AAB70733.1; -.
GO; GO:0003677; F:DhA binding; IEA.
InterPro; IPR001334; E6.
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EMBL; U34114; AAA91661.1; -.
EMBL; U34125; AAA91672.1; -.
EMBL; U34130; AAA91671; -.
EMBL; U34130; AAA91678.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6DBA CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein E6.
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Best Local Similarity
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NCBI_TaxID=10581;
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 91:868-874(2002).
EMBL; AF404698; AAL01353.1; -.
GO; GO:0002577; F:DNA Loll nucleus; IEA.

Pfam; PF00518; E6; 1.
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.,
Esth-Giraldo E., Giraldo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
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EMBL, AF003015; AAB70732.1; --
GO, GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                 100.0%; Score 50; DB 2; Length 143; 100.0%; Pred. No. 0.62; tive 0; Mismatches 0; Indels
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Pred. No. 0.65;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQÜENCE 143 AA; 17274 MW; SFB0F7E1EC6DBA82 CRC64;
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SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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(TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel, 19, Last seq
01-OCT-2003 (TrEMBLrel, 25, Last ann
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MEDLINE=21846229; PubMed=11857370;
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nes 9; Conservative
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Best Local Similarity
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MEDLINE=20112892; PubMed=10644829;
MAID MIN. Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analyais of human papillomavirus type 16 B6 variants in relation to 13 Standard L.J., Meijer C.J., Malboomers J.M.;

"Gon Virol. 81:317-325(2000).

"REMBL, AJ388066; CAB45104.1; -..

"REMBL, AJ388066; CAB45124.1; -..

REMBL, AJ388066; CAB45124.1; -..

RO, GO:0003677; F:DNA binding; IEA.

"RO, GO:0003677; F:DNA binding; IEA.

"RICHERPO: IPR001334; B6.

"REMBL PRO0188 B6.

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100.0%; Pred. No. 0.65;
tive 0; Mismatches 0; Indels
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077816;
065-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruses; dsNNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
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Best Local Similarity 100.
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Search completed: June 28, 2005, 23:28:13 Job time : 55.1 secs

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Lipie Page Blank (uspto)

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A;Cross-references: UNIPROT:Q18957; EMBL:Z75710; PIDN:CAB00025.1; GSPDB:GN00019; CESP:D1(A;Experimental source: clone D1081
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                                                        C;Genetics:
A;Gene: CESP:D1081.4
A;Map position: 1
A;Introns: 25/2; 40/3; 72/3; 114/3; 139/3; 167/3; 227/2; 326/1; 352/3; 376/2; 403/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein DKFZp434C091.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
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A;Reference number: Z17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 55.6%; Pred. No. 3.2e+02; Similarity 55.6%; Pred. No. 3.2e+02; S. Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                          66.7%; Score 36; DB 2; Length 421;
71.4%; Pred. No. 3.18+02;
tive 1; Mismatches 1; Indels
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A;Experimental source: cultivar Columbia; BAC clone T1E22
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A;Experimental source: adult testis; clone DKFZp434C091
                                                                                                                                                                                             Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 62.5%;
Matches 5; Conservative
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CSACCRQS 455
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A,Molecule type: mRNA
A,Residues: 1-438 <POU>
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A:Residues: 1-651 <BEV>
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A, Note: T1E22.110
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A, Map position:
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A,Residues: 22-83,'N' <JOU>
C,Comment: The functional molecule consists of two nonidentical chains, C9S3 chain 1 and c involved in disulfide bonds.
C,Superfamily: snake toxin
C,Superfamily: snake toxin
C,Keywords: heterodimer; venom
F;1-21/Domain: signal sequence #status predicted <SIG>
F;2-86/Product: venom protein C9S3 chain 1 #status experimental <MAT>
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                                                                                                                                                              A;Cross-references: UNIPROT:P17696; EMBL:X51467; NID:g62761; PIDN:CAA35830.1; PID:g62762
R;Joubert, F.J.; Viljoen, C.C.
Hoppe-Seyler's Z. Physiol. Chem. 360, 1075-1090, 1979
A;Title: The amino-acid sequence of the subunits of two reduced and S-carboxymethylated A;Reference number: A91679; MUID:80070629; PMID:511106
                               Title: Nucleotide sequence encoding a 'synergistic-like' protein from the venom glande
Reference number: S09235; MUID:90221903; PMID:2326204
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Start codon: TTG
C;Superfamily: Ruminococcus flavefaciens cellulose 1,4-beta-cellobiosidase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 36; DB 1; Length 86; 44.4%; Pred. No. 1.3e+02; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 2; Length 352
Pred. No. 2.8e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Dobson, R. submitted to the EMBL Data Library, July 1996 A;Reference number: Z19256 A;Accession: T20315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
55.6%;
     Nucleic Acids Res. 18, 1639, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-352 <WAN>
A;Cross-references: EMBL:X51944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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75 CVKCCKTDR 83
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                                                                                                              Molecule type: mRNA
Residues: 1-86 <ROW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                    Accession: S09235
                                                                                                                                                                                                                                                                                                         Accession: A01679
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Search completed: June 28, 2005, 23:32:12
Job time : 12.05 secs
                                                                                         Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 71...
Best Local Si Conservative
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252 CLSCCTS 258
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81 CIYCCRS 87
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A,Map position: 2
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hypothetical protein F6E21.40 - Arabidopsis thaliana (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: Arabidopsis thaliana (mouse-ear cress) (5.5pecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 (5.5pecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 (5.5pecies: 10-1066 #s.) Faris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrosubmitted to the Protein Sequence Database, June 1999 #seference number: 216533 #Aceterence number: 216533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T2II.110 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004 (C;Accession: T49879 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le A;Reference number: 224493 A;Accession: T49879
                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 4
A;Introns: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1
                                                                                                                                                                                                                                                                 A;Residues: 1-670 <BEV>
A;Cross-references: UNIPROT:Q9M090; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
A;Experimental source: cultivar Columbia; BAC clone F6E21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-898 <WIL>
A;Cross-references: EMBL:AL021448; PIDN:CAA16276.1; GSPDB:GN00023; CESP:Y2H9A.1
A;Experimental source: clone Y2H9A
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A;Molecule type: DNA
A;Residues: 1-1075 <BEV>
A;Croser-references: UNIPROT:Q9LY20; EMBL:AL163912; GSPDB:GN00063; ATSP:T211.110
A;Experimental source: cultivar Columbia; BAC clone T211
C;Genetics:
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 66.7%; Score 36; DB 2; Length 898; Best Local Similarity 71.4%; Pred. No. 4.6e+02; Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 670;
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Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Wallis, J.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z20237
A;Accession: T26577
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141 VSCCRSS 147
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A, Gene: CESP: Y2H9A.1
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Cipacession: H84839
Riin, X.; Kaul, S.; Rouneley, S.D.; Shea, T.P.; Benitco, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Nature, J.S.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Residues: 1-107 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: 081483; GB: AE002093; NID: 93894195; PIDN: AAC78544.1; GSPDB: GN(C; Genetics:
                            A;Map position: 5
A;Introns: 411/2; 456/2; 504/3; 604/3; 685/1; 731/3; 768/3; 786/1; 822/3; 865/3; 895/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            late embryogenesis abundant M10 protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                 Score 36; DB 2; I
Pred. No. 5.1e+02;
1; Mismatches 1;
A; Gene: ATSP: T211.110
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Sequence 6, Appliance 14, Appliance 14, Appliance 10, Appliance 11, Appliance 12, Appliance 12, Appliance 12, Appliance 13, Appliance 14, Appl

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

Run on:

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US-10-484-063-9

Sequence 9, Application US/10484063

Publication Wo. US20050048467A1

Publication Wo. US20050048467A1

GENERAL INFORMATION:

APPLICANT: TOTOLERN US. USLLERMO

APPLICANT: TOTOLERN MICHELE

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: USC.560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: ECT/US02/23198

PRIOR PRILING DATE: 2001-07-19

PRIOR PILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 9: 27

SEQ ID NO 9: 27

SEQ ID NO 9: 27
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6 US-10-653-595-213
7 US-10-899-214145
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7 US-10-144-65786
7 US-10-141-645-72
7 US-10-141-645-72
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7 US-10-141-645-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human papillomavirus
  Best Local Similarity 100.
Matches 9; Conservative
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61
137
210
210
245
1368
1368
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    Query Match
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Sequence 64, Appl
Sequence 20, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 16, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 4, Appli
                                                                                           June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_RBW PUB.Pepp:*
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              GenCore version 5.1.6
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US-10-938-249-513
US-10-976-570-44
US-10-477-390-6
US-10-484-063-20
US-10-484-063-27
US-10-858-384-2
US-10-367-057-16
US-10-367-309A-1
US-09-367-309A-1
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                1717557 seqs, 384547976 residues
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                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Seguence 265982, Seguence 357597,

Sequence

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Gaps

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US-10-177-390-6
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PUDILication No. U220040170644A1

GENERAL INFORMATION:

APPLICANT: OF UZ20040170NL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: BOUNGALLE-WRATILLE, Sandra

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: GUILLET, Jaan-Gerard

TITLE OF INVENTION: MAXEURE OF PEPPLIGAS derived from E6 and/or E7

TITLE OF INVENTION: papillomavirus proteins and uses thereof

TITLE OF INVENTION WINNER: US/10/476,570

CURRENT APPLICATION NUMBER: PC/FR02/01533

PRIOR APPLICATION NUMBER: PC/FR02/01533

PRIOR APPLICATION NUMBER: PC/FR02/01533
us-10-938-249-513

us-10-938-249-513

publication No. US2005003969A1

Sequence 513, Application US/1038249

publication No. US2005003969A1

GENERAL INCRNATION: Peter S.

APPLICANT: Babinowitz, Joshua D.

APPLICANT: Rabinowitz, Joshua D.

APPLICANT: Schwelzer, Johannes

APPLICANT: Schwelzer, Johannes

APPLICANT: Abrantion: Collagorial in Hematopoietic

TITLE OF INVENTION: Molecular Interactions in Hematopoietic

TITLE OF INVENTION: Molecular Interactions in Hematopoietic

TITLE OF INVENTION: Molecular Interactions in Hematopoietic

TITLE OF INVENTION: Molecular Interactions in Hematopoietic

FILE REFERENCE: 2000-11-80

FRIOR FILING DATE: 2000-10-10

PRIOR APPLICATION NUMBER: US 60/134,114

PRIOR FILING DATE: 1999-05-14

PRIOR FILING DATE: 1999-05-14

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/16,498

PRIOR APPLICATION NUMBER: US 60/16,498

PRIOR FILING DATE: 1999-10-29

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: US 60/10,453

PRIOR PLING DATE: 1999-10-13

PRIOR APPLICATION NUMBER: US 60/10,453

PRIOR PLING DATE: 2000-01-14

PRIOR APPLICATION NUMBER: US 60/10,453

PRIOR APPLICATION NUMBER: US 60/10,505

PRIOR APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158 US-10-476-570-44
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US-10-484-063-20

i Sequence 20, Application US/10484063

j Publication No. US20050048467A1

j GENERAL INFORMATION:
    APPLICANT: TORTOLERO-LUNA, GUILLERMO
    APPLICANT: FOLLEN, MICHELE
    TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
    TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
    FILE REFERENCE: UTSC:560US
    CURRENT APPLICATION NUMBER: PCT/US02/23198
    FRIOR APPLICATION NUMBER: PCT/US02/23198
    FRIOR APPLICATION NUMBER: 60/306,809
    RATOR FILING DATE: 2002-07-19
    FRIOR PLING DATE: 2002-07-20
    NUMBER OF SEQ ID NOS: 27
    SEQ ID NO 20
    LENGTH: L151
    SEQ ID NO 20
    LENGTH: L151
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Sequence 6, Application US/1017390

Sequence 6, Application US/1017390

Publication No. US20030143743A1

GENERAL INFORMATION:

APPLICANT: Schuler, Gerold

APPLICANT: N.V. Antwerps Innovatiecentrum

TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

TITLE OF INVENTION: Polynuclectides by Electroporation

FILE REFRENCE: 021505wo/JH/ml

CURRENT APPLICATION NUMBER: US/10/177,390

CURRENT FILING DATE: 2002-06-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                         100.0%; Score 54; DB 16; Length 24; 100.0%; Pred. No. 1.9;
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; ORGANISM: Human papillomavirus
US-10-484-063-20
                                                                                              LENGTH: 24
TYPE: PRT
ORGANISM: artificial sequence
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
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Best Local Similarity 100.

Matches 9; Conservative
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Best Local Similarity
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APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Lide HPV E6 and E7 genes and proteins useful for vaccination FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: 18/10/472,724
CURRENT APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 171
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                                                                                                                                                                                                 0; Indels
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                                                                                                                           US-10-367-057-16
; Sequence 16, Application US/10367057; Publication No. US20050100554A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10472724
Publication No. US20040171806A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-367-057-16
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Sequence 27, Application US/10484063

Sequence 27, Application US/10484063

Sequence 27, Application US/10484063

Sequence 27, Application OF USZO050048467A1

SEQUENCE OF UNIVERSION:

APPLICANT: TORTOLENE OF UNIVERSION:

APPLICANT: FOLLEN, MICHELE

TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: METHODS AND COMPOSITIONS GROWTHS, INCLUDING CIN

TITLE OF INVENTION: PRR-CANCENOUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: USC.560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2004-01-16

PRIOR FILING DATE: 2002-07-19

PRIOR PLING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 27

SEQ ID NO 27
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APPLICANT: CHOPFIN, JEANNINE
APPLICANT: CHOPFIN, JEANNINE
APPLICANT: CHOPFIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 5058-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 3.2
                                                Gaps
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Score 54; DB 17; Length 151;
Pred. No. 7.5;
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                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10858384
Publication No. US20050033025A1
    Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REPERBNES: 1845124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
FRIOR APPLICATION NUMBER: US/09/581,976
PRIOR APPLICATION NUMBER: DCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius ; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type ; OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 54; DB 17; Length 273; 100.0%; Pred. No. 12;
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Sequence 10, Application US/10000903

Publication No. US2002018221A1

GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Combardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT APPLICATION NUMBER: US/10/000,903
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FRASEQ for Windows Version 3.0
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; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity luv.
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
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LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 54; DB 9; Length 266; 100.0%; Pred. No. 11;
                                                                                         APPLICANT: MACFALLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
TITLE OF INVENTION: UNBER: US/09/367,309A
CURRENT FILIGH DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR PLING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-13
PRIOR PLING DATE: 1998-02-14
SPIOR APPLICATION NUMBER: AU PO 5178
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATCHTIN OF: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bruck, Claudine
APPLICANT: Bruck, Claudine
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human papillomavirus type 16
                       Sequence 1, Application US/09367309A
Publication No. US20020081329A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/1000903
Publication No. US20020182221A1
GENERAL INFORMATION:
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Best Local Similarity 100...
Best 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo sapien
US-10-000-903-4
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Pusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
US-10-899-771-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Best Local Similarity 100.0%; Pred. No. 15; Length 371;
Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 54; DB 17; Length 292; Best Local Similarity 100.0%; Pred. No. 12; Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE SPERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 371
                                                                                               CURRENT PILICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-10-000-903-6
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Search completed: June 29, 2005, 05:18:16 Job time : 117.15 secs

249 CMSCCRSSR 257

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BDWARDS, Stirling John
APPLICANT: BDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 266
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APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
FILE OF INVENTY PAPLICANTON: VUMBER: US/09/359,382
CURRENT PEPLICANTON NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICANTON NUMBER: US/08/60,165
EARLIER PELING DATE: 1999-12-20
EARLIER FILING DATE: 1999-12-20
EARLIER PELING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTING DATE: 1994-12-20
SOFTWARE: PALENTING DATE: 1994-12-20
SOFTWARE: PALENTING DATE: 1994-12-20
SEQ ID NO 10
LENGTH: 266
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100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels
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US-09-359-382-10
                                                                                                                                                                         Sequence 10, Application US/08860165A
Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09359382
Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: EDWARDS, Stirling John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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1 CMSCCRSSR 9
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                                              81 CMSCCRSSR
                                                                                                                                                    US-08-860-165-10
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US-09-359-382-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-12
                                                                                                                                                                                                                                                                         APPLICANT: EDRARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB Elizabeth Ann
APPLICANT: WEBB Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1999-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1999-12-20
EARLIER PILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 12
LENGTH: 172
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APPLICANT: BUDARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels
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CURRENT FILING DATE: 1999-07-23
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER PELING DATE: 1995-12-20
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 12
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                                                                                                                                                                                  Sequence 12, Application US/08860165A Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09359382 Patent No. 6306397
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ORGANISM: Artificial Sequence
                                                                    143 CMSCCRSSR 151
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                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                              RESULT 5
US-08-860-165-12
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Unery Match 100.0%; Score 54; DB 3; Length 371; Best Local Similarity 100.0%; Pred. No. 3.6; Matches 9; Conservative 0; Mismatches من تمثمار
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                                                      GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: General, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER: FASTSEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
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VGS-03-485-885-6

Sequence 6, Application US/09485885

Patent No. 6342224

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Delisse, Anne-Marie Eva Fernande

APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45.07

CURRENT APPLICATION NUMBER: US/09/485,885

CURRENT FILING DATE: 1999-08-17

PRIOR FILING DATE: 1999-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1999-08-22

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 6

SEQ ID NO 6
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US-09-485-885-14
Sequence 14, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
  Sequence 10, Application US/09485885
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CMSCCRSSR 9
                        Patent No. 6342224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-485-885-6
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                                                                                                                                                                                                                                APPLICANT: MALLIARGS, JUM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 01722/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR PILING DATE: 1999-02-19
PRIOR PILING DATE: 1999-02-19
PRIOR PILING DATE: 1997-02-19
NUMBER: OF SEQ ID NOS: 6
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 1
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 54; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 2.8; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Lambaranie Bracie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE REFERENCE: B45107
CURRENT APPLICATION NUMBER: U9/09/485,885
CURRENT APPLICATION NUMBER: U5/09/485,885
CURRENT FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1999-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
TYPE: PRI
TYPE: PRI
TYPE: PRI
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                            Sequence 1, Application US/09367309A
Patent No. 642807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/09485885; Patent No. 6342224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 CMSCCRSSR 151
143 CMSCCRSSR 151
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                                                                                                                      US-09-367-309A-1
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US-09-485-885-10
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CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun STREET: 233 South Wacker Drive, 6300 Sears Tower CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIF: 60606-6402
CONPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: PFLING DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO DATE: CHICAGO 
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CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 98
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NAME: Williams Jr., Joseph A.
REGISTATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27013/34028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Papillomavirus sylvilagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
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LENGTH: 98 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                               US-09-382-616A-1
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US-09-820-764-4
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                                                                                                                                                                                                                                                                                                                                                                MEANUI INFORMATIONE, ROBERT
APPLICANT: FINDLE,
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBINIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 53; DB 3; Length 98 Best Local Similarity 100.0%; Pred. No. 0.023; Matches 9; Conservative 0; Mismatches 0; Indels
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Patent No. 6200746
EBNERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/075,541D

FILING DATE: 10-JUN-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU pk 3876

FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DCt/augl/00575

FILING DATE: 12-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: NADEL, ALAN S

REGISTRATION: NUMBER: 27,363

REFERENCE/DOCKET NUMBER: 8795-4

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PANTICH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 MARKET STREET, 36TH FLOOR CITY: PHILADELPHIA STATE: PENNSYLVANIA
                                                                                                                                                                                                                                     US-08-075-541D-42; Sequence 42, Application US/08075541D; Patent No. 6183745; GENERAL INFORMATION: APPLICANT: TINDLE, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ 1D NO: 42: SEQUENCE CHARACTERISTICS: LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SC
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MOLECULE TYPE: peptide
                                                                                        19 TIDLYCYEQ 27
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                                      1 TTDLYCYEQ 9
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STRANDEDNESS: si
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APPLICANT: Chu, N. Randall
APPLICANT: Mizer, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/00201
CURRENT PILING DATE: 2000-007-10
FRIOR PILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 98
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,764
FILING DATE: 30-Mar-2001
CLASSIFCATION CURREN: US/09/820,764
FILING DATE: 10-Mar-2001
RRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
Sequence 4, Application US/09820764
Patent No. 6352696
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 53; DB 3; Length 98; 100.0%; Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                              NUMBER OF SEQUENCES: 28
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Best Local Similarity 100.
Matches 9; Conservative
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; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match
Best Local Similarity 100.0%; Score 53; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLXCYEQ 9

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Db 19 TTDLYCYEQ 27

Search completed: June 28, 2005, 21:33:31
Job time: 17 secs
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Sequence 25612, Application US/09252991A

Patent No. 655178

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERCIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marc J. Whenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                   APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 100.
Matches 9; Conservative
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86 CCACCRSAR 94
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ORGANISM: Homo sapien
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STRAIN-HPV16; TISSUB-Cervical;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
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STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
Papillomavirus.
NCBI_TaxID=10566;
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Q1-NOV-1996 (TrEMBLrel. 0
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E6 protein (Fragment).
Human papillomavirus.
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Q80883, Q1-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
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9; Conservative
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NCBI_TaxID=10566;
SEQUENCE
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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1: uniprot_sprot:*
2: uniprot_trembj:*
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Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL, AF404692; AAL01342.1; -
GO; GO:0042025; C:host cell nucleus; IEA.
GG; GO:0003677; F:DNA binding; IEA.
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C0919D6;
C01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
E6 protein (Fragment).
Viruses; dsDMA viruses, no RNA stage; Papillomaviridae; Papillomavirus.
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FAURE TAXID=10581;
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                                                    100.0%; Score 52; DB 2; Length 90; 100.0%; Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Calutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL. 114516; AAB60570.1; -.
                                                                                                                                                                                                                                                                     Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10566;
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90 90
90 AA, 10964 MW; BC2531643ACBA76C CRC64;
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91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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MEDLINE=21846229; PubMed=11857370;
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STRAIN-HPV16; TISSUE-Cervical tissue;
STRAIN-HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (GEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14514; AAB60568.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IRR001334; E6.
Pfam; PF00518; E6; 1.
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Papillomavirus.
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90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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01-OCT-2003 (TrEMBLrel. 25, Last ann
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
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Human papillomavirus.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec

US-08-170-344-57

1 SCCRSSRTR 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
i: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C;Accession: T47947
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet; submitted to the Protein Sequence Database, January 2000
A;Reference number: Z24480

A;Accession: T47947 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-212 <DEH>

hypothetical protein F2A19.150 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

T47947

hypothetical prote	lysine-tRNA ligase	acrogranin - guine	tegument protein 6	transcription regu	aminoglycoside 6'-	hypothetical prote	hypothetical prote	keratin high-sulfu	high-sulfur wool m	high-sulfur wool m	high-sulfur wool m	high-sulfur wool m	ultra-high-sulfur	weakly transcripti	transcription regu
T18667	S14834	148141	855659	AD3622	T01788	S42858	AD3436	KRSHHC	147111	147109	147108	147112	A45910	AH1452	A11088
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359	576	591	3436	95	206	61	87	152	152	152	152	152	186	231	231
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33	33	33	33	32.5	32.5	32	32	32	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SEE>
A; Cross-references: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G333032
B; Cross-references: UNIPROT: P03126; GB: K02718; NID: G333031; PIDN: AAA46939.1; PID: G333032
B; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
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                                                  C;Species: human papilionavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T1042; T1042;
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Reference number: A23355; MUID:85246220; PMID:2990099
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A;Molecule type: DNA
A;Residues: 1-158 <KEN>
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Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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Dypothetical protein At2g46160 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: D84899
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Residues: 1-214 <STO>
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Crispecies: Brucella melitensis
Crispecies: Brucella melitensis
Crispecies: Brucella melitensis
Crispecies: Brucella melitensis
Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Crispecies: Cr
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein SC1A11.02c SC1A11.02c - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: 134649
R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.submitted to the EMBL Data Library, January 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:AL035205; PIDN:CAA22742.1; GSPDB:GN00070; SCOEDB:SC1A11.02c
A;Experimental source: strain A3(2)
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Score 37; DB 2; Length 870;
Pred. No. 1e+02;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: 221551
A;Accession: T34649
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-152 <8EE>
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       74.0%;
85.7%;
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6; Conservative
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Best Local Similarity 75.0°
                                          Similarity 85.7 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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A,Map position: 2
       Query Match
Best Local S:
Matches 6
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A;Experimental source: clone T26H8
R;Basham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ciptures Advantage Mart 1993 Marguence_revision 18-Nov-1994 #text_change 15-Mar-2004
Cipture: 04-Mar-1993 Marguence_revision 18-Nov-1994 #text_change 15-Mar-2004
Cipture: 04-Mar-1993 Marguence_revision 18-Nov-1994 #text_change 15-Mar-2004
Cipture: 07-Mart 1992 Marguence_revision 18-Nov-1994 Marguence 18-Mart 1995
A; Titure: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide.
A; Reference number: A42112; MUD:92184794; PMID:1371999
A; Retains preliminary
A; Molecule type: nucleic acid; protein
A; Residues: 1-837 axul>
A; Resperimental source: intestinal
A; Experimental source: intestinal
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A,Molecule type: DNA
A,Residues: 1-870 < WIZ.>
A,Residues: 1-870 < WIZ.>
A,Cross-references: EMBL:Z81142; PIDN:CAB03512.1; GSPDB:GN00023; CESP:ZK1037.11
A,Experimental source: clone ZK1037
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25338; T27667
R;Mortimore, B.
Submitted to the EMBL Data Library, November 1996
A;Reference number: 220018
A;Reference number: Z20018
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-870
A;Molecule type: DNA
A;Residues: 1-870
A;Molecule type: DNA
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A;Introns: 161/1; 162/3; 212/3; 233/3; 301/3; 517/2; 562/3; 578/1; 825/2
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       A,Cross-references: UNIPROT:Q9M313; EMBL:AL132962
A,Experimental source: cultivar Columbia; BAC clone F2A19
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Pred. No. 43;
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submitted to the EMBL Data Library, October 1996
A;Reference number: 220401
A;Accession: T27667
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                                                                                                                A;Map position: 3
A;Note: F2A19.150
F;132-183/Domain: RING finger homology <RRN>
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C;Species: Rattus norvegicus (Norway rat)
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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50 CCRASRLR 57
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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A; Residues: 1-114 < KAW>
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.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-98 <RES>
A,Cross-references: UNIPROT:Q16303; GB:S76942; NID:g913280; PIDN:AAB33728.1; PID:g913281
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C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase
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A,Residues: 1-1905 <OHT>
A,Cross-references: UNIPROT:Q91823; GB:D38175; NID:g961514; PIDN:BAA07374.1; PID:g961515
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Neuron 14, 1189-1199, 1995
A;Title: Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via
A;Reference number: I51553; MUID:95329274; PMID:7605632
A;Accession: I51553
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Hum. Mol. Genet. 3, 2207-2212, 1994
A.Title: Human dopamine D4 receptor gene: frequent occurrence of a null allele and obser
A;Reference number: I54366; MUID:95187162; PMID:7881421
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Cross-references: GB:AE008917; PIDN:AAL53200.1; PID:g17984074; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plexin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Homo sapiens (man)
Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                        Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Pred. No. 78;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: vertebrate rhodopsin C; Keywords: neurotransmitter receptor
                                                                                                                                                                                                 Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                      72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%;
ilarity 85.7%;
Conservative (
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SCCRSPQT 1513
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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hes 6; Conser
                                                                                                             Status: preliminary
                                                                                                                               Molecule type: DNA
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CJACCESSION: C70575
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Riftle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                C;Accession: D72600
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9YC19; DDBJ:AP000061; NID:g5104821; PIDN:BAA80258.1; PID:dl(
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hair keratin cysteine rich protein - sheep
hair keratin cysteine rich protein - sheep
(;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
(;Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
(;Accession: S60314
C;Accession: S60314
R;Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                      C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 141;
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hypothetical protein APE1268 - Aeropyrum pernix (strain K1)
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Pred. No. 62;
1; Mismatches
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Search completed: June 28, 2005, 23:32:13 Job time : 12.05 secs
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A;Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-ri
A;Reference number: S60314; MUID:94149288; PMID:7508963
A;Accession: S60314
                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-151 <FRA>
A;Cross-references: UNIPROT:Q28576; EMBL:X73462; NID:g512030; PIDN:CAA51841.1; PID:g5120
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glucose starvation-induced protein (clone pZSS3) - maize (fragment)
C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S60454; S49585
R;Chevaller, C.; Bourgeois, E.; Pradet, A.; Raymond, P.
Plant Mol. Biol. 28, 473-485, 1995
A;Title: Molecular cloning and characterization of six cDNAs expressed during glucose st
A;Reference number: S60453; MUID:95359405; PMID:7632917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-166 <DIE>
A;Cross-references: UNIPROT:O13522; EMBL:U32274; NID:g927313; PID:g2194162; GSPDB:GN000d
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A;Molecule type: mRNA
A;Residues: 1-229 cRHS>
A;Cross-references: UNIPROT:Q41855; EMBL:X82617; NID:g575425; PIDN:CAA57939.1; PID:g5754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, July 1995
A;Description: The sequence of S. cerevisiae cosmids 9481, 9509, 9926, 9461, and lambda
A;Reference number: S69665
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C;Date: 22-Ang-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S69692
R;Dietrich, F.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YDR396w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                              70.0%; Score 35; DB 2; Length 151;
100.0%; Pred. No. 73;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: MIPS:YDR396w
A;Cross-references: SGD:S0002804
A;Map position: 4R
C;Superfamily: Saccharomyces hypothetical protein YDR396w
                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
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59 ACCRASRS 66
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Best Local Similarity
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RESULT 15 G97530

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probable zinc-binding alcohol dehydrogenase [imported] - Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens G;Accession: G97530

R;Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Accession: G97530

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Accession: G97530

A;Feference: DNA

A;Feference: DNA

A;Feference: DNA

A;Fesidues: 1-371 cKUR>
A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE07869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE07869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; GB:AE07869; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

A;Coss-references: UNIPROT:Q8UF19; PIDN:AAK87200.1; PID:g15156478; GSPDB:GP

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Sequence 6, Appli Sequence 10, Appli Sequence 14, Appli Sequence 11, Appl Sequence 213, Appl Sequence 211, Appl Sequence 211, Appl Sequence 6786, A Sequence 6786, A Sequence 18537, Sequence 196497, Sequence 196497, Sequence 196497, Sequence 105833, Sequence 160786, Sequence 160786, Sequence 160786, Sequence 230614, Sequence 230614, Sequence 250250, Sequence 250250, Sequence 250250, Sequence 250250, Sequence 250250, Sequence 160782, Sequence 250250, Sequence 250250, Sequence 13533,

3 US-10-899-771-4
3 US-10-899-771-10
3 US-10-809-771-10
3 US-10-899-771-10
3 US-10-899-771-6
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4 US-09-397-945-213
5 US-10-653-595-213
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6 US-10-425-114-65786
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6 US-10-437-963-199754
6 US-10-437-963-199754

Sequence 310834, Sequence 135875, Sequence 294572, Sequence 310833 Sequence 186241

US-10-437-963-135435 US-10-425-115-310834 US-10-437-963-135875

ALIGNMENTS

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Sequence 9, Application US/10484063
; Sequence 9, Application WJ.10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: PRE-CANCEROUS GROWTHS, INCLUDING CIN
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; TITLE OF INVENTION NUMBER: US/10/484,063
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; IND NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Human papillomavirus
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Matches 9; Conservative
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Sequence 513, App
Sequence 6, Appli
Sequence 20, Appl
Sequence 27, Appl
Sequence 1, Appli
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB_pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB_pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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100.0%; Score 50; DB 17; Length 16; 100.0%; Pred. No. 1;

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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 15:
TYPE: PRT
CREANTSM: Human papillomavirus
US-10-484-063-20
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 44
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Maxuure of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45656-5071-US
CURRENT APPLICATION NUMBER: DC110/476,570
PRIOR PPLICATION NUMBER: PCT/PRO2/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
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                                               Sequence 513, Application US/10938249

Publication No. US20050037969A1

GENERAL INFORMATION:
APPLICANT: Exhinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: 020054-001130US
CURRENT APPLICATION NUMBER: US/10/938,249
CURRENT FILING DATE: 2000-10130US
CURRENT PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/134,114
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
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Matches 9; Conservative
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| NUMBER OF SEQ ID NOS: 63
| SOFTWARE | PREMELIN VET. 2.1
| SECTION 0.44
| DANIEL OF SEQ ID NOS: 63
| SOFTWARE | PREMELIN VET. 2.1
| SEQ ID NO.44
| DANIEL SECTION 0.44
| DANIEL
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GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Sur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT APPLICATION NUMBER: PCT/EP02/03271
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
IEBNGTH: 171
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100.0%; Score 50; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                         APPLICANT: Cuthill, Scott;

APPLICANT: Uackson, Amanda;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, Chan Eng

TITLE OF INVENTION: Complexes and Methods of Using Same;

FILE REFERENCE: 21402-559

CURRENT APPLICATION NUMBER: US/10/367,057

CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SEQ ID NO 16

LENGTH: 158
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                                                                                                                                                                                    Sequence 16, Application US/10367057
Publication No. US20050100554A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10472724
Publication No. US20040171806A1
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Best Local Similarity 100.
                                                    145 SCCRSSRTR 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16
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Sequence 27, Application US/10484063

Sequence 27, Application US/10484063

Publication No. US20050048467A1

SEQUENCAL

APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORFOLENC-LUNA, GUILLERMO

APPLICANT: FOLILEN, MICHELE

TITLE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:56008

CURRENT FILING DATE: 2004-01-16

PRIOR FILING DATE: 2003-07-19

PRIOR FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARRE PRICATION NUMBER: 60/306,809

PRIOR FILING DATE: 2001-07-20

SOFTWARRE PRICATION NUMBER: 00/306,809
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APPLICANT: BUNGGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: ER 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTI OF VET. 3.2
                                                          Gaps
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Query Match
100.0%; Score 50; DB
Best Local Similarity 100.0%; Pred. No. 6.1
Matches 9; Conservative 0; Mismatches
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; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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; Publication No. US20050033025A1
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: 1845124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
RICOR APPLICATION NUMBER: US/09/581,976
RRICOR FILING DATE: 2000-06-20
RRICOR FILING DATE: 1999-12-18
PRIOR PELING DATE: 1999-12-18
PRIOR PELING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type; OTHER INFORMATION: 16)
US-10-899-771-4
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100.0%; Score 50; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 50; DB 17; Length 273; 100.0%; Pred. No. 9.7;
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Sequence 10, Application US/10000903

Publication No. US2002018221A1

GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Carard, Catherine Marie Eva RepricANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FRAELSQ for Windows Version 3.0
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US-10-899-71-10
'Sequence 10, Application US/10899771
'Publication No. US20050031638A1
'GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 9; Conservative
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ORGANISM: Homo sapien
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LENGTH: 292
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                   Sequence 1, Application US/09367309A; Sequence 1, Application US/09367309A; Publication No. US20020081329A1; Publication No. US20020081329A1; GENERAL INFORMATION:
APPLICANT: MALLIARGS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES; PILE REFERENCE: 017227/0149; PILE REFERENCE: 017227/0149; PRICHERY APPLICATION NUMBER: US/09/367,309A; CURRENT FILING DATE: 1999-08-11; PRIOR APPLICATION NUMBER: PGT/AU98/00080; PRIOR FILING DATE: 1999-02-13; PRIOR PLICATION NUMBER: AU PO 5178; NUMBER OF SEQ ID NOS: 6; SOFTWARE: Patentin Ver: 2.1; FEMALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 50; DB 9; Length 266; 100.0%; Pred. No. 9.5;
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Denibardo Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-000-903-4
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us-08-170-344-57.rapb

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## APPLICANT: Gerard, Catherine Marie Ghislaine
### TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
### TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
### FILE REPERBUCE: 845124
### CURRENT APPLICATION NUMBER: US/10/899,771
### CURRENT APPLICATION NUMBER: US/09/581,976
### PRIOR APPLICATION NUMBER: US/09/581,976
### PRIOR PLIING DATE: 1090-06-20
### PRIOR PLIING DATE: 1990-12-18
### PRIOR PLIING DATE: 1997-12-24
### PRIOR PLIING DATE: 1997-12-24
### NUMBER OF SEQ ID NOS: 28
### SEQ ID NO 10
### SEQ ID NO 10
### SEQ ID NO 10
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CRGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
CRGANISM: OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
CTHER INFORMATION: 16)
US-10-899-771-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10009903
Sequence 6, Application US/10009903
Publication No. US2002018221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE PRIOR PRIOR SAPIEN
US-10-000-903-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Gaps

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0; Indels

0; Mismatches

Search completed: June 29, 2005, 05:18:16 Job time : 116.15 secs

251 SCCRSSRTR 259

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Life bade Blauk (nebto)

21791, A 58297, A 6, Appli 6, Appli 25071, A

Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

Scoring table:

Searched:

Title: Perfect score:

Sequence:

OM protein

Run on:

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Length 21;
                                                                                                                                                                                                                                                                                                                                              GEGUENCE 167, Application US/08934915

Sequence 167, Application US/08934915

GENERAL INFORMATION:
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: BARILLOMAVINUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: T1775 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STREET: T4775 U.S. HWY. 19 NORTH, SUITE 500
CITY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: RIORY disk
COUNTRY: U.S.A.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: IBM PC compatible
OPERATION VUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLEASIFICATION NUMBER: US/08/934,915
FILING DATE: 32-SEP-1997
CLEASIFICATION NUMBER: US/08/934,915
FILING DATE: ATTORNEY, AND ATTORNEY, AGENT NUMBER: 37,133
REPERBENCY DOCKET NUMBER: 37,133
REPERBENCY DOCKET NUMBER: 37,133
REPERBENCY DOCKET NUMBER: 1046 6
                                     US-09-074-114-6
US-09-252-991A-25071
US-09-252-991A-29444
US-09-252-991A-29444
US-09-270-767-35721
US-09-270-767-35721
US-09-252-991A-28100
US-09-252-991A-28110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50; DB 2;
Pred. No. 0.31;
                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
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 MOLECULE TYPE: peptide
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Best Local Similarity
US-08-934-915-167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
 RESULT 1
Sequence 167, App
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
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21156, A
33122, A
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30039, A
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6, Appli
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                                                                                            June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 12,
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Sequence 10,
Sequence 10,
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Sequence
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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-980-523A-2
US-08-316-239B-3
US-08-316-239B-4
US-08-860-165-12
US-09-359-382-12
US-09-359-382-12
US-09-360-165-10
US-09-360-165-10
US-09-360-165-10
US-09-485-885-4
US-09-485-885-4
US-09-485-885-14
US-09-485-885-14
US-09-485-885-14
US-09-252-991A-21156
US-09-252-991A-31124
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US-09-270-767-47906
US-09-252-991A-26200
US-09-252-991A-18341
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US-09-252-991A-30039
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US-09-489-039A-12930
US-09-252-991A-30960
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                                                                                                                                                                                                                                                       513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                  protein search, using sw model
                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                      US-08-170-344-57
50
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Match Length
                                                                                                                                                                                                              BLOSUM62
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100.0
100.0
82.0
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Score

Result No.

Gaps

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APPLICANT: Parmenter, Cheryl A.

TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 50; DB 1; Length 162; Best Local Similarity 100.0%; Pred. No. 1.6; Matches 9; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 50; DB 1; Length 162; 100.0%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08316239B Patent No. 5679509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wheeler, Cosette M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35.205
REFERENCE/DOCKET NUMBER: UN-
                                                                                                                                                                                                                                                not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 817-9453
TELEPAX: (703) 803-9387
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                           not relevant
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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TOPOLOGY: not
                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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COUNTRY:
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APPLICANT: Warmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
                                                                                                                                                                                                               Sequence 2, Application US/09980523A

Sequence 2, Application US/09980523A

Patent No. 6783763

GENERAL INFORMATION:

APPLICANT: GIOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILET, JEAN-GERARD

APPLICANT: GONNAN, FRANCINE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WOB1 AO INS

CURRENT PLILING DATE: 2002-04-29

PRIOR FILING DATE: 2002-04-29

PRIOR PLILING DATE: 1999-06-03

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PALENTIN VINCHER PRODUCTION VINCHER OF SEQ ID NOS: 24

SEQ ID NO 2

LENGTH: 158
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            Gaps
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          Indels
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ZIP: 20120-3400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
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0
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08316239B; Patent No. 5679509; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human Papillomavirus US-09-980-523A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 SCCRSSRTR 153
                                                                                                    8 SCCRSSRTR 16
                                                       1 SCCRSSRTR 9
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          6
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          Matches
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Gaps

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; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
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Sequence 10. Application US/09359382

Patent No. 6306397

GENERAL INPORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: OF INVENTION: VARIANTS OF HUMAN PAPLILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-07-23
EARLIER FILING DATE: 1995-12-20

NUMBER OF SEQ ID NOS: 27

SEQTHARE: DatentIN Ver. 2.0

SEQ ID NO 10

LENGTH: 266
                                                                                                                                                                                                                                         APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WASB, Slizabeth Ann
APPLICANT: WASB, Elizabeth Ann
APPLICANT: FARZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFRENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 50; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 2.4; Matches 9; Conservative 0; Mismatches 0; Indels
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ORGANISM: Human papillomavirus type 16
                                                                                                                                                                     Sequence 10, Application US/08860165A Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.v
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1 SCCRSSRTR
                                            83 SCCRSSRTR
                                                                                                                                                                                               Patent No. 6004557
GENERAL INFORMATION:
                                                                                                                                             US-08-860-165-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: WEBB. Elizabeth Ann
APPLICANT: FRAZER. Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPERENCE: 01722/7018
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
FEARLIER PELICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157/94
EARLIER PILING DATE: 1994-12-20
MUMBER OF SEQ ID NOS: 27
COFFWARD FILING DATE: 1994-12-20
MUMBER OF SEQ ID NOS: 27
COFFWARD FILING DATE: 1994-12-20
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Patent No. 6004557
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 50; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT PELICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
BARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PELICATION NUMBER: PCT/AU95/00868
EARLIER PELICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/09359382
Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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SEQ ID NO 12
LENGTH: 172
                                                         145 SCCRSSRTR 153
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                     SCCRSSRTR
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100.0%; Score 50; DB 3; Length 292; 100.0%; Pred. No. 2.6;
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Sequence 10, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: 194500-02-18
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FaetSEQ for Windows Version 3:0
LENGTH: 292
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Patent No. 6434224

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Delisse, Anne-Marie Eva Fernande

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Jembardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

FILE REPERBNCE: B45107

CURRENT APPLICATION NUMBER: OFT/EP98/05285

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1998-08-17

PRIOR PLIING DATE: 1998-08-17

PRIOR POLICATION NUMBER: GB 9717953.5

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FRAESEQ for Windows Version 3.0

LEMOTE - 27
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Homo sapien
US-09-485-885-10
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US-09-485-885-14
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US-09-485-885-6
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0
                                                                                                                                                                                                                                                    APPLICANT: MACEARLAN, RODERICK I.
APPLICANT: MALIAROS, JIM
TITLE OF INVENTION: CRELATING IMMUNOSTIMULATING COMPLEXES
TITLE OF INVENTION: CRELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR PILING DATE: 1997-02-19
NUMBER OF SEO ID NOS: 6
SOFTWARE: PATENTIN VOS: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 50; DB 4; Length 266; Best Local Similarity 100.0%; Pred. No. 2.4; Matches 9; Conservative 0; Mismatches 0; Indels
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Patent No. 634224

GENERAL INFORMATION:
APPLICANT:
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Selva, Vaccine
FILE REFERENCE: B45107

CURRENT APPLICATION NUMBER: C1989/05285
FRIOR FILING DATE: 1998-08-17
FRIOR PILING DATE: 1998-08-17
FRIOR PILING DATE: 1998-08-17
FRIOR APPLICATION NUMBER: GB 9717953.5

NUMBER OF SEQ ID NOS: 23
SEQ ID NOS: 23
SEQ ID NOS: 23
SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                        ; Sequence 1, Application US/09367309A; Patent No. 6428807
; GENERAL INFORMATION:
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     SCCRSSRTR 153
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US-09-485-885-4
                                                                                                                    RESULT 9
US-09-367-309A-1
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US-09-485-885-10
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US-09-485-885-4
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; Sequence 21156, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REPERBENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21156
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Sequence 31122, Application US/09252991A
Sequence 31122, Application US/09252991A
Sequence 31122, Application US/09252991A
Setent No. 6551795
SERENCE INCRMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
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Pred. No. 27;
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                APPLICANT: Cabezon Silva, Teresa APPLICANT: Cabezon Silva, Teresa APPLICANT: Delisse, Anne-Marie Eva Fernande APPLICANT: Gerard, Catherine Marie Ghislaine APPLICANT: Lombardo-Bencheikh, Angela TITLE OF INVENTION: Vaccine FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: G8 9717953.5
PRIOR APPLICATION NUMBER: G8 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 390
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21156
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Best Local Similarity 77.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapien
US-09-485-885-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-21156
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec

Title: Perfect score:

US-08-170-344-56 54 1 CMSCCRSSR 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	protein E6 - human	hypothetical prote			cyc02 protein prec	etical p	venom protein C983	cellulose 1,4-beta	hypothetical prote	_		_	_	_	Φ	hair keratin cyste			LIM-protein FHL3,	hypothetical prote	hypothetical prote	υ	astB/chuR-related	muscarinic acetylc	muscarinic recepto	muscarinic acetylc	muscarinic acetylc	בומיופים היהיות	
SUM	ID	WEWLHS	T25338	T33488	T08179	JQ0877	C71460	V6EP9A	811926	T20315	T12494	T48256	T10666	T26577	T49879	H84839	S60314	869692	139526	T09504	H72593	T34080	G97530	H72266	A31897	151837	803608	A24325	A29514	
	DB	-	~	7	7	7	7	Н	7	~	~	7	7	~	7	~	~	7	~	~	~	~	~	7	7	~	7	7	N	
	Length	158	870	747	640	101	591	86	352	421	438	651	670	868	1075	107	151	166	194	280	280	309	371	442	460	460	460	460	460	
de	Query Match	100.0	83.3	77.8	72.2	68.5	68.5	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	64.8	64.8	64.8	64.8	•	64.8	•	64.8	64.8	64.8	64.8	64.8	64.8	64.8	
	Score	54	45	42	39	37	37	36	36	36	36	36	36	36	36	32	35	35	35	32	35	32	35	35	35	35	35		35	
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hypothetical prote subtilisin-like pr	nypolnetical prote venom protein C9S3 hypothetical prote	probable membrane hypothetical prote	E6 protein - human small hydrophobic	ultra-high-sulfur late competence op	hypothetical prote hypothetical prote	glucose starvation pteridine reductas	collagen - nematod
T10539 A39490	124463 V6EP92 A90507	S54085 T30606	W6WL18 JQ1625	A45910 S39864	T34341 E84560	S60454 D97497	A44984
211	7 - 7	00		0 0	0 0	0 0	0
730	63 129	139	158	189	190	229	. 295
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	0 E0 E0						
30	337 4	365	37 38	39 40	41 42	4. 4. 8. 4.	45

ALIGNMENTS

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A;Accession: A03682
A;Molecule type: DNA
A;Robert type: DNA
A;Robert type: DNA
A;Robert type: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A;Robert type 16 genome acts at the level
A;Robert type 16 genome acts at the level
A;Robert type 16 genome acts at the level
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                                                                                          C; Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Moleculue type: DNA
A;Residues: 1-159 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
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                                                                                                                                                R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G. Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
W6WLHS
protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
                                                                                                                        C; Accession: A03682; T10427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 CMSCCRSSR 151
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Best Local Similarity
Matches 9; Conserv
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RESULT 2

Apportetical protein ZK1037.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25338; T27667
R;Mortimore, B.
Swhitted: Dt the RMBL Data Library, November 1996
A;Reference number: Z20018
A;Reference number: Z20018
A;Reference number: T25338
A;Reference number: L25018
A;Robecule type: DNA
A;Robecule type: DNA
A;Residues: 1-870 <WIL> T25338

us-08-170-344-56.rpr

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72.2%;
66.7%;
  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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57 CVRCCRSA 64
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                                                                                             1 CMSCCRSSR
                                                                                                                                      573 CCRCCRGSR
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A;Molecule type: DNA
A;Residues: 1-591 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-101 < KOD>
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JQ0877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CT875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
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C;Species: Chlamydomonas reinhardtii
C;bate: 11-Unn-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08179
R;Gloeckner, G.; Beck, C.F.
submitted to the EMBL Data Library, October 1996
A;Description: Wolecular characterization of a gene (LRG5) involved in blue light signal
A;Reference number: Z16399
A,Cross-references: UNIPROT:Q9XTQ4, EMBL:Z82057, PIDN:CAB04861.1, GSPDB:GN00023, CESP:ZK
A,Experimental source: clone T26H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-747 <fULJ.
A;Residues: 1-747 <fULJ.
A;Cross-references: UNIPROT:Q97ZL0; EMBL:AF098986; PIDN:AAC67425.1; GSFDB:GN00028; CESP:A;Experimental source: strain Bristol N2; clone C36C9
                                                                                                                                                                                                  A;Cross-references: EMBL:Z81142; PIDN:CAB03512.1; GSPDB:GN00023; CESP:ZK1037.11
A;Experimental source: clone ZK1037
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A;Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:g1644369; PID:g1644370
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C16C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                     A;Map position: 5
A;Introns: 161/1; 162/3; 212/3; 233/3; 301/3; 517/2; 562/3; 578/1; 825/2
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                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fulton, B.; Martin, J.; O'Brien, D.
submitted to the RMEL bata Library, October 1998
A;Description: The sequence of C. elegans cosmid C36C9.
A;Reference number: Z21357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.8%; Score 42; DB 2; ilarity 75.0%; Pred. No. 65; Conservative 1; Mismatches 1
                                                                                         A,Reference number: 220401
A,Accession: T27667
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 45; DB 2; 77.8%; Pred. No. 28;
                                              R;Basham, V.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: X
A;Introns: 171/3; 427/1; 563/1; 627/2; 686/1
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CMSCCRSSR 9
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Best Local Similarity
6, Conserve
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                                                                                                                                                            A; Molecule type: DNA
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cycol protein precursor - Madagascar periwinkle
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: J00877
B;Kodama, H.; Ito, M.; Hattori, T.; Nakamura, K.; Komamine, A.
B;Date: John Pebruary 1991
A;Description: Isolation of genes that are preferrentially expressed at the G1/S boundary
A;Reference number: J00877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:084883; GB:AE001361; GB:AE001273; NID:g3329348; PIDN:AAC6847? A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      venom protein C9S3 chain 1 precursor - eastern green mamba
C;Species: Dendroaspis angusticeps (eastern green mamba)
C;Dacies: 19-Feb-1984 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: S09235; A01679
R;Rowan, E.G.; Ducancel, F.; Doljansky, Y.; Harvey, A.L.; Boulain, J.C.; Menez, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%; Score 37; DB 2; Length 591;
62.5%; Pred. No. 2.7e+02;
ive 1; Mismatches 2; Indels
Score 39; DB 2; Length 640;
Pred. No. 1.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P25923
A;Experimental source: strain B, cell suspension culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: cycc2
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-101/Product: cyc02 protein #status predicted <MAT>
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us-08-170-344-55.rpr

Matches

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transcription-repair coupling factor Cj1085c [imported] - Campylobacter jejuni (strain NC C;Species: Campylobacter jejuni (strain NC C;Species: Campylobacter jejuni (strain NC C;Species: Campylobacter jejuni (strain NC C;Species: Campylobacter jejuni (strain NC C;Accession: H81311 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrelj Nature 403, 665-668, 2000 A;Title: The genome sequence of the food-borne pachogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9PNK9; GB:AL113077; GB:AL111168; NID:g6968444; PIDN:CAB7334(
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-148 <DEL>
A,Residues: 1-148 <DEL>
A,Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g39699; C,Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: human papillomavirus type 37
C.Species: human papillomavirus type 37
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
E.Jelius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A.Specription: Primer-directed sequencing of human papillomavirus types.
A.Reference number: $36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Es protein - human papillomavirus type 53
C;Species: human papillomavirus type 53
C;Species: human papillomavirus type 53
C;Species: Peb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S35527
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Reference number: S36469
A;Reference number: S36469
A;Accession: S35527
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A,Gene: mfd, Cj1085c
C,Superfamily: transcription-repair coupling protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.2%; Score 36; DB 2; 55.6%; Pred. No. 7.7; iive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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                                                                           148 HVDQGQRFH 156
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119 HVDENKRFH 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                            1 HLDKKORFH
                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: H81311
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-978 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                            C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RhPV 1 genomic sequence and an integration loc A;Reference number: A38503; MUID:91135018; PMID:1847267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: C40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma A;Reference number: A40509; MUID:91374616; PMID:1716694
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E6 protein - rhesus papillomavirus
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                Gaps
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C;Superfamily: papillomavirus E6 protein
C;Kywowats. DNA binding; early protein; transforming protein; zinc finger
F;60-96/Region: zinc finger CCCC motif
F;133-169/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Reference number: A38502; MUID:91135017; PMID:1847266; Accession: A38502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein – human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P27962; GB:M73258
C;Superfamily: papillomavirus B6 protein ·
C;Keywords: DNA binding; early protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
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Pred. No. 3.3;
2; Mismatches
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Pred. No. 3.3;
2; Mismatches
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                                                                                                                                                                                                                                                                       73.1%;
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Similarity 66.7%;
6; Conservative 2
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                                                                                                                                                                                                                                                                                                                           6; Conservative
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120 HLNSKRRFH 128
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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Best Local Similarity
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Residues: 1-191 <OST>
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Residues: 1-158 <REU>
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Matches

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us-08-170-344-55.rpr

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Search completed: June 28, 2005, 23:32:11
Job time : 12.05 secs
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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nes 5; Conservative
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427 NLDKEQKYH 435
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-499 <GLA>
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A,Status: preliminary
A,Molecule type: DNA
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A;Gene: CC3192
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A;Molecule type: DNA
A;Residues: 1-154 <DELD:
A;Cross-tences: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: T00065
R;Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.; DNA Resses, T.; 1997
BNA Ray 30-313, 1997
A;Title: Prediction of the coding sequences of unidentified human genes. VIII. 78 new cd. A;Reference number: Z14084; MUID:98116655; PMID:9455477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1172 <1SH>
A;Cross-references: UNIPROT:Q8WXX7; EMBL:AB007902; NID:g2662164; PIDN:BAA23714.1; PID:g2
A;Experimental source: brain
C;Genetics:
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C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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C;Species: human papillomavirus type 45
C;Date: 20-Reb-1995 #sequence_revision 20-Reb-1995 #text_change 09-Jul-2004
C;Accession: 836561
                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
                                                                                                                                                                                  Gaps
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C;Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
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Pred. No. 70;
3; Mismatches 1; Indels
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                                                                                                                                      Length 154;
                                                                                                                                                                                  2; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                  69.2%; Score 36; DB 2;
66.7%; Pred. No. 8;
vative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein KIAA0442 - human (fragment)
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Best Local Similarity 55.6%;
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Best Local Similarity 66.79
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Matches 6; Conserv
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A; Molecule type: DNA
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Gaps

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C;Accession: F87644
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.
B.; Laub, M.T.; DeBoy, R.T.; Doddson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon;
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: G82923
R;Glass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, Rebruary 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A;Reference number: A82870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9A3L1; GB:AE005673; NID:g13424868; PIDN:AAK25154.1; GSPDB:G
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C,Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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55.6%; Pred. No. 45;
ive 4; Mismatches 0; Indels
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Pred. No. 36;
1; Mismatches
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 [2002].
EMBL; AF404702; AAL01361.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; E:DNA binding; IEA.
Pfam; PF00518; E6; 1.
NON TER
1 1 SEQÜENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(202).
EMBL; AF404698; AAL01353.1; -.
EMBL; AF404698; AAL01353.1; -.
EMBL; AF404698; Chost cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
PFam; PF00518; E6; 1.
Gaps
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Q919C4;
01-DEC-2001 (TYEMBLrel. 19, Created)
01-DEC-2001 (TYEMBLrel. 19, Last sequ)
01-OCT-2003 (TYEMBLrel. 25, Last sequil-OCT-2003 (TYEMBLrel. 25, Last ann
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MEDLINE=21846229; Pubmed=11857370;
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Best Local Similarity 100...
Best of Conservative
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Best Local 9; Conservative
9; Conservative
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                                                                                 123 CMSCCRSSR 131
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E6 protein (Fragment)
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NCBI_TaxID=10581;
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01-DEC-2001
01-DEC-2001
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Q919B6
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MEDLINE=21846229; PubMed=11857370;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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                   DB 2; Length 130;
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100.0%; Pred. No. 0.98;
tive 0; Mismatches 0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
B6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
                                                                                                                                                                                                                                                                                                                 (TrEWBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEWBLrel. 25, Last annotation update)
                     Score 54; DB 2;
Pred. No. 0.98;
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130 AA.
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Best Local Similarity 100.0%; Pi
Matches 9; Conservative 0;
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Q919D2;
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"Human papilomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
J. virol. 69:7743-7753(1995).
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U34114; AAA91661.1; -.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 Aa; 18292 MW; 35012A9E01993C35 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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nes 9; Conservative
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           136 CMSCCRSSR 144
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MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Tornesello M.L., Giraldo G.,
Eraldo G.,
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
EMBL, AF003015; AAB70732.1; --
GO, GO:0042025; C:host call nucleus; IEA.
GO: GO:0042025; C:host call nucleus; IEA.
InterPro, IPR001334; E6.
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MEDLINE=974374; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo G., Giraldo G.,
Beth-Giraldo E., Giraldo G.,
Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL; AF003016; ABAF0733.1;
EMBL; AF003016; ABAF0733.1;
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; B6.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
Human papillomavirus type 16.
Viruges: deDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6DBA CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
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E6 protein.
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MEDLINE=20112892; PubMed=10644829;
A van Dulin M., Snijders P.J., Voseen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
T. "Analysis of human papillomavirus type 16 B6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
T. "Analysis of human papillomavirus type 16 B6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
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05-JUL-2004 (TrENBLrel. 27, Created)
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05-JUL-2004 (TrENBLrel. 27, Last annotation update)
E6 oncoprotein (E6 protein).
E6 oncoprotein (E6 protein).
Fuman papillomavirus type 16.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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Ponglikitmongkol M., Vaeteewoottacharn K.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18334 MW; FF9F2A2FCEBA6C02 CRC64;
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Virology 14 A;Title: Hu	as, to uman pa	1-185, apilloma	1985 avirus	t XI	Virology 145, 181-185, 1985 A;Title: Human papillomavirus type 16 DNA sequence.		
A;Reference	e numbe	er: A22:	355; ML	E E	:85246220; PMID:2990099		
A, Molecule	type:	DNA					
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A;Cross-rei R;Kennedy,	rerence I.M.;	es: UNII Haddow,	PROT: PO	ยี่	26; GB:KO2718; NID:g333031; Lements, J.B.	PIDN:AAA46939.1; PI	PID:9333032
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A; Accession	n: T10	427	•				
A;Status: I	prelim.	inary; t	ranslė	ate	Status: preliminary; translated from GB/EMBL/DDBJ		
A;Residues:	1-15	8 <ken></ken>			•		
A;Cross-rei	ference	es: EMBI	J: K0271	. 81	Cross-references: BMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032	1; PID:9333032	
C, Genetics:	·						
A;Gene: 50 C:Superfamily: papillomavirus E6 protein	. i	anilloma	atr ive	8	protein		
C, Keywords	DNA	pinding,	early	3 2	Keywords: DNA binding; early protein; zinc finger		
F:37-73/Region: zinc finger CCCC motif	gion:	zinc fir	iger CC	ပ္ပင်			
F ; 110-146/1	TOT Fou	. 21112	Tafir	į			
Query Match Best Local Matches	tch al Simi 9;	similarity 100 9; Conservative	100.0%; 100.0%; /ative	* *	; Score 52; DB 1; Length 1; Pred. No. 0.0052; 0; Mismatches 0; Indels	158; .s 0; Gaps 0;	
ò	1 HE	HLDKKQRFH	6				
Db 1	125 HLI	5 HLDKKQRFH	133				
C E-HODG							

WeWEJI

E protein - human papillomavirus type 31

C;ppecies: human papillomavirus type 31

C;bpecies: human papillomavirus type 31

C;bate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

A;clate: number: A94398; MulD:89299478; PMID:2545036

A;Reference number: A94398; MulD:89299478; PMID:2545036

A;Status: translation not shown

RESULT 2

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A;Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877 R;Cole, S.T.; Danos, O. J. Mol. Biol. 193, S99-608 and comparative analysis of the human papillomavirus type 18 A;Reference number: A92937; MUID:87283882; PMID:3039146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
R;Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the pp. A;Reference number: A92791; MUID:86306665; PMID:3018129
A;Contents: annotation; identification of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
BmbO J. 6, 139-144, 1987.
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A;Reference number: A91068; MUID:87218459; PMID:3034571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A33502
R;Volpers, C; Streck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26165; G26251
submitted to the EMBL Data Library, August 1993
A; Reference number: 836469
A; Reference number: 836469
A; Reference number: 836579
A; Status: preliminary
A; Molecule type: DBL
A; Residues: 1-155 < DBL>
A; Residues: 1-155 < DBL>
A; Residues: 1-155 < DBL>
C; Superfamily: papillomavirus E6 protein
C; Repwords: DNA binding; arrly protein; transforming protein; zinc finger
E; 33-69/Region: zinc finger CCCC motif.
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Keywords: DNA binding; early protein; transforming protein; zinc finger
F;12-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
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                                                                                                                                                                                                                                                                                                                                                         Length 155
                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                      76.9%; Score 40; DB 1; 66.7%; Pred. No. 1.3; tive 2; Mismatches
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3; Mismatches
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Pred. No. 3
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Best Local Similarity 66.70,
Best Local Similarity 66.70,
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A;Molecule type: DNA
A;Residues: 1-158 <COL>
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hes 6; Conserv
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A; Residues: 1-158 <SEE>
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     A;Molecule type: DNA
A;Residues: 1-149 <GGL.
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: host Homo sapiens (man)

C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C; Accession: E40824; 836521

R; Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

K; Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, R.A.; Dubensky, T.W.

A; Title: The phylogenetic relationship and complete nucleotide sequence of human papillo

A; Reference number: A40824; MUID:92124753; PMID:1310198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-149 < MAR.
A; Cross-reference: UNIPROT: P27228; GB: M74117; NID: g333050; PIDN: AAA46966.1; PID: g333051
R; Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A; Description: Primer-directed sequencing of human papillomavirus types.
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                                                                                                         C;Superfamily: papillomavirus E6 protein
C;Keywords: DA binding; early protein; zinc finger
E;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain 35H
C; Superfamily: papillomavirus E6 protein
C; Rywords: DNA binding; early protein; zinc finger
F; 30-66/Region: zinc finger CCCC motif
F; 103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                  Score 48; DB 1;
Pred. No. 0.031;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein - human papillomavirus type 35
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A;Residues: 1.155 cLOB>
A;Cross.references: UNIRROT:P24836
R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                  92.3%;
88.9%;
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                    8; Conservative
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|HLEEKKRFH 126
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A;Accession: S36521
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Best Local Similarity
Matches 8; Conserv
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A,Molecule type: DNA
A,Residues: 1-149 <DEL>
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:866-874(2002).
EMBL; AF404699; AAL01355.1; -
GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21846229; PubMed=11857370; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 52; DB 2; Length 130; 100.0%; Pred. No. 0.017; ive 0; Mismatches 0; Indel8
0; Indels
                                                                                                                                                                                                                                    0919C0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                   130 AA
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0; Mismatches
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EMBL, AR404700, AAL01357.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.

Pfam; PF00518; E6; 1.

NON TER 1

SEQUENCE 130 AA; 15779 MW; 26D0147D39
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9; Conservative
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nes 9; Conservative
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                                                                                          97 HLDKKORFH 105
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                                               1 HLDKKORFH
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0919C2;
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Matches
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404701; AAL01359.1; -.
GO; GO:000257; C:host cell nucleus; IEA.
PF00518; E6; 1.
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                 Query Match 100.0%; Score 52; DB 2; Length 103; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 9; Conservative 0; Mismatches 0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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Best Local Similarity
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MEDLINE=21846229; PubMed=11857370;
MEDLINE=21846229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868=874(2002).
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
Beam; PPRO5187; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868=874(2002).

GO; GO:0042702; AAL01361.1;

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; debNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TAXID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                               138 AA.
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Matches 9; Conservative
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MEDLINE=21846229; PubWed=11857370;
MALTS K.J., Thompson C.H., Cossatt Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874[20-2].
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:001877; F:DNA binding; IEA.
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SEQÜENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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Watts K.J. Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97.868-874(2002).
BMBL; AAF04695; AAL0147.1;
GO, GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
FFEM: PFEM: B6; 1.
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SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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97 HLDKKORFH 105
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NCBI_TaxID=10581;
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Gaps

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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.,
"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer 1801868-874 (2002)
EMBL, AP404698, AAL01353.1.
GO; GO: 0042025; C:host cell nucleus; IEA.
GO; GO: 0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
NON TER
1 1
SEQÜENCE 143 AA; 17274 MW; 5FB0F7E1ECGDBA82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

100.0%; Score 52; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels
                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TremBurel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
 143 AA.
 PRT;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21846229; Pubmed=11857370;
PRELIMINARY;
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0; Gaps

Search completed: June 28, 2005, 23:28:13 Job time : 56.1 secs

्राह bade Blank (nebto)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec Run on:

US-08-170-344-55 52 Title: Perfect score:

1 HLDKKORFH 9 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1717557 seqs, 384547976 residues Searched:

1717557 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT TRMP PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

			_	_	_		_	_			
	App]	App	App]	App	App	Appli	App	App	Appli	App	2, Appli
	42,	41,	26,	10,	40,	9	20,	27,	7	16,	
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence
ΩΙ	US-10-476-570-42	US-10-476-570-41	US-10-476-570-56	US-10-858-384-10	US-10-476-570-40	US-10-177-390-6	US-10-484-063-20	US-10-484-063-27	US-10-858-384-2	US-10-367-057-16	US-10-472-724-2
DB	16	16	16	17	16	14	17	11	11	11	16
* Query e Match, <u>L</u> ength DB I	14	20	22	22	23	151	151	151	158	158	171
% Query Match,	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	52	52	52	52	52	52	52	52	52	52	52
Result No.	-	7	9	4	Ŋ	9	7	80	6	10	11

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Gaps

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Query Match 100.0%; Score 52; DB 16; Length 14; Best Local Similarity 100.0%; Pred. No. 0.0081; Matches 9; Conservative 0; Mismatches 0; Indels

۳4,	Sequence 4, Appli	1 =	ø,	ý	7	7	23	2	9	5	2	23	N	18	78	54		1336,	e 8156,	Sequence 4398, Ap	m	1426	25(~	8	236	ģ	4	4	39	129
US-09-367-309A US-10-000-903	7 US-10-899-771-4	US-10-899-771	US-10	US-10	2	-10	US-1	-10	US-1	US-1	US-1	US-1(SD	US-10	ns	US-10	S US-10-425-115-291659	US-09-925-301-1336		Sn	ä	an	ns	US-10-37	US-10	/ US-10-732-923-2363	ns	ns	US-10-193-764	ns	US-10-437-963-129618
133	17	11	13	17	13	17	14	16	16	13	17	13	17	14	-	15	Н	σ	٦	16	-	-	15	Н	Н	٦	П	7	Ä	14	16
266	273	292	371	371	390	390	10	158	172	. 278	278	383	383	15	15	978	229	231	960	1266	1281	51	165	299	509	535	895	897	1005	101	1215
100.0	0.00	100.0	100.0	100.0	100.0	100.0	84.6	75.0	75.0	75.0	75.0	75.0	75.0	71.2	71.2	71.2	69.2	69.2	69.2	69.2	69.2	67.3	67.3		67.3	67.3	67.3	67.3	67.3	67.3	67.3
52	2 2	25	52	25	52	25	44	39	39	39	39	39	39	37	37	37	36	36	36	36	36	35	35	35	35	35	35	35	35	35	32
13 2	1.4 4. c	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 124-138
US-10-476-570-42
                                                                                                                                                                                                                                                                 GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLEBER, GENTAR

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: MAXLURE of peptides derived from B6 and/or E7

TITLE OF INVENTION: MAXLURE of peptides derived from Se thereof

FILE REFERENCE: 4553-5071-US

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT PILING DATE: 2003-11-04

PRIOR APPLICATION NUMBER: FR 01 05980

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 42

LENGTH: 14

MANDEL OF MADEL US-10-476-570-42
; Sequence 42, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
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us-08-170-344-55.rapb

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TYPE: PRT
ORGANISM: Artificial Sequence
                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                             HLDKKORFH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 HLDKKORFH 16
                                                                                                                                     1 HLDKKORFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-858-384-10
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LENGTH: 23
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
US-10-476-570-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                          APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MOURGAULT-VILLADA, Isabelle
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
ITILE OF INVENTION: Mixture of peptides derived from E6 and/or E7
ITILE OF INVENTION: Mixture of peptides derived from E6 and/or E7
ITILE OF INVENTION: Mixture of peptides derived from E6
ITILE OF INVENTION: Mixture of peptides derived from E6
ITILE OF INVENTION: Mixture of peptides
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NOS: 63
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/10476570

PUBLICATION NO. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

APPLICANT: MAILLERE, Bernard

APPLICANT: MOUSLLE TOURGAUT-VILLADA,

APPLICANT: POUVELLE-T, Jean-Grand

APPLICANT: GUILLET, Jean-Grand

APPLICANT: POUVELLE TOUR LOSS AND TOUR

TITLE OF INVENTION: MAXULE OF EPOPTIONS

CURRENT APPLICATION NUMBER: PCT/FR02/01533

FRIOR PELICATION NUMBER: PR 01 05980

PRIOR APPLICATION NUMBER: PR 01 05980

PRIOR APPLICATION NUMBER: PR 01 05980

PRIOR APPLICATION NUMBER: PR 01 05980

NUMBER OF SEQ ID NOS: 63

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO SECOND NOS: 63

LENGTH . 22
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                                                                                                                                                                                         ; Sequence 41, Application US/10476570 ; Publication No. US20040170644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: artificial sequence
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ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                            1 HLDKKORFH 9
HLDKKQRFH 9
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAUIT-VILLADA, Isabelle
APPLICANT: BOURGAUIT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maximure of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maximure of peptides derived from E6 and/or E7
TITLE OF INVENTION: Maximure of peptides derived from E6
TITLE OF INVENTION WINDER: US/10/476,570
CURRENT PILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SED ID NOS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BUURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: DARTICULARLY IN VACCINATION
FILE REPREBNCE: 2058-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: PS/907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 10
LINGTH: 22
                                                                   Gaps
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100.0%; Score 52; DB 16; Length 22; 100.0%; Pred. No. 0.013; ive 0; Mismatches 0; Indels
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Sequence 40, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
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; Sequence 10, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
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ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
    118 HLDKKQRFH 126
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                                                                                                                                                                                            GENERAL INFORMATION:
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; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140
US-10-476-570-40
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APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: MITHELE
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2002-01-16
PRIOR PLLING DATE: 2002-07-19
PRIOR PLLING DATE: 2002-07-19
PRIOR PILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Eucaryotic Cells with Linear
                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 52; DB 14; Length 151; 100.0%; Pred. No. 0.088; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                 Query Match 100.0%; Score 52; DB 16; Length 23; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                      Sequence (A Application US/1017390)

Publication No. US20030143743A1

GENERAL INFORMATION:

APPLICANT: Schuler, Gerold

APPLICANT: N.V. Antwerps Innovatiecentrum

TITLE OF INVENTION: Improved Transfection of Eucaryotic Cel

TITLE OF INVENTION: Polymucleotides by Blectroporation

FILE REFERENCE: 021505wo/JH/ml

CURRENT FILING DATE: 2012-06-20

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.1

SEQUENCE: CONTROL OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
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; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Human papillomavirus
US-10-484-063-20
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Matches 9; Conservative
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HLDKKQRFH 16
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Gaps

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1 HLDKKORFH 9

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                                                                                                     APPLICANT: SASTEY, K. JAGANNADHA
APPLICANT: SASTEY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHEBE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR PALLING DATE: 2004-01-19
PRIOR PLLING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
: SOFTWARE: Patentin Ver. 2.1
: LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR PRILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 3.2
SEQ ID NO 2
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100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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; ORGANISM: Human papillomavirus type 16
US-10-484-063-27
US-10-484-063-27; Application US/10484063; Publication No. US20050048467A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10858384; Publication No. US20050033025A1; GENERAL INFORMATION:
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Similarity 100.0%; Score 52; DB 9; Length 266;
9; Conservative 0; Mismatches 0: Indels
  ; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES; FILE REFERENCE: 01727/0149; CURRENT APPLICATION NUMBER: US/09/367,309A; CURRENT FILING DATE: 1999-08-11; PRIOR APPLICATION NUMBER: PCT/AU98/00080; PRIOR FILING DATE: 1998-02-13; PRIOR FILING DATE: 1997-02-19; RRIOR FILING DATE: 1997-02-19; NUMBER: OF SEQ ID NOS: 6; SOFTWARE: PALENTIN Ver. 2.1; SEQ ID NO: 1 LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DALGA, CAGGALLIGARIS APPLICANT: CADEZON SILVA, TETEBA APPLICANT: Delisse, Anne-Marie Eva Fernande APPLICANT: Delisse, Anne-Marie Eva Fernande APPLICANT: Gerard, Catherine Marie Ghislaine APPLICANT: Lombardo-Bencheikh, Angela TITLE REFERENCE: B45107 CURRENT APPLICATION NUMBER: US/10/000,903 CURRENT FILING DATE: 2001-10-01 PRIOR PLLING DATE: 1990-08-17 PRIOR PLLING DATE: 1997-08-22 PRIOR PLLING DATE: 1997-08-22 PRIOR FILING DATE: 1997-08-22 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 273
                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
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125 HLDKKQRFH 133
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ORGANISM: Homo sapien
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Best Local Similarity
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US-10-000-903-4
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US-10-899-771-4
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Publication No. US20040171806A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
TITLE OF INVENTION: MOBBER: US/10/472,724
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFWWARE: Patentin version 3.2
SEQ ID NO 2
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RESULT 10
US-10-367-057-16

i Sequence 16, Application US/10367057
i Publication No. US20050100554A1
i GENERAL INFORMATION:
i APPLICANT: Cuthill, Scott;
i APPLICANT: Guthill, Scott;
i APPLICANT: Lewin, David A.;
i APPLICANT: Looi, Chean Eng
i TILE Of INVENTION: Complexes and Methods of Using Same;
i TILE PERERNE: 21402-259
i CURRENT APPLICATION NUMBER: US/10/367,057
i PRIOR PILING DATE: 2003-02-14
i NUMBER OF SEQ ID NOS: 198
i SSOFTWARE: CURASEQLIST Version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09367309A; Publication No. US20020081329A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HLDKKORFH 9
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Search completed: June 29, 2005, 05:18:15 Job time : 116.15 secs

250 HLDKKORFH 258

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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
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Sequence 1426, Ap
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                                                                                    June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
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Sequence 23,
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-4563
US-09-471-276-1426
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US-09-601-729-278
US-09-980-523A-10
US-08-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-08-350-316-12
US-08-359-382-12
US-09-359-382-10
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US-09-359-382-10
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US-08-934-915-166
US-08-934-915-166
US-08-94-915-166
US-08-94-915-166
US-08-94-915-106
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Maximum Match 100%
Listing first 45 summaries
                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 200000000
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52
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Match Length
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Perfect score:
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No.
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ALIGNMENTS

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Sequence 223, Application US/08159339A
| Sequence 223, Application US/08159339A
| Patent No. 6037135
| GENERAL INFORMATION:
| APPLICANT: Rabbo, Ralph T.
| APPLICANT: Sette, Alessandro
| APPLICANT: Sette, Alessandro
| TITLE OF INVENTION: USes
| TITLE OF INVENTION: USes
| TORRESPONDENCE ADDRESS:
| TOWNERS OF SEGUENCES: 1234
| COUNTRY: USA
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TYPE: PRT
ORGANISM: Human Papillomavirus
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ORGANISM: Human Papillomavirus
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                  8 HLDKKQRFH 16
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                                                                                                                                                                                                                              1 HLDKKORFH
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SEQ ID NO 10
LENGTH: 22
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APPLICANT: LOING, ESTELLE
APPLICANT: LOING, ESTELLE
APPLICANT: LOING, ESTELLE
APPLICANT: GUILLET, JEAN GERARD
TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: USG/09/601,729
PRIOR PILING DATE: 1992-02-05
PRIOR PLING DATE: 1992-02-06
PRIOR PLING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SEQ ID NO 278
LENGTH: 20
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| Sequence 10. Application US/09980523A
| Patent No. 6783763
| GENERAL INFORMATION:
| APPLICANT: GHORPIN, JEANNINE
| APPLICANT: GOURGAULT VILLADA, ISABELLE
| APPLICANT: GUILLET, JEAN-GERARD
| APPLICANT: GUILLET, JEAN-GERARD
| APPLICANT: FERRIES, ESTELLE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR DSE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR DSE
| TITLE OF INVENTION: PROTEINS OF HPV, THEIR DSE
| TITLE OF INVENTION: PRICE NOB! AO INS
| CURRENT APPLICATION NUMBER: US/09/980,523A
| CURRENT FILING DATE: 2000-05-31
| PRIOR FILING DATE: 1999-06-03
| NUMBER OF SEQ ID NOS: 24
| SOFTWARE: PATENTIN VET. 2.1
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US-09-601-729-278
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                                                100.0%; Score 52; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                           0; Indels
                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                         Sequence 278, Application US/09601729
Patent No. 683952
GENERAL INFORMATION:
APPLICANT: THIAM, KADER
APPLICANT: ANTHAUT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: CONG, ESTELLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                      Local Similarity
      US-08-159-339A-223
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                                                  Query Match
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TYPE: PRT
ORGANISM: Artificial Sequence
         not relevant
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                                                                                                                                                                                                                   1 HLDKKQRFH 9
                          MOLECULE TYPE:
HYPOTHETICAL:
US-08-316-239B-4
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APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cherly A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B FILING DATE: 30-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35.205
REPRENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                              UNME-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
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ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08316239B
Patent No. 5679509
                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION UNDMERE: 35,205
REFRENCE/DOCKET NUMBER: UNWE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEPAK: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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TYPE: amino acid
STRANDEDNESS: not releva
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Gaps
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; Sequence 12. Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: ERAZER.
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT APPLICATION NUMBER: US/08/359,082
ERALIER APPLICATION NUMBER: US/08/860,165
ERALIER PILING DATE: 1997-09-22
ERALIER PILING DATE: 1997-09-22
ERALIER PILING DATE: 1997-09-22
ERALIER PILING DATE: 1997-09-22
ERALIER PILING DATE: 1997-12-20
ERALIER PILING DATE: 1994-12-20
MUMBER OF SEQ ID NOS: 27
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US-08-860-165-12

Sequence 12, Application US/08860165A

Patent No. 6004557:
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBS. Elizabeth Ann
APPLICANT: WEBS. Elizabeth Ann
APPLICANT: WEBS. Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722//130
FURRENT FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER PILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
ENEGTH: 172
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Query Match

100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels
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100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels
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Sequence 10, Application US/08860165A Patent No. 6004557
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LENGTH: 266
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| Sequence 10. Application US/08117083
| Patent No. 5719054
| GENERAL INFORMATION: | APPLICANT: Boursnell, Michael E. | APPLICANT: Boursnell, Michael E. | APPLICANT: Inglis, Stephen C. | APPLICANT: Inglis, Stephen C. | APPLICANT: Mirco, Alan J. | TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins | VUMBER OF SEQUENCES: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 71 | CORRESPONDENCE ADDRESS: 72 | CORRESPONDENCE ADDRESS: 73 | CORRESPONDENCE ADDRESS: 74 | CORRESPONDENCE ADDRESS: 75 | CORRESPONDENCE ADDRESS: 76 | CORRESPONDENCE ADDRESS: 77 | CORRESPONDENCE ADDRESS: 78 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS: 70 | CORRESPONDENCE ADDRESS:
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                                                                                                                                                         Query Match 100.0%; Score 52; DB 3; Length 172; Best Local Similarity 100.0%; Pred. No. 0.034; Matches 9; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: /note= "Xaa refers to stop codon in
OTHER INFORMATION: the open reading frame."
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRIATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                      ) ORGANISM: Human papillomavirus type 16
US-09-359-382-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58783
TELECOMMUNICATION INFORMATION:
TELEPRX: 415-398-3249
TELER: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 182 amino acida
TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                     63 НЕДККОКРН 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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    TYPE: PRT
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RESULT 10 US-08-860-165-10

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
GENERAL INFORMATION:
APPLICANT: EDMARDS, Stirling John
APPLICANT: EDMARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT APPLICATION VUMBER: US/08/660,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENTH: 266
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US-09-359-382-10
Sequence 10, Application US/09359382
Sequence 10, Application US/09359382
Sequence 10, Application US/09359382
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB. Flizabeth Ann
APPLICANT: WEBB. Flizabeth Ann
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
BARLIER APPLICATION NUMBER: PCT/AU95/00868
BARLIER APPLICATION NUMBER: PCT/AU95/00868
BARLIER FILING DATE: 1995-12-20
BARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
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ORGANISM: Human papillomavirus type 16
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 9; Conservative
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US-09-367-309A-1
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Gaps

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100.0%; Score 52; DB 3; Length 292; 100.0%; Pred. No. 0.055;
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TILLE OF INVENTION: Vaccine
TILLE OF INVENTION: VACCINE
TILLE OF INVENTION WIMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
FRIOR FILLING DATE: 1990-0-17
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR FILLING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
                       TITLE OF INVENTION: Vaccine
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
NUMBER OF SEQ ID NOS: 23
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
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       Lombardo-Bencheikh, Angela
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Job time : 18.05 secs
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US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
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Best Local Similarity 100..
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapien
US-09-485-885-10
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US-09-485-885-6
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                                                               APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REPERENCE: 107227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT PILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN OF: 2.1
SEQ ID NO : 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE SEFERENCE: B45:107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT PILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOSTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Bruck, Claudine
APPLICANT: Delisse, Anne-Marie Eva Fernande; APPLICANT: Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Patent No. 6342224
Patent No. 6428807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
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Best Local Similarity 100.
Matches 9; Conservative
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CORGANISM: Homo sapien
US-09-485-885-4
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US-09-485-885-4
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ö Gaps ö 100.0%; Score 52; DB 3; Length 371; 100.0%; Pred. No. 0.069; 0; Indels

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Q8b564 Q8bb19 Q8bb20 Q8bb21 Q9w8c3 Q9w931

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DB 2; Length 81;
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14515; AAB60569.2; -..
GO; GO:000477; F. Chost cell nucleus; IEA.
GO; GO:000377; F. DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE=Cervical;
Haegert D.G., Galutira D.F., Younghusband B.H.;
SUbmitred (SEP-194) to the EMBL/GenBank/DDBJ databases.
EMBL; U14511; AAB60565.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
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Human papillomavirus.

Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

Papillomavirus.

NCBI_TaxID=10566;
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Papillomavirus.
NCBI_TaxID=10566;
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Last annotation update)
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Last annotation update)
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100.0%; Pred. No. 0.2;
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Q8B564
Q8BB19
QBBB20
QBBB21
Q9W8C3
Q9WMP2
Q9WMP3
Q9WMP5
VE6 HPV16
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Q8QHTO
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les 9; Conservative
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      - protein search, using sw model
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illarity 100.0%; Pred. No. 0.22;
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STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (GEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14514; AAB60568.2;
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STRAIN-HPV16; TISSUB-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1;
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Q80887; O. Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
EG protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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90 AA, 11021 MW, 47F42BBEFACCCC01 CRC64;
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91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
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GO; GO:003677; F:DNa binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
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Pfam; PF00518; E6; 1.
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NCBI_TaxID=10566;
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STRAIN=HPV16; IISSUE-Cervical tissue;
STRAIN=HPV16; IISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghushand B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513; AAB60567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IFR001334; E6.
Pfam; PF00518; E6; 1.
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STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Calutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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Papillomavirus.
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84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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GO; GO:003677; F:DNA binding; IEA.
Interpro; IPR001334; E6.
Pfam; PF00518; E6; 1.
GO, GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
NON TER 1 1
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SEQÜENCE 84 AA; 10177 MW; SAB6B
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MEDINE-2186219: PubMed=11857370;
Watts K.J. Thompson C.H., Cosaart Y.E., Rose B.R.;
Watts K.J. Thompson C.H., Cosaart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:866-874 (2002)
Int. J. Cancer 97:866-874 (2002)
GO: GO:00042025; C:host cell nucleus; IEA.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
Pfam; PRODSIB; E6; 1.
NON TER
SEQÜENCE 130 AA; 15792 MW; BGC2147D227EEDDC CRC64;
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404701; AAL01359.1; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNA binding; IEA.
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                0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
86 protein (Fragment)
 Pred. No. 0.25;
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                         52 LIRCINCOK 60
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NCBI_TaxID=10581;
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NCBI_TaxID=10581;
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Q919B4
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404692; AAL01342.1; -.
GO; GO:000257; C:host cell nucleus; IEA.
PF00518; E6; 1.
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              Query Match 100.0%; Score 51; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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60; G0:0042025; Cibost cell nucleus; IEA.
GO; 60:0003677; F:DNA binding; IEA.
Pfam; PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;
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Best Local Similarity 100...
9; Conservative
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76 LIRCINCOK 84
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Watts K.J., Thompson C.H., Cosart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404696; AAL01349.1; -..
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404695; AAL01347.1;
GO, GO:0003677; F:DNA binding; IEA.
Fram, PF00518; E6; 1.
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0919C9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OFC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment to Fragment type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, FAF04699; AAL01355.1;

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

Pfam; PF00518; E6; 1.

1 SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Human papillomavirus type 16.
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| December 201902 | PRELIMINARY; | PRT; | 138 AA. |
| December 301902 | PRELIMINARY; | PRT; | 138 AA. |
| December 301902 | PRELIMINARY; | PRT; | 138 AA. |
| December 3010 (TrEMBLrel. 19; Last sequence update) |
| December 3010 (TrEMBLrel. 19; Last sequence update) |
| December 3010 (TrEMBLrel. 19; Last annotation update) |
| December 3010 (TrEMBLrel. 19; Last annotation update) |
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Search completed: June 28, 2005, 23:28:12 Job time : 55.1 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec Run on:

US-08-170-344-54 51 Title: Perfect score:

1 LIRCINCOK 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB & Maximum DB &

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
	51	100.0	158	-	Wewlhs	protein E6 - human
7	45	88.2	149	Н	W6WL35	ein -
m	43	84.3	158	ч	W6WL18	protein -
4	43	84.3	158	N	836561	protein -]
S	42	82.4	149	Н	W6WL31	E6 protein - human
9	41	80.4	75	~	E91249	ü
7	40	78.4	119	7	S47942	റ
œ	40	78.4	119	7	S50634	ribosomal protein
6	39	76.5	103	~	108775	hypothetical prote
10	39	76.5	149	н	W6WL33	,
11	39	76.5	4	Н	W6WL58	E6 protein - human
12	38	74.5	113	7	T43515	ribosomal protein
13	38	74.5	119	7	T37896	40s ribosomal prot
14	38	74.5	120	~	T39095	40s ribosomal prot
15	38		230	N	C90266	-2
16	38	74.5	559	7	T33347	hypothetical prote
17	37	72.5	0	N	T26806	
18	37	72.5	4	N	836515	,
19	37	72.5	191	Н	W6WLR1	E6 protein - rhesu
20	37	72.5	311	7	B84428	hypothetical prote
21	37	72.5	1932	~	T25525	
22	36	70.6	120	~	T14466	Φ
23	36	70.6	133	~	AB3465	н
24	36	70.6	153	7	S36503	
25	36	70.6	198	~	S48236	SNM1 protein - yea
56	36	70.6	274	~	T34004	
27	36	70.6	795	~	T48252	eceriferum3 (CER3)
28	36	•	902	7	B84652	TU.
29	35	9.89	38	7	S07972	н

RESULT 2

A;Status: translation not shown

A; Accession: E40824

probable ribosomal ORF MSV256 hypothe	rotein	E6 procein - numan hypothetical prote	recepin - human	gag polyprotein -	hypothetical prote	hypothetical prote	URBS1 protein - sm	hypothetical prote	hypothetical prote	conserved hypothet	gag polyprotein -	gag polyprotein -	hypothetical prote
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133	142	314	451	206	695	797	950	23	63	67	73	75	89
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35	S	ກຕ	32	32	32	32	32	34	34	34	34	34	34
30 31	32	3.5 4.6	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                   C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
MyMolecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
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                                                                          R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G. Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily; papillomavirus E6 protein
Keywords: DNA binding; early protein; zinc finger
E;37-73 Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
E6 - human papillomavirus type 16
es: human papillomavirus type 16
                                                               C; Accession: A03682; T10427
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Rigoldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1889
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A;Reference number: A94398; MUID:89299478; PMID:2545036
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                                                                                                                                                                                                                          A;Residues: 1-158 <DEL.
A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g3970;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916 C;Comment: This protein may be involved in the oncogenic potential of this virus. C;Superfamily: papillomavirus B6 protein C;Superfamily: papillomavirus B6 protein C;Superfamily: papillomavirus P6;Protein; zinc finger CCCC motif F;30-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                 R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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Pred. No. 7.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2
Pred. No. 5.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W6WL31
E6 protein - human papillomavirus type 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Species: human papillomavirus type 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.4%;
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 84.3%;
Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.00.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 LIRCLRCOK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Likcircon 108
                                                                                                                              A;Reference number: S36469
A;Accession: S36561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-149 <GOL>
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A Molecule type: DNA
A, Residues: 1-75 < HAY>
                                                                                                                                                                                                A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A32444
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E91249
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Shabo J. 6, 139-144, 1987
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16
A;Reference number: A91068; MUID:87218459; PMID:3034571
A;Molecule type: DNA
A;Residues: 1-149 <MAR>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-158 <COL>
A; Residues: 1-158 <COL>
A; Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
A; Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
B; Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A; Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the 3, Reference number: A92791; WUID:86306665; PID:3018129
A; Contents: annotation; identification of the protein
C; Superfamily: papillomavirus E6 protein
C; Superfamily: papillomavirus E7 protein
E; Reywords: DNA binding; early protein; transforming protein; zinc finger.
F; Reywords: Zinc finger CCCC motif
F; 105-141/Region: zinc finger CCCC motif
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A,Cross-references: UNIPROT: P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877
R;COLe, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A,Title: Nucleotide sequence and comparative analysis of the human papillomavirus type
A,Reference number: A92937; MUID:87283882; PMID:3039146
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C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
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C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.149 - CEBL>
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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                                                                                         R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types. A;Reference number: S36469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.3%; Score 43; DB 1; Length 158; 77.8%; Pred. No. 5.5;
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1; Mismatches
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Matches 7; Conserv
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A;Residues: 1-149 cCCL>
A;Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
E;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33,
A;Reference number: A93020; MUID:86200464; PMID:3009902
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                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein DKFZp586C1620.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
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                                                                                                                             Score 40; DB 2; Length 119;
Pred. No. 13;
2; Mismatches 1; Indels
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A;Residudes: 1-103 «MAN-
A;Cross-references: UNIPROT:Q9Y3X7; EMBL:AL050144
A;Experimental source: adult uterus; clone DKFZp586C1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T08775
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z16471
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22;
                                   A,Map position: 5R
C;Superfamily: rat ribosomal protein S26
C;Keywords: cytosol; protein biosynthesis; ribosome
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Pred. No. 17;
3; Mismatches
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               A;Cross-references: SGD:S0000933; MIPS:YER131w
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Pred. No.
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C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.5%;
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                                                                                                                                Query Match
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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21 VRCVNCSK 28
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Best Local Similarity
7; Conserve
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27 VQCINCEK 34
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A; Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of 8.cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-119 <BRU>
| Cross-references: EMBL:Z72711; NID:g1322808; PIDN:CAA96901.1; PID:g1322809; MIPS:YGL18
| Experimental source: strain S288C
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                                                                                                                                                                                                                                                                                                                                                                            R;Wu, M.; Tan, H.
Bubmitted to the EMBL Data Library, June 1994
A.Description: Disruption of RPS26 in Saccharomyces cerevisiae results in the formation
A;Reference number: S47942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda
A;Reference number: S50437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-119 <BER>
A;Cross-references: EMBL:X91489; NID:g1143557; PIDN:CAA62786.1; PID:g1143559
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64183
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                                                                                                                                                                                                                                                 ribosomal protein S26.e.A, cytosolic - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G1355; protein YGL189c
C;Species: Saccharomyces cerevisiae
C;Date: 11-Nov-1994 #sequence revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: S47942; S61129; S64206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae)
N;Atternate names: protein YER131w
N;Atternate names: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: 28-Jan_1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
                                        Gaps
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                                        Indels
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13;
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Keywords: cytosol; protein biosynthesis; ribosome
               Pred. No. 6.6; Hismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB;
Pred. No. 13;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: SGD:S0003157; MIPS:YGL189c
A,Map position: 7L
85.7%; Fic.
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Best Local Similarity 62.5%;
Matches 5; Conservative 2
                                     Conservative
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57 IRCVNCQ 63
       Best Local Similarity
Matches 6; Conserv
                                                                                   2 IRCINCQ 8
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A;Residues: 1-119 <DIE>
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Cispecies: Schizosaccharomyces pombe
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
Cibacession: T39099
A.Reference number: Z21827
A.Reference number: Z21827
A.Reference number: Z21827
A.Reference number: Z21827
A.Roseion: T39095
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Roseion: J-120 are DNA
A.Residues: 1-120 are DNA
A.Residues: J-120 ar
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Cispecies: Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cispecies: Sulfolobus solfataricus
Cipate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
Cipate: 20266
Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Y Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-230 «KUR»
A;Cross-references: UNIPROT:097212; GB:AE006641. NID:gl3814322; PIDN:AAK41386.1; GSPDB:GP
C;Genetics:
A;Gene: hdrC-2
                                                                                                                                                                                                                                                                                                                                                               40s ribosomal protein s26 - fission yeast (Schizosaccharomyces pombe)
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74.5%; Score 38; DB 2; Length 120;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels
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Pred. No. 43;
2; Mismatches
   Pred. No. 27;
2; Mismatches
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Job time : 12.05 secs
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66.7%;
62.5%;
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Best Local Similarity 66.7
Matches 6; Conservative
   Best Local Similarity 62.5
Matches 5; Conservative
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21 VRCINCSR 28
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21 VRCINCSR 28
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                                                                                                            2 IRCINCOK 9
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A;Molecule type: DNA
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T39095
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C;Superfamily: papillomavirus E6 protein
C;Kwywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCC motif
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A;Experimental source: strain 972h-; cosmid c1805
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C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43515
R;Kawamukai, M.
submitted to the EMBL Data Library, July 1999
A;Description: S. pombe ribosomal protein S26 homolog.
A;Reference number: Z22530
A;Accession: T43515
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
   C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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C;Superfamily: rat ribosomal protein S26
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22;
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A;Reference number: Z21752
A;Accession: T37896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-119 < RIE>
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                  C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
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A;Residues: 1-113 <KAW>
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A;Molecule type: DNA
A;Residues: 1-149 <KIR>
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Matches 7; Conservative
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Best Local Similarity 62.5
Matches 5, Conservative
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15 VRCINCSR 22
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A; Introns: 42/1
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June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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51
                                                                                                                                                                                                                                 1 LIRCINCOK 9
                                                                                                                                                                                          Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                        Scoring table:
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Run on:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

/ cgn2 6/ptodata/1/pubpaa/USO9B FUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USO9E PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USO9E PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USO9E PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USO0B PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USO0B PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOB PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBCOMB.pep: , / cgn2 6/ptodata/1/pubpaa/USOOE PUBM.pep: , / cgn2 6/ptodata/1/pubma/USOOE PUBM.pep: , / cgn2 6/ptodata/1/pubm Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

Description	Sequence 39, Appl	Sequence 8, Appli	Sequence 60, Appl	Sequence 13, Appl	Sequence 6, Appli	Sequence 20, Appl	Sequence 27, Appl	Sequence 2, Appli	Sequence 16, Appl	Sequence 2, Appli	Sequence 1, Appli
ΩI	US-10-476-570-39	US-10-484-063-8	US-10-476-570-60	US-10-476-570-13	US-10-177-390-6	US-10-484-063-20	US-10-484-063-27	US-10-858-384-2	US-10-367-057-16	US-10-472-724-2	US-09-367-309A-1
DB	16	17	16	16	14	11	17	17	17	16	0
Query Match Length DB	15	20	22	29	151	151	151	158	158	171	266
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	51	51	51	51	51	51	51	51	51	51	51
Result No.	7	8	m	4	ស	9	7	80	σ	10	11

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Gaps

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Query Match 100.0%; Score 51; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.18; Matches 9; Conservative 0; Mismatches 0; Indels

Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appli Sequence 13, Appl Sequence 153, Appl Sequence 157, Appli Sequence 157, Appli Sequence 157, Appli Sequence 157, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 23, Appli Sequence 25, Appli Sequence 251, Appli Sequence 655, Appli Sequence 655, Appli Sequence 655, Appli	28660 15640
US-10-000-903-4 US-10-899-771-4 US-10-899-771-4 US-10-899-771-10 US-10-899-771-6 US-10-899-771-6 US-10-899-771-6 US-10-899-771-6 US-10-899-771-14 US-10-899-771-14 US-10-751-845-153 US-10-751-845-153 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-899-771-21 US-10-751-845-158 US-10-751-845-158 US-10-751-845-158 US-10-767-701-53503 US-10-751-846-116-317008 US-10-221-378-655 US-10-221-378-655	-10-425-115-28 -10-437-963-15
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0.000000000000000000000000000000000000	44
U U U U U U U U U U U U U U U U U U U	388
11111111122222222222222222222222222222	. 4. 4. 3. 4. 7.

ALIGNMENTS

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 101-115 US-10-476-570-39
                                                                                                      ## APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
## APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
## APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
## APPLICANT: MAILLEBE, Mernard
## APPLICANT: BOUNGAULT-VILLADA, Isabelle
## APPLICANT: BOUNGAULT-VILLADA, Isabelle
## APPLICANT: BOUNGAULT-MORATILLE, Sandra
## APPLICANT: GUILLE-MORATILLE, Sandra
## APPLICANT: GUILLE-MORATILLE, Sandra
## APPLICANT: GUILLET, Jean-Gerard
## TITLE OF INVENTION: MAKTURE of peptides derived from E6 and/or E7
## TITLE OF INVENTION: MAKTURE of peptides derived from E6 and/or E7
## TITLE OF INVENTION: MAKTURE of peptides derived from E6 and/or E7
## TITLE OF INVENTION: MAMBER: US/01/476,570
## CURRENT PILING DATE: 2003-11-04
## PRIOR PILING DATE: 2003-11-04
## PRIOR PILING DATE: 2001-05-04
## NUMBER OF SEQ ID NOS: 63
## SOFTWARE: PatentIN Ver. 2.1
## SEQ ID NO 39
## LEASTH IS
Sequence 39, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
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3 LIRCINCOK 11
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US-10-476-570-60
                                                                                                                                                                      Sequence 8, Application US/10484063
; Sequence 8, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
    APPLICANT: SASTRY, K. JAGANNADHA
    APPLICANT: TORTOLERO-LUNA, GUILLERMO
    APPLICANT: FOLLEN, MICHELE
    ITILE OF INVENTION: PRE-CANCEROUS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
    ITILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
    FILE REFERENCE: UTSC:560US
    CURRENT APPLICATION NUMBER: US/10/484,063
    CURRENT PILING DATE: 2004-01-16
    PRIOR PILING DATE: 2004-01-16
    PRIOR PILING DATE: 2002-07-19
    RIOR PILING DATE: 2001-07-20
    NUMBER OF SEQ ID NOS: 27
    SOFTWARE: Patentin Ver. 2.1
    SEQ ID NO 8
    LENGTH: 20
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| Sequence 60, Application US/10476570
| Publication No. US20040170644A1
| GENERAL INFORMATION:
| APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
| APPLICANT: MATILERE, Bernard
| APPLICANT: BOURGAUT-VILLE-MARATILE.
| APPLICANT: BOURGAUT-VILLE-MARATILE.
| APPLICANT: BOURGAUT-VILLE-MARATILE.
| APPLICANT: GUILLET, Jean-Gerard
| TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
| TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7
| TITLE OF INVENTION: Maxture of peptides derived from E6
| TITLE OF INVENTION: MARER: US/10/476,570
| FILE REFERENCE: 45636-5071-US
| CURRENT FILING DATE: 2003-11-04
| PRIOR FILING DATE: 2003-11-04
| PRIOR FILING DATE: 2003-0-04
| NUMBER OF SEQ ID NOS: 63
| SEQ ID NO 60
| LEASTH APPLICATION NUMBER: FR 01 05980
| SEQ ID NO 60
| LEASTH APPLICATION NUMBER: PRIOR FILING DATE: 2003-0-04
| NUMBER OF SEQ ID NOS: 63
| LEASTH APPLICATION NUMBER: PRIOR FILING DATE: 2003-0-04
| SEQ ID NO 60
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100.0%; Score 51; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 51; DB 17; Length 20; Best Local Similarity 100.0%; Pred. No. 0.24; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: artificial sequence
                            11 LIRCINCOK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LIRCINCOK 9
1 LIRCINCOK 9
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13
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Publication No. US20030143743A1

GENERAL INFORMATION:

APPLICANT: Schuler, Gerold

APPLICANT: Schuler, Gerold

TITLE OF INVENTION: Improved Transfection of Bucaryotic Cells with Linear TITLE OF INVENTION: Polynucleotides by Electroporation

FILE REFERENCE: 021505wo/JH/ml

CURRENT APPLICATION NUMBER: US/10/177,390

CURRENT PILING DATE: 2002-06-20

NUMBER OF SEO ID NOS: 34

SOFTWARE: Patentin Ver. 2.1
                                                                                 APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Gernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
ITILE OF INVENTION: Mixture of peptides derived from E6 and/or E7
ITILE OF INVENTION: Mixture of peptides derived from E6 and/or E7
ITILE OF INVENTION: MIXTURE DEPLICANTION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
FRIOR FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR APPLICATION NUMBER: PCT/FR02/01533
SOFTWARE: PARCHIN VOR. 2.1
SSOFTWARE: PARCHIN VOR. 2.1
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100.0%; Score 51; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels C
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TYPE: PRT
ORGANISM: Human papillomavirus type 16
Sequence 13, Application US/10476570; Publication No. US20040170644A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uvery Match
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0. 77471
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j Sequence 16, Application US/10367057

j Publication No. US20050100554A1

j GENERAL INFORMATION:

j APPLICANT: Cuthill, Scott;

j APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, Complexes and Methods of Using Same;

TITLE OF INVENTOR: Complexes and Methods of Using Same;

FILE REFERENCE: 21402-559

CURRENT FILING DATE: 2003-02-14

PRIOR PRILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 16

SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
APPLICANT: CHOCK TO THE CARACITES APPLICANT: BOURGAULT VILLADA, ISABELLE APPLICANT: GUILLET, JEAN-GERARD APPLICANT: GUILLET, JEAN-GERARD APPLICANT: COUNAN, FRANCINE APPLICANT: CONNAN, FRANCINE APPLICANT: CONNAN, FRANCINE TITLE OF INVENTION: PATTICULARLY IN VACCINATION FILE OF INVENTION: PATTICULARLY IN VACCINATION FILE OF INVENTION PARTICULARLY IN VACCINATION FILE OF INVENTION NUMBER: US/10/858,384

CURRENT PILING DATE: 1909-06-03

NUMBER OF SEQ ID NOS: 24

SOFTHARE: PATCHING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SEQ ID NO S: 24

LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LIRCINCOK 9
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US-10-472-724-2
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Publication No. US20050048467A1

GENERAL INFORMATION:
APPLICANT: ADGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
CURRENT APPLICATION NUMBER: PCT/US02/23198
FRIOR FILING DATE: 2002-07-19
FRIOR PELLOR DATE: 2002-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 27
LENGTH: 151
LENGTH: 151
                                                                                                   ; APPLICANT: SASTRY, K. JAGANNADHA;
APPLICANT: SASTRY, K. JAGANNADHA;
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: TORTOLERO-LUNA, GUILLERMO
TITLE OF INVENTION: MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HEV-ASSOCIATED
TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REPERENCE: UTSC:560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2002-01-16
PRIOR PRILING DATE: 2002-01-19
PRIOR PLILING DATE: 2002-07-19
PRIOR PLILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTION OFF: 2.1
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US-10-484-063-27
                              Sequence 20, Application US/10484063 Publication No. US20050048467A1 GENERAL INFORMATION:
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Publication No. US20050033025A1
GENERAL INFORMATION:
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; ORGANISM: Human papillomavirus
US-10-484-063-20
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-000-903-4
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100.0%; Score 51; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels (
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APPLICANT: MALLIAROS, UIM
FILLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILLE REPERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT PELING DATE: 1999-08-11
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1999-02-13
PRIOR PILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTING DATE: 1997-02-19
SOFTWARE: PATENTING DATE: 1997-02-19
SOFTWARE: PATENTING DATE: 1997-02-19
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SEQ 1D NO 2
LENGTH: 171
                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Synthetic Construct US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Human papillomavirus type 16 US-09-367-309A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09367309A, Publication No. US20020081329A1, GENERAL INFORMATION:
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Publication No. US20020182221A1
GENERAL INFORMATION:
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Best Local Similarity
9; Conserv?
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** APPLICANT: Dalemans, Wilfried L.J.

** APPLICANT: Dalemans, Wilfried L.J.

** APPLICANT: Dalemans, Milfried L.J.

** APPLICANT: Dalemans, Milfried L.J.

** APPLICANT: Dalemans, Compositions Compising Human Papilloma Virus Proteins

** TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins

** TITLE OF INVENTION: DATE: DALEMAN AND AND APPLICATION NUMBER: US/10/899, 771

** CURRENT APPLICATION NUMBER: US/09/881, 976

** PRIOR PLING DATE: 1908-12-18

** PRIOR PLING DATE: 1989-12-18

** PRIOR PLING DATE: 1999-12-24

** NUMBER OF SEQ ID NOS: 28

** NUMBER: FastSEQ for Windows Version 3.0

** SEQ ID NO 4-4

** SEQ ID NO 4-4

** SEQ ID NO 4-4
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Bva Fernande
APPLICANT: Carbardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR FILING DATE: 1998-08-17
PRIOR PLLING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
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i Sequence 10, Application US/10000903
i Publication No. US20020182221A1
i GENERAL INFORMATION:
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Publication No. US20050031638A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
....hes 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                        TYPE: PRT
ORGANISM: Homo sapien
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US-10-899-771-10

Sequence 10, Application US/10899771

Sequence 10, Application US/10899771

Sequence 10, Application US/10899771

Sequence 10, Application Wo. US20050031638A1

GENERAL INFORMATION:

APPLICANT: Gerard, Catherine Marie Ghislaine

TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide

TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide

TITLE OF INVENTION: UMBER: US/10/899,771

CURRENT APLICATION NUMBER: US/09/581,976

FRIOR APPLICATION NUMBER: PCT/EP98/08563

FRIOR FILING DATE: 1998-12-18

FRIOR FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 10

LENGTH: 292
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CTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
CHER INFORMATION: 16)
US-10-899-771-10
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100.0%; Score 51; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEG for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-10
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ORGANISM: Artificial Sequence
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Search completed: June 29, 2005, 05:18:15 Job time : 117.15 secs

232 LIRCINCOK 240

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1 LIRCINCOK 9

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Sequence 79, Appl Sequence 165, Appl Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 14, Appli Sequence 14, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 21,  Appli Sequence 516, Appli
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-934-915-165
US-08-316-233A-2
US-08-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-09-155-12
US-09-155-12
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US-09-155-10
US-09-165-10
US-08-159-339A-569
US-08-159-339A-569
US-08-159-339A-90
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US-09-132-210-333
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No.
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Sequence 45114, A Sequence 43718, A Sequence 5522, Ap Sequence 31938, A Sequence 1155, A Sequence 11, Applisequence 1, Applisequence 1, Applisequence 6011, Applisequence 6011, Applisequence 6011, Applisequence 6011, Aps			
28 38 74.5 44 4 US-09-270-767-45114 29 38 74.5 84 4 US-09-270-767-45114 31 36 70.6 269 4 US-09-328-0324-9691 32 36 70.6 269 4 US-09-328-0324-9691 33 36 70.6 504 4 US-09-270-767-35938 34 35 68.6 121 4 US-09-270-767-35938 35 35 68.6 121 4 US-09-248-796A-19706 35 35 68.6 133 4 US-09-248-796A-19706 35 35 68.6 133 4 US-09-732-210-1578 37 35 68.6 133 4 US-09-732-210-1578 38 34 66.7 35 3 US-09-057-486-1 41 34 66.7 72 4 US-09-107-522A-4927 42 34 66.7 72 4 US-09-107-522A-4927 43 34 66.7 72 4 US-09-107-522A-4927 44 34 66.7 72 4 US-09-270-767-40981 45 34 66.7 92 4 US-09-270-767-40981	ALIGNMENTS	RESULT. 19.6-08-159-39A-79 19.6-08-159-39A-79 19.6-08-159-39A 19.6-08-159-31155 19.6-08-159-315A 19.6-08-150-315A 10.6-08-150-315A ; STRANDEDNESS: single ; TOPOLGGY: linear ; MOLECULE TYPE: peptide	

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USA
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STREET: 61
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STATE:
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                                     100.0%; Score 51; DB 3; Length 10; 100.0%; Pred. No. 0.015;
                                                                               0; Indels
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                                                                                                                                                                                                                                                     Sequence 165, Application US/08934915
| Ratent No. 5932412
| CENERAL INFORMATION:
| APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA |
| APPLICANT: DILLNER, LENA |
| APPLICANT: DILLNER, LENA |
| TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8, |
| TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR |
| TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR |
| TITLE OF INVENTION: DIAGNOSTIC PURPOSES |
| CORRESPONDENCE ADDRESS: ADDRESSEE: ADDRESSEE: ADDRESSEE: AMSON & ASSOCIATES, P.A.
                                                                                                                                                                                                                                                                                                                                                                                    SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                             0; Mismatches
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COMPUTER: IBM PC compatible

OPERATION SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FLING DATE: 22-5EP-1997

CLASSIFICATION: 435

PRIOR APPLICATION APPR:

APPLICATION NUMBER: 07/949,836

FLING DATE: APPLICATION NUMBER: 07/949,836

FLING DATE: APPLICATION NUMBER: 07/949,836

FLING DATE: APPLICATION THORMATION:

NAME: LOUISE A. FOULCH

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 165: SEQUENCE CHARACTERISTICS:
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                                                                             9; Conservative
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COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                              2 LIRCINCOK 10
                                                                                                                     1 LIRCINCOK 9
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GY: linear
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Matches 9; Conserv
                                                        Best Local Similarity
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US-08-934-915-165
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US-08-159-339A-79
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                                       Query Match
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Sequence 2, Application US/09980523A Patent No. 6783763 GENERAL INFORMATION:

RESULT 3 US-09-980-523A-2

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Conservative
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Best Local Similarity
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Matches 9; Conserv
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LENGTH: 172
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APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated wi
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                      Gaps
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                                                                            100.0%; Score 51; DB 1; Length 162; 100.0%; Pred. No. 0.23;
                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: PROPER FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-860-165-12
Sequence 12, Application US/08860165A
Patent No. 6004557
Patent No. ROPASTION:
APPLICANT: EDWARDS, Stirling John
                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08316239B
Patent No. 5679509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 81-9453
TELEFAX: (703) 80-9387
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                  9, Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                Best Local Similarity
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HYPOTHETICAL:
// MOLECULE TYPE:
// HYPOTHETICAL:
US-08-316-239B-3
                                                                                                                                                                                                                                                    RESULT 5
US-08-316-239B-4
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                                                                              Query Match
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US-09-359-382-12

Sequence 12, Application US/09359382

Sequence 12, Application US/09359382

GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
CURRENT FRAZER, 1an

STILLE REFERENCE: 017227/0148
CURRENT FILING DATE: 1994-07-23

BARLIER APPLICATION NUMBER: US 08/860,165

BARLIER FILING DATE: 1995-12-20

BARLIER FILING DATE: 1995-12-20

BARLIER FILING DATE: 1994-12-20

BARLIER FILING DATE: 1994-12-20

MUMBER OF SEQ ID NOS: 27

SEQTWARE: PatentIn Ver. 2.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
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APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 3; Length 172; 100.0%; Pred. No. 0.25;
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                                                                                 CURRENT APPLICATION NUMBER: US/08/860,165A CURRENT FILING DATE: 1997-09-22 EARLIER APPLICATION NUMBER: PCT/AU95/00668 EARLIER FILING DATE: 1995-12-20 EARLIER APPLICATION NUMBER: AU PNO157 EARLIER FILING DATE: 1994-12-20 WUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 10, Application US/08860165A
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GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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Gaps

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100.0%; Score 51; DB 4; Length 266; 100.0%; Pred. No. 0.38;
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Sequence 6, A2224

GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: General Catherine Marie Eva Rernande
APPLICANT: Gerand, Catherine Marie Chislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFRENCE: B45107

CURRENT APPLICATION NUMBER: US/09/485,885

CURRENT PILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1998-08-27

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabescon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTON: Vaccine
FILE REFERENCE: B45107
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
FRICH APPLICATION NUMBER: PCT/AU98/00080
FRICH APPLICATION NUMBER: PCT/AU98/00080
FRICH APPLICATION NUMBER: AU PO 5178
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
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Beet Local Similarity 100.00
Beet Accal Similarity 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapien
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GENERAL INFORMATION:
APPLICANT: BUNANDS, Stirling John
APPLICANT: BUNANDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: FRAZER, Ian
ITILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1999-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
EARLIER FILING DATE: 1994-12-20
SOFUNDREN OF SEQ ID NOS: 27
SOFUNDREN OF SEQ ID NOS: 27
LENGTH: 266
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                                    APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 51; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 0.38; Matches 9; Conservative 0; Mismatches 0; Indels
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Patent No. 6428807;
GENERAL INFORMATION:
APPLICANT: MACFALLAROS, JIM
APPLICANT: MALLAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
                                                                                                                                    CURRENT PELICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 266
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US-09-359-382-10
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Patent No. 6306397
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ORGANISM: Artificial Sequence
   APPLICANT: WEBB, Elizabeth Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
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Pred. No. 4.1e+05;
1; Mismatches 1
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
                                                                                                                                                                                                                                                 Mismatches
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100.0%; Score 51;
Best Local Similarity 100.0%; Pred. No. 0
Matches 9; Conservative 0; Mismatche
      PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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PRIOR APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-A0(2-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 569, Application US/08159339A
Patent No. 6037135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.3%;
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Grey, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 576-0300
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LENGTH: 9 amino acids
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Best Local Similarity 77.8
Matches 7; Conservative
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                     232 LIRCINCÓK 240
                                                                                        LENGTH: 390
TYPE: PRT
CRGANISM: Homo sapien
US-09-485-885-14
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STRANDEDNESS: sir
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APPLICANT: Kubo, 1
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Patent No. 634224
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
GREECANT: Buck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TILLE OF INVENTION: Vaccine
FILE REFERNCE: B45107
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Buck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
ITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FRAESEQ for Windows Version 3.0
LENGTH: 371
                                                                                                                                                                                                                                                                                                              Mismatches
PRIOR APPLICATION NUMBER: PCT/EP98/05285 PRIOR FILING DATE: 1998-08-17 PRIOR PILING DATE: 1997-08-22 NUMBER OF SEQ ID NOS: 23 SOFTHARE: PASESEQ for Windows Version 3.0 SEQ ID NO 10
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Patent No. 6342224
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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US-09-485-885-6
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09wmp5
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Q8bb20
                          Q8bb21
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=HPVI6; TISSUE=Cervical tissue;
STRAIN=HPVI6; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, U14515; AAB60569.2; -.
GO; GO:000477; F. Chost cell nucleus; IEA.
GO; GO:000377; F. EDM binding; IEA.
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STRAIN=HPV16; TISSUE-Cervical;
STRAIN=HPV16; TISSUE-Cervical;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14511; AAB60565.2; --
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no RNA stage; Papillomaviridae;
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9784 MW; DDSFEDBC9F845B97 CRC64;
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ilarity 100.0%; Pred. No. 0.0098;
Conservative 0: Mismatel
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                                                                                                                                                 ALIGNMENTS
                          QBB21
Q9W8C3
Q9W931
Q9WMP2
Q9WMP3
Q9WMP3
V9WMP5
VEG HPV16
Q8JMU8
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Human papillomavirus.
Viruses; daDNA viruses, nv
Papillomavirus.
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E6 protein (Fragment).
Human papillomavirus.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
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Best Local Similarity
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NCBI_TaxID=10566;
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Copyright (c) 1993 - 2005
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STRAIN=HPV16; TISSUE=Cervical tissue;
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (GSP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1; -.
GO; GO:0004277; F. Chost cell nucleus; IEA.
GO; GO:0003677; F: DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE=Cervical tissue;
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (GSP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, U14514; AAB60566.2; -
GO, GO:000477; F.Nak abinding; IEA.
GO, GO:000377; F.DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses, dsDNA viruses, no RNA stage, Papillomaviridae;
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SEQÜENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
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90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
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91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
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Q80885;
01-NOV-1996 (TrEMELrel. 01, Created)
01-NOV-1996 (TrEMELrel. 01, Last sequence update)
01-OCT-2003 (TrEMELrel. 25, Last annotation update)
E6 protein (Fragment).
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Last annotation update)
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NCBI_TaxID=10566;
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NCBI_TaxID=10566;
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100.0%; Score 54; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -. GENGT CON CONTRAINT CONTRAINT CAN BURN CONTRAINT; FINAL binding; IEA.
INTERPRO! IPR001334; E6.
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STRAIN-HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghubband B.H.;
Submitted (SPP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, 104513; AAB60567.2; ...
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IFRR001334; E6.
Pfam; PF00518; E6; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; deDNA viruses, no RNA stage; Papillomaviridae;
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Papillomavirus.
                    Interpro; IPR001334; B6.
Pfam; PF00518; B6; 1.
NON TER 84 84
NON TER 84 84
SEQÜENCE 84 AA; 10177 MW; SAB6B896468E1CAA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0003677; F:DNA binding; IEA
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Human papillomavirus.
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MEDINE=2186229; Numbed=11857370; Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-874 (2002).

EMBL, AF404701, AAL01359.1; ---
GO, GO:0042025; C:host cell nucleus; IEA.
GO, GO:0003677; F:DNA binding; IEA.
Ffam, PRO0518; E6; 1.

NON TER.
SEQÜENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404700; AAL01357.1;
GO; GO:0003677; F:Dost cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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                       0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E procein (Fragment).
Human papillomavirus type 16.
Viruges; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
  Pred. No. 0.016;
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                     0; Mismatches
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  100.0%;
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Best Local Similarity 100.0%;
Matches 9; Conservative (
Best Local Similarity 100.
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                                                             1 QOYNKPLCD 9
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                                                                                                                                                                                                                                                                                                                                                                       Papillomavirus
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Q919C0
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Q919B8
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MEDLINE=21846229; PubMed=11857370;

Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL, FA040704; AAL01165.1;

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:005677; F:DNA binding; IEA.

PÉRM; PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
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                Query Match
100.0%; Score 54; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                          49 QQYNKPLCD 57
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404694; AAL01345.1;
GO; GO:000257; C:host cell nucleus; IEA.

Péam; PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404695; AAL01347.1; -..
GO; GO:0042055; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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C Q919D2;
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T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
T 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
E 6 protein (Fragment).
S Human papillomavirus type 16.
C Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
C Papillomavirus.
X NCBI_TaxID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=21846229; PubMed=11857370;
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E6 protein (Fragment).
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MEDLINE=21846229; PubMed=11857370;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF046699; AAL01355.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0043677; F:DNA binding; IEA.
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MEDLINE=21846229; PubMed=11857370;
MEDLINE=21846229; PubMed=11857370;
Matte K.J., Thompson C.H., Cossatt Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868=874(2002).
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0018; E6; 1.
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E6 protein (Fragment).
Human papillomavirus type 16.
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Search completed: June 28, 2005, 23:28:12 Job time : 55.1 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec Run on:

US-08-170-344-53 54

1 QQYNKPLCD 9 Title: Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable membrane protein YMR162c - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein YM8520.11c
C;Species: Saccharomyces cerevisiae
C;Species: O8-Jul.1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54520; S54607
R;Huft, S; Bowman, S.
RyHuf, S; Bowman, S.
A;Reference number: S54510

RESULT 2

S54520

A, Accession: S54520 A, Molecule type: DNA A, Residues: 1-1656 < HUN>

hypothetical prote	hypothetical prote	cathepsin L (EC 3.	thymidine phosphor	thymidine phosphor	exodeoxyribonuclea	hypothetical prote	hypothetical prote	probable chaperone	hypothetical prote	beta-N-acetylhexos	retrovirus-related	hypothetical prote	hypothetical prote		hypothetical prote
T11222	T05461	A53810	AG2592	A97375	NCEC7	T16546	F96802	G83305	T04562	JC7821	GNLRL1	C72534	T30065	WEWLC1	AD2197
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284	287	339	438	438	456	477	481	627	627	191	1260	29	127	150	202
61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	61.1	59.3	59.3	59.3	59.3
33	33	33	33	33	33	33	33	33	33	33	33	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	42

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SEES
A; Residues: 1-158 <SEES
A; Cross-treferences: UNIRROT: P03126; GB: K02718; NID: g333031; PIDN: AAA46939.1; PID: g333032
R; Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
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protein B6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: K02718; NID: 9333031; PIDN: AAA46939.1; PID: 9333032
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A;Molecule type: DNA
A;Residues: 1-158 <KEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: papillomavirus E6 protein
Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
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A,Molecule type: protein
A,Residues: 28-102 <001>
A,Residues: 28-102 <001>
A,Residues: 28-102 <001>
A,Residues: 28-102 <001>
A,Residues: 37-57 <002>
R,When, P; Rose, J; Love, R; Wei, C.H.; Wang, B.C.
R,Chen, P; Rose, J; Love, R; Wei, C.H.; Wang, B.C.
A,Title: Reactive sites of an anticarcinogenic Bowman-Birk proteinase inhibitor are simil A,Reference number: A42052, MUD19-2112932; PMID: 370730
A,Title: Reactive sites of an anticarcinogenic Bowman-Birk protein regulates endogeneous proteinase during germination, stores sulf C,Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology C,Keywords: duplication; seed; serine proteinase inhibitor; Bowman-Birk inhibitor repeat homology F,227/Domain: signal sequence #status predicted <816>
F,1-27/Domain: Signal Sequence #status P,1-27/Domain: Signal Sequence #status P,1-27/Dom
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Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID: 20406833; PMID: 10952301
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                  Rjodani, S.; Ikenaka, T.
1. Biochem. 83, 737-745, 1978
A;Title: Studies on soybean trypsin inhibitors. XII. Linear sequences of two soybean dout
A;Reference number: A01303, MID:78150870; PMID:641033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;44-70/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;71-96/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;73-97,44-59,47-93,49-57,67-74,71-86,76-84/Disulfide bonds: #status experimental F;51/Inhibitory site: Arg (trypsin) #status predicted F;78/Inhibitory site: Arg (trypsin) #status predicted
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82310
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                                                                                     A;Cross-references: EMBL:X68706; NID:g18571; PIDN:CAA48657.1; PID:g18572
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                                                                                                                                A; Experimental source: clone pB26
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38 EYSKPCCD 45
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Matches 5; Conserv
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A, Molecule type: DNA
A, Residues: 1-412 <HEI>
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N;Contains: proteinase inhibitor (Bowman-Birk) E-I (PI-II)
C;Species: Glycins max (soybean)
C;Date: 24-Apr-1984 #sequence revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: 832243; JC2224; A01303; B01303; S29559
C;Accession: 832243; JC2224; A01303; B01303; S29559
Existing to the EMBL Data Library, October 1992
A;Description: Molecular cloning of a gemonic DNA encoding the soybean bowman-birk prote
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R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Biosci. Biotechnol. Biochem. 58, 843-846, 1994
A;Title: Nucleotind sequence homology of cDNAs encoding soybean Bowman-Birk type protein
A;Reference number: JC2224; MUID:94289861; PMID:7764974
A;Cross-references: UNIPROT:Q12674; GB:Z49705; EMBL:Z49700; NID:g825556; PID:g825567; EM
A;Experimental source: strain AB972
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A;Status: mRNA
A;Molecule type: mRNA
A;Residues: 1-83 <JOUN
A;Cross-references: UNIPROT:P01064; EMBL:M20733; NID:g169946; PIDN:AAA33954.1; PID:g1699
C;Supperfamily: Bowman-Birk proteshanse inhibitor; Bowman-Birk inhibitor repeat homology
F;25-51/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;52-77/Domain: Bowman-Birk inhibitor repeat homology <BB12>
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C;Species: Glycine max (soybean)
C;Date: 02-01993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S07941
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of CDNA encoding the soybean protease inhibitors PI IV
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Pred. No. 69;
3; Mismatches 1; Indels
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F/510-526/Domain: transmembrane #status predicted <TM2>
F/1323-1339/Domain: transmembrane #status predicted <TM3>
F/1373-1339/Domain: transmembrane #status predicted <TM4>
F/1400-1416/Domain: transmembrane #status predicted <TM4>
F/1401-1452/Domain: transmembrane #status predicted <TM5>
F/1436-1452/Domain: transmembrane #status predicted <TM5>
F/1474-1490/Domain: transmembrane #status predicted <TM5>
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Pred. No. 9.7;
2; Mismatches
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A,Map position: 13R
f,Keywords: transmembrane protein
F,454-470/Domain: transmembrane #ste
F;510-526/Domain: transmembrane #ste
F;133-1339/Domain: transmembrane #ste
F;1373-1389/Domain: transmembrane #ste
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55.6%;
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Best Local Similarity 55.0
Pest Local Si Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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132 ERFNKPYCD 140
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A; Molecule type: DNA
A; Residues: 1-102 <SON>
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A; Gene: CT858

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Genetics

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hypothetical 23.6K protein - turkey herpesvirus
NiAlternate names: ORE2 protein
Cispecies: turkey herpesvirus
Cibate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
Cibate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
Cibate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
Cibate: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
Airtile: The complete sequence and gene organization of the short unique region of herpes Airtile: The complete sequence and gene organization of the short unique region of herpes Airtile: The complete sequence and gene organization of the short unique region of herpes Airtile: The complete sequence and gene organization of the short unique region of herpes Airtile: The complete sequence and gene organization of the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and the short unique region of herpes and 
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RjFraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.N.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A, Filtle: The minimal gene complement of Mycoplasma genitalium.
A, Reference number: A64200; MUID:96026346; PMID:7569993
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A;Cross-references: UNIPROT:Q88519; EMBL:X68653; NID:g406783; PIDN:CAA48613.1; PID:g40678
A;Experimental source: strain FC126
C;Superfamily: Marek's disease virus minor virion protein
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C;Species: Methanothermus fervidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: C37777
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 36;
1; Mismatches 1; Indels
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                                                       Indels
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                    Pred. No. 16;
1; Mismatches
83.3%; Fig.
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Best Local Similarity 75.0%;
Matches 6; Conservative
                                                       Conservative
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174 EQYWKPLC 181
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                 Best Local Similarity
Matches 5; Conserv
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nes 6, Conserv
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                                                                                                                                                       53 NKPICD 58
                                                                                                                 4 NKPLCD 9
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      Molecule type: DNA
Residues: 1-1289 <CZI>
Cross-references: UNIPROT:Q08748; EMBL:Z75204; NID:g1420655; PID:g1420656; GSPDB:GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: T10785
R;Marro, P.; Metraux, J.P.; Sticher, L.
Submitted to the EMBL Data Library, March 1997
A;Description: Isolation of a novel cucumber cDNA associated with systemic acquired resi
                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE001359; GB:AE001273; NID:g3329331; PIDN:AAC68456.1; PID:g332933
A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            '; Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004; Accession: 867200
'; Catepluch, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobiasch, E. ubmitted to the Protein Sequence Database, July 1996
'; Reference number: 867194
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C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:024512; EMBL:U93586; NID:92406581; PID:92406582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A;Map position: 15R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 87;
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Pred. No. 1.3e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 2;
Pred. No. 63;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: mRNA; Residues: 1-87 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: strain S288C
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 71.4%,
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Best Local Similarity 66...
6; Conservative
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562 KRYNKPLLD 570
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Accession: T10785
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484 QYSKPIC 490
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                                                                                                                                                                                                                                                                                                               Status: preliminary
Molecule type: DNA
Residues: 1-609 <ARN>
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Genetics:

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Query Match

Gaps

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Protein serine carboxypeptidase T18K17.4 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Dara-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
C;Accession: B96759
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A;Residues: 1-438 <STO>
A;Cross-references: UNIPROT:Q9CAU2; GB:AE005173; NID:g6598854; PIDN:AAF18708.1; GSPDB:GN(
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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Species: 3-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: BB1723
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 200
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                           Fig. 12.15,47/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status experimental Fig. 12.15,47/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 19,4,37,41/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 10,113/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 10,113/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 10,129,122,256/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 219,222,256/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 25,249,252/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 25,233,331/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 25,325,328,331/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 25,329,325,328,331/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 36,394,397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 36,394,397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 36,394,397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 36,394,397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status predicted Fig. 397,40/Binding site: 4Fe-4S cluster (Cy8) (covalent) #status 
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Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches
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C;Superfamily: Serine carboxypeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references. UNIPROT: 049180; GB:M34016; NID:g149803; PIDN:AAA72833.1; PID:g149806 C; Superfamily: polyferredoxin 6x2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology C; Superfamily: polyferredoxin 6x2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology cFER1> F; 2-55/Domain: ferredoxin 2[4Fe-4S] homology cFER2> F; 68-125/Domain: ferredoxin 2[4Fe-4S] homology cFER3> F; 209-263/Domain: ferredoxin 2[4Fe-4S] homology cFER3> F; 209-263/Domain: ferredoxin 2[4Fe-4S] homology cFER5> F; 277-342/Domain: ferredoxin 2[4Fe-4S] homology cFER6> F; 358-412/Domain: ferredoxin 2[4Fe-4S] homology cFER6>
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A;Cross-references: UNIPROT:Q50784; GB:J04540; NID:g149730
A;Cross-references: UNIPROT:Q50784; GB:J04540; NID:g149730
A;Cross-references: UNIPROT:Q50784; GB:J04540; NID:g149730
A;Experimental source: strain Delta H
A;Note: the sequence is revised in GenBank entry MBFMVRH, release 109.0, (PID:g149734)
B;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Q1u, D.S.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
Xi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautctrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: H69017
A;Status: nucleic acid sequence not shown; translation not shown
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A;Residues: 1-95, G', 97-412 «MTH>
A;Cross-Terences: BS.AE000883; GB:AE000666; NID:g2622231; PIDN:AAB85622.1; PID:g262223
A;Experimental source: strain Delta H
R;Hedderich, R.; Albracht, S.P.J.; Linder, D.; Koch, J.; Thauer, R.K.
EASE Lett. 298, 65-68, 1992
A;Title: Isolation and characterization of polyferredoxin from Methanobacterium thermoau
A;Reference number: S20413; MUID:92183831; PMID:1312016
R;Steigerwald, V.J.; Beckler, G.S.; Reeve, J.N.
J. Bacteriol. 172, 4715-4718, 1990
A;Title: Conservation of hydrogenase and polyferredoxin structures in the hyperthermophi A;Reference number: A37777; MUID:90330590; PMID:2115877
A;Accession: C37777
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: G30315; H69017; $20413
R;Reeve, J.N.; Beckler, G.S.; Cram, D.S.; Hamilton, P.T.; Brown, J.W.; Krzycki, J.A.; Ko Proc. Natl. Acad. Sci. U.S.A. 86, 3031-3035, 1989
A;Title: A hydrogenase-linked gene in Methanobacterium thermoautotrophicum strain delta-A;Reference number: A30315; MUD:89240669; PMID:2654933
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F;69-125/Domain: ferredoxin 2[4Fe-4S] homology <FER.2
F;39-195/Domain: ferredoxin 2[4Fe-4S] homology <FER.3
F;209-264/Domain: ferredoxin 2[4Fe-4S] homology <FER.3
F;208-343/Domain: ferredoxin 2[4Fe-4S] homology <FER.3
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A,Residues: 1-2,'V',4-28 <HED>
A,Cross-references: PIDN:AAB21772.1; PID:g247131
A,Experimental source: strain Marburg, DSM 2133
C,Genetics:
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Best Local Similarity
6; Conserve
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                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-412 <STE>
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Gaps

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0; Indels

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transcription factor REST (version 2) - human (fragment)
N;Alternate names: neural-restrictive silencer factor; RE1-silencing transcription factor;Saceise: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 2.3-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: 138755
R;Schoenherr, C.J.; Anderson, D.J.
R;Schoenherr, C.J.; Anderson, D.J.
A;Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multip
A;Reference number: 138754; MUID:95176234; PMID:7871435
A;Accession: 138755
A;Accession: 138755
A;Accession: Liany
A;Molacule type: mRNA
A;Residues: 1-681 <RES>
A;Cross-references: UNIPROT:Q12957; EMBL:U13879; NID:g606947; PIDN:AACS0115.1; PID:g6069
A,Residues: 1-601 <TET>
A,Residues: 1-601 <TET>
A,Cross-references: UNIPROT:Q9PL60; GB:AE002292; GB:AE002160; NID:g7190286; PIDN:AAF3911
A,Experimental source: strain Nigg (MoPn)
C,Genetics:
A,Gene: TC0248
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A,Cross-references: GDB:702138
A,Map position: 4q12-4q12
C,Keywords: transcription regulation
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Search completed: June 28, 2005, 23:32:09 Job time: 12.05 secs

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June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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Sequence 13,
Sequence 55,
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Sequence 38,
Sequence 35,
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/ Cgn2_6/ptodata_A/pumpaa_(USO9B_PUBCOMB.pep:
/ Cgn2_6/ptodata_A/pumpaa_(USO9B_NEW_PUB.pep:
/ Cgn2_6/ptodata_A/pumpaa_(USIOM_PUBCOMB.pep:
/ Cgn2_6/ptodata_A/pumpaa_(USIOM_PUBCOMB.pep:
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/ Cgn2_6/ptodata_A/pumpaa_USIOM_PUBCOMB.pep:
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/ Cgn2_6/ptodata_A/pumpaa_USIOM_PUB.pep:
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/NEO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-476-570-35
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US-10-476-570-13
US-10-476-570-13
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US-10-177-390-6
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Sequence 16, Appl Sequence 2, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appl Sequence 13, Appl Sequence 13028, Sequence 13106, Sequence 29823, Sequence 29823, Sequence 29823, Sequence 45211, A Sequence 246016, Sequence 246016, Sequence 246016, Sequence 246016, Sequence 215491, Sequence 150743, Sequence 150743, Sequence 11804, Sequence 11804, Sequence 11804, Sequence 211911, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11801, Sequence 11804, Ap	
US-10-367-057-16 US-10-367-309-18 US-10-90-367-309A-1 US-10-90-367-309A-1 US-10-90-903-4 US-10-909-771-4 US-10-909-771-4 US-10-909-771-16 US-10-909-771-16 US-10-909-771-14 US-10-909-771-14 US-10-909-771-14 US-10-909-771-14 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-133006 US-10-479-96-13491 US-10-425-114-6912 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-2119811 US-10-425-115-219811 US-10-425-115-219811	
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112 112 123 133 133 133 133 133 133 133	

ALIGNMENTS

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; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 93-107
US-10-476-570-37
                                                                                                      APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: POUNELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: MAXEURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXEURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXEURE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXEURE of 1004/04/76,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
FRIOR FILING DATE: 2003-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN OF 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 54; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 9; Conservative 0; Mismatches 0; Indels
Sequence 37, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: artificial sequence
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LENGTH: 15
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Gaps

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Sequence 6, Appli Sequence 20, Appl Sequence 27, Appl Sequence 2, Appli

100.0 100.0 100.0

100.0

Sequence 8

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TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of the artificial sequence: peptide E6 97-111
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLER, Bernard
APPLICANT: MAILLER, Bernard
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
TITLE OF INVENTION: papillomavirus proteins and uses thereof
TITLE OF INVENTION: MARBER: 2001-103
FILLE REFERENCE: 45636-507-103
FRICA PAPLICATION NUMBER: PR 01 05980
FRICA APPLICATION NUMBER: FR 01 05980
FRICA APPLICATION NUMBER: PR 01 05980
FRICA APPLICATION NUMBER: FR 01 05980
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLER, Bernard
APPLICANT: MAILLER, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
APPLICANT: GUILLET, Gand-Gerard
TITLE OF INVENTION: papillomavirus proteins and uses thereof
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 4556-5071-US
CURRENT APPLICATION NUMBER: PC1/FR02/01533
PRIOR PLILING DATE: 2002-05-03
PRIOR PLILING DATE: 2002-05-03
PRIOR PELING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE PATENTIN VET. 2.1
SEQ ID NOS: 63
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                                                                                                                                                                                                                                                                          Sequence 38, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
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ORGANISM: artificial sequence
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QOYNKPLCD 9
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Description of the Artificial Sequence: Peptide fragment
for E6 of HPV
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Best Local Similarity 10v...
                                                                                                                                                                                                                           18 QQYNKPLCD 26
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                                                                                                 Query Match
Best Local·Similarity
Matches 9; Conserv
    OTHER INFORMATION:
COTHER INFORMATION:
US-10-858-384-8
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APPLICANT: CONMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: MAILIERE, Bernard
APPLICANT: MAILIERE, Bernard
APPLICANT: MAILIERE, Bernard
APPLICANT: MAILIERE, Bernard
APPLICANT: MOURGAUL-VILLADA, Isabelle
APPLICANT: POUVELLE-WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mapplicant us proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT FILING DATE: 2003-11-04
PRIOR PRICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 55
LENGTH: 29
                                                        Gaps
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APPLICANT: CHOPPIN, JEANNINE

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: CONDAN, FRANCINE

APPLICANT: CONDAN, FRANCINE

APPLICANT: CONDAN, FRANCINE

APPLICANT: CONDAN, FRANCINE

TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN

TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE

FILE REFERENCE: 0508-1037-1

CURRENT APPLICATION NUMBER: US/10/858,384

CURRENT FILING DATE: 1999-06-03

PRIOR FILING DATE: 1999-06-03
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    Length 29;
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    100.0%; Score 54; DB 16; 100.0%; Pred. No. 0.013;
                                                   0; Mismatches
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; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
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Publication No. US20050033025A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: artificial sequence
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Best Local Similarity 100..
مار و 9; Conservative
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SOFTWARE: Patentin Ver. 3.2
                                                   9; Conservative
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Query Match
Best Local Similarity
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LENGTH: 29
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i Sequence 20, Application US/10484063

j Publication No. US20050048467A1

j GENERAL INFORMATION:

j APPLICANT: SASTRY, K. JAGANNADHA

j APPLICANT: PORTOLENE

j TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

j TITLE OF INVENTION: METHODS AND COMPOSITIONS GROWTHS, INCLUDING CIN

j TITLE OF INVENTION: METHODS AND COMPOSITIONS GROWTHS, INCLUDING CIN

j TITLE OF INVENTION: METHODS AND COMPOSITIONS GROWTHS, INCLUDING CIN

j TITLE OF INVENTION NUMBER: US/10/484,063

j CURRENT APPLICATION NUMBER: US/10/484,063

j CURRENT FILING DATE: 2004-01-16

j PRIOR APPLICATION NUMBER: 60/306,809

j PRIOR FILING DATE: 2001-07-20

j NUMBER OF:SEQ ID NOS: 27

j SEQ ID NOS: 27

j SEQ ID NOS: 27

j ENGTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schuler, Gerold
APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
TITLE OF INVENTION: Polynucleotides by Electroporation
FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
SUTREEN FILING DATE: 2002-06-20
SOFTWARE: Patentin Ver. 2.1
                                                                   Gaps
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1 Similarity 100.0%; Score 54; DB 17; Length 29; Similarity 100.0%; Pred. No. 0.013; 9; Conservative 0; Mismatches 0; Indels
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Publication No. US20030143743A1
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; ORGANISM: Human papillomavirus
US-10-484-063-20
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US-09-367-309A-1
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US-10-472-724-2
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                                                                                                                  Sequence 27, Application US/10484063
; Sequence 27, Application US/10484063
; Publication No. USZO050048467A1
; GENERAL INFORMATION:
APPLICANT: TOTOLERNO MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE REFERENCE: UTSC.56003
TITLE REFERENCE: UTSC.56003
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: EG/306,809
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PARENTIN Ver: 2.1
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Publication No. US20050033025A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GHORMATION:
APPLICANT: GUILLET, JEANNINE
APPLICANT: GUILLET, JEANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE BE PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION HOMBER: US/10/858,384
CURRENT FILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR APPLICATION OF: 3.2
SOFTWARE: PATENTING DATE: 1999-06-03
SOFTWARE: PATENTING DATE: 1999-06-03
SOFTWARE: PATENTING DATE: 1999-06-03
SOFTWARE: PATENTING DATE: 1999-06-03
SOFTWARE: PATENTING DATE: 1999-06-03
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Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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US-10-484-063-27
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; ORGANISM: Human Papillomavirus
US-10-858-384-2
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90 QQYNKPLCD 98
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Sequence 2, Application US/10472724
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
    APPLICANT: Cid-Arregul, Angel
; APPLICANT: Cid-Arregul, Angel
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 2
; LENGTH: 171
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100.0%; Score 54; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels C
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US-10-367-057-16

Sequence 16, Application US/10367057

Sequence 16, Application US/10367057

Publication No. US20050100554A1

GENERAL INFORMATION:

APPLICANT: Cuthill, Scott;

APPLICANT: Lewin, David A.;

APPLICANT: Lewin, David A.;

APPLICANT: Conj. Chean Eng

TITLE OF INVENTOR: Complexes and Methods of Using Same

FILE REFERENCE: 21402-559

CURRENT FILING DATE: 2003-02-14

PRIOR PAPLICATION NUMBER: 05/256,911

PRIOR APPLICATION NUMBER: 60/256,911

PRIOR PLILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 198

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 16

1, ENGTW. 1 = 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Synthetic Construct US-10-472-724-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09367309A, Publication No. US20020081329A1, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MACFARLAN, RODERICK I. APPLICANT: MALLIAROS, JIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 QQYNKPLCD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 QOYNKPLCD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 158
TYPE: PRT
CRGANISM: Homo sapiens
US-10-367-057-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QQYNKPLCD 9
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Search completed: June 29, 2005, 05:18:14 Job time : 116.15 secs

203 QQYNKPLCD 211

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37773, A 52990, A 7233, Ap

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

OM protein

Run on:

Sequence:

Searched:

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Score 54; DB 2; Length 20;
Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC, PURPOSES
CORRESPONDENCE ADDRESS:
ADDRESSE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWARER
STATE: FLORIDA
US-09-949-016-8616
US-09-029-047C-2
US-09-029-047C-2
US-09-180-039A-10910
US-08-565-386-8
US-09-270-767-44293
US-09-270-767-4293
US-09-270-767-45891
US-09-270-767-61424
US-09-270-767-61824
US-09-270-767-61824
US-09-120-365-80
US-09-150-365-80
US-09-150-365-80
US-09-150-365-80
US-09-150-365-80
US-09-515-039-80
                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEE-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,133
R: 1946.6
                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 45, Application US/08934915; Patent No. 5932412; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REPERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
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MOLECULE TYPE: peptide
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Best Local Similarity
   US-08-934-915-45
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   Sequence 164, App
Sequence 233, App
Sequence 43, Appl
Sequence 40613
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55829, A
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4, Appli
12, Appli
12, Appl
10, Appl
11, Appli
4, Appli
6, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, P
Sequence 2, P
Sequence 3, P
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Sequence 12, Sequence 12,
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Sequence 10,
Sequence 1,
Sequence 4,
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Sequence
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-934-915-45
US-09-980-523A-8
US-09-316-239B-4
US-08-316-239B-4
US-08-316-239B-4
US-08-860-165-12
US-09-359-382-10
US-09-359-382-10
US-09-359-382-10
US-09-485-885-4
US-09-485-885-14
US-09-486-885-14
US-09-270-767-40613
US-09-270-767-55829
US-09-270-176-55829
US-09-270-133A-2
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US-09-873-155A-50
US-09-949-016-6644
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                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                     513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                               US-08-170-344-53
54
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                                                                                                                                                                                                                   1 QQYNKPLCD 9
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Match Length
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                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                    Scoring table:
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Result No.

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ALFLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
SUBPERMENTIAL OF SEQUENCES: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL NO. 56/930.
GENERAL INFORMATION:
APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 54; DB 1; Length 162; 100.0%; Pred. No. 0.0079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTOMNEY/AGENT INFORMATION:
NAME: Jageiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET UNMBER: 35,205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
100.0%; Pred. No. 0.0077; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            Sequence 3, Application US/08316239B Patent No. 5679509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08316239B Patent No. 5679509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 162 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: not relevant
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                              1 QQYNKPLCD
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Matches 9; Conserv
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                                                                                                                                                                                                             RESULT 4
US-08-316-239B-3
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GOUNGAULT VILLADA, ISABELLE
APPLICANT: GUNNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE BG AND E7
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILLE REFERENCE: WOB1 AO INS
CURRENT PELLING DATE: 2002-04-29
FRIOR FILLING DATE: 2002-06-31
FRIOR PELLOGATION NUMBER: FCT/FRO0/01513
FRIOR PELLOGATION NUMBER: F 99/07012
FRIOR APPLICATION NUMBER: F 99/07012
FRIOR FILLING DATE: 1999-06-03
FRIOR APPLICATION NUMBER: F 99/07012
FRIOR FILLING DATE: 1999-06-13
FRIOR FILLING DATE: 1999-06-13
FRIOR FILLING DATE: 1999-06-13
FRIOR FILLING DATE: 1999-06-13
FRIOR FILLING DATE: 1999-06-13
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APPLICANT: CHOPPIN.

APPLICANT: CHOPPIN.

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEBAN-GERARD

APPLICANT: GUILLET, JEBAN-GERARD

APPLICANT: GUILLET, JEBAN-GERARD

APPLICANT: GUILLET, JEBAN-GERARD

TITLE OF INVENTION: POLYTEPITOPIC PROTEIN FRACHENTS OF THE E6 AND E7

TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PRATICULARLY IN VACCINATION

FILE REFERENCE: WOBL AO INS

CURRENT FILING DATE: 2002-04-29

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 2.1

SOFTWARE: PALENTIN VET: 2.1

SECTIVAL: PROTEIN VET: 2.1
  Gaps
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Indels
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0,0013;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 54;
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                                                                                                                                                                                                   US-09-980-523A-8; Sequence 8, Application US/09980523A: Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09980523A Patent No. 6783763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Human Papillomavirus
US-09-980-523A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
9; Conservative
                                                                                                    6 QQYNKPLCD 14
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                                                1 QQYNKPLCD 9
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MEDLINE=21046229; PubMed=11857370;
Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL, AR404701; AAL01359.1; -..
GO; GO:0003677; P:DNA binding; IEA.
PFam; PF00518; E6; 1.
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"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).
EMBL; AF404700; AAL01357.1;
GO; GO:0042025; C:host cell nucleus; IEA.

PF605, GO:0003677; F:DNA binding; IEA.
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100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches, 9; Conservative 0; Mismatches 0; Indels
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                   0; Indels
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 procein (Fragment)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses, dsDNA viruses, no RNA stage, Papillomaviridae,
Papillomavirus.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
 Pred. No. 0.16;
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                   0; Mismatches
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MEDLINE=21846229; PubMed=11857370;
100.08;
 Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
                                                                                                                                                                      PRELIMINARY;
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                                                                      65 TTLEQQYNK 73
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                                                   1 TTLEQOYNK
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                                                                                                                                                                                                                                                                                                       Papillomavirus.
NCBI_TaxID=10581;
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Q919C0;
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Q919C0
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Q919B8
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            Query Match 100.0%; Score 47; DB 2; Length 91; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Human papillomavirus type 16.
Viruees; debNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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EMBL, AR404703, AAL01343.1; -.
GO, GO:0042025; C:host cell nucleus; IEA.
GO, GO:0003677; F:DNA binding; IEA.
PFam; PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;
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                                                                               1 TTLEQQYNK 9
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Best Local Similarity
9; Conserve
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NCBI_TaxID=10581;
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SEQUENCE FROM N.A.

MEDLINE=21846229; PubMed=11857370;

WALTS K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874 (2002).

EMBL; AAF04695; AAL01347.1; ---

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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                                                                                   0919D0 PRELIMINARY; PRT; 130 AA.
0919D0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Matches 9; Conservative
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Matches 9; Conservative
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ID 09
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**REQUENCE FROM N.A.*

**R MEDLINE=21846229; PubMed=11857370;

**RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

**RI "Sequence variation and physical state of human papillomavirus type 16

**RI "Sequence variation and physical state of human papillomavirus type 16

**RI "Sequence variation and physical state of human papillomavirus type 16

**RI "Sequence variation and physical state of human papillomavirus type 16

**RI "Sequence variation and physical state of human papillomavirus type 16

**RI "Cancer 97:868-874(2002)

**REMBL; AR404699; AAL01355.1; --

**DR GO; GO:0003677; P:DNA binding; IEA.*

**DR GO; GO:0003677; P:DNA binding; IEA.*

**DR Pfam; PFF00518; E6; 1.

**NN TRR "C.T."

**TOTA MW; 26D0147D396B0929 CRC64;
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MEDLINE-21846229; PubMed=11857370;

Watta K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watta K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868 874 (2002).

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0018; E6; 1.

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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Frament)
Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus type 16.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                         65 TTLEQOYNK 73
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1 TTLEQQYNK 9
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NCBI_TaxID=10581;
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0919C2
AC 0919C2;
DT 01-DEC.;
DT 01-DEC.;
DE E6 prott
OC Viruses
OC Papilles
OC Papilles
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EMBL; AF404694; AAL01345.1; -..
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:005677; F:DNA binding; IEA.
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0919D2 PRELIMINARY; PRT; 138 AA.
0919D2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
Human papillomavirus type 16.
Viruses; dsNNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
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Search completed: June 28, 2005, 23:28:12 Job time : 56.1 secs

78 TTLEQQYNK 86

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8 a

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C.Species: Mycobacterium tuberculosis
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C.Accession: C70791
R.fole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome & A.Reference number: A70500; MuID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: O69650; GB: AL022121; GB: AL123456; NID: 93261559; PIDN: CAA18006
A; Experimental source: strain H37RV
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibbolist Listeriophage Al18) homolog lin2412 [imported] - Listeria innocua (strain Clip1126; C; Species: Listeria innocua cravision 27-Nov-2001 #text_change 09-Jul-2004 [C; Accession: AG1733]
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fshii, H.; D.; Jones, L.M.; Karst. U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
C;Species: Saccharomyces cerevisiae
C;Dates: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C;Accession: S6702
R;Dietrich, F.S.
submitted to the EMBL Data Library, August 1995
submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 9410
                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q04049; EMBL:U33007; NID:g927685; PIDN:AAB64856.1; PID:g92765
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 2; I
Pred. No. 1.1e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2;
Pred. No. 89;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                      A;Cross-references: SGD:S0002827; MIPS:YDR419w
A;Map position: 4R
                                                                                                                                                                                                                                                                                                                                                                                                                             72.3%;
85.7%;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.3
Best Local Similarity 77.6
Matches 7; Conservative
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134 STLEQQYVK 142
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Best Local Similarity (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 LEQEYNK 436
                                                                                                                                                                                    A, Accession: S69702
A, Molecule type: DNA
A, Residues: 1-632 < DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LEQOYNK 9
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                        A; Gene: SGD: RAD30
                                                                                                                                                                                                                                                                                               C,Genetics:
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AG1733
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Molecule type: DNA
;Residues: 1-526 <WILD.
;Cross-references: UNIPROT: 023333; EMBL: Z75554; PIDN: CAA99954.1; GSPDB: GN00023; CESP: ZC
;Experimental source: clone ZC455
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C.pares: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C.Accession: T27581
R.Lightning, J.
submitted to the EMBL Data Library, June 1996
A.Reference number: 220390
                                                                                                                                                                                                                                                                                                                                              glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola
C;Species: Prevotella ruminicola
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:P95544; EMBL:U82240; NID:g1772844; PID:g1772845: Experimental source: strain B14
                                                                                                          Gaps
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S69702
hypothetical protein YDR419w - yeast (Saccharomyces cerevisiae)
                                                    72.3%; Score 34; DB 2; Length 407; 66.7%; Pred. No. 56; 2; Indels ative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 2C455.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNAA;Residues: 1-444 <WEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2;
Pred. No. 62;
3; Mismatches
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55.6%; Pred. No. 73;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: T10487
R;Wen, Z.T.; Morrison, M.
Bubmitted to the EMBL Data Library, December 1996
A;Reference number: Z17049
A;Accession: T10487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: gdhA
C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 5
A;Introns: 47/3; 123/1; 153/1; 389/3
C;Superfamily: glucuronosyltransferase
  A; Experimental source: isolate FCBR
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                           Query Match
Best Local Similarity 66.7.
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Best Local Similarity 55.6
Matches 5; Conservative
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Matches 5, Conservative
                                                                                                                                                                                          | :|| |||
249 TEIEQNYNK 257
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TTLDEEFNK 287
                                                                                                                                                            1 TTLEQOYNK 9
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Score 33; DB 2; Pred. No. 67; 1; Mismatches

70.2%;

Conservative

Query Match Best Local Similarity ''''' 6; Conserv'

246 LEOKYNK 252

3 LEQQYNK 9

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NyAlternate names: acetohydroxy acid isomeroreductase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Decies: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S30145; S34640; S36884
R;Curien, G.; Dumas, R.; Douce, R.
Plant Mol. Biol. 21, 717-722, 1993
A;Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy aci
A;Reference number: S30145; MUID:93192533; PMID:8448371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-284,'R'. 286-591 <DUM>
A;Residues: 1-284,'R'. 286-591 <DUM>
A;Cross-references: EMBL:X68150; NID:9288062; PIDN:CAA48253.1; PID:9288063
R;Dumas, R.; Curien, G.; DeRose, R.T.; Douce, R.
Biochem. J. 294, 821-828, 1993
A;Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and characte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Introns: 99/3, 130/3, 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
C; Superfamily: plant ketol-acid reductoisomerase; ketol-acid reductoisomerase homology C; Keywords: Ciloroplast; isoleucine-valine biosynthesis; isomerase, oxidoreductase F; 1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
F; 68-591/Product: ketol-acid reductoisomerase #status predicted <NNP>
F; 123-321/Domain: ketol-acid reductoisomerase homology <KAR>
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A;Residues: 1-578,'A',580-591 <DU2>
A;Cross-references: EMBL:X69880; NID:g402551; PIDN:CAA49506.1; PID:g402552
                                                                                                                                                                                                                                                                                                 ketol-acid reductoisomerase (EC 1.11.86) precursor - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S36884; MUID: 93393563; PMID: 8379936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 28, 2005, 23:32:08
Job time: 12.05 secs
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1es 6; Conservative
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A; Residues: 1-591 < CUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S30145
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Matches
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A;Residues: 1-310 <GLA>
A;Residues: 1-310 <GLA>
A;Cross-references: UNIPROT:Q928X0; GB:AL592022; PIDN:CAC97639.1; PID:g16414934; GSFDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein gp49 [Bacteriophage Al18] homolog lmo2317 [imported] - Listeria monocytogenes (e
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06825
R;Zhu, X.
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A;Reference number: 215837
A;Accession: 106825
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Reddues: 1-581 <ZHU-
A;COSB-references: UNIPROT:082043; EMBL:Y17796; PIDN:CAA76854.1
A;Experimental source: cv. G2
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Score 33; DB 2; Pred. No. 70; 1; Mismatches

70.2%; 85.7%;

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Query Match

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C;Superfamily: plant ketol-acid reductoisomerase; ketol-acid reductoisomerase homology C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase F;113-311/Domain: ketol-acid reductoisomerase homology <KAR>

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A; Gene: pgaair

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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; --
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:003677; F:DNA binding; IEA.
InterPrc; IFR001334; E6.
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513, ARB60567.2; -
GO; GO:0042025; C:host cell nucleus; IEA.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                 E6 protein (Fragment).

Human papillomavirus.

Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

NCBI_TaxID=10566;
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Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874 (2002).
EMBL; AF404703; AR101563.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; P:DNA binding; IEA.
Pfam; PF00518; B6; 1.

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MEDLINE=21846229; PubMed=11857370;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).

EMBL; AF4046923; AL01342.1; ---
GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.
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Human papillomavirus type 16.
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                              99 AA; 12005 MW; C2B96025EC370E38 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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"Sequence variation and physical state of human papillomavirus type 16
"Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates [2002].
Int. J. Cancer 97:868-874 [2002].
EMBL, AF404704, AAL01365.1;
-C. GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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STRAIN=HPV16; TISSUE-Cervical tissue;
STRAIN=HPV16; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14514; AAB60568.2; ---
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IFR001334; E6.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
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MEDLINE=21846229; PubMed=11857370;
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MEDLINE=96079021; PubMed=7494284;
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Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
EMBL. AR003016; AAB70733.1;
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                          100.0%; Score 45; DB 2; Length 130; 100.0%; Pred. No. 0.11;
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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EMBL, AF404695, AAL01347.1; -.

GO; GO:0042025; C:host cell nucleus; IEA.

GO; GO:0003677; F:DNA binding; IEA.

Pfam; PP00518; E6; 1.

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SEQÜENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
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SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein.
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                                                    0; Mismatches
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MEDLINE=97437474; PubMed=9292007;
                                                   9; Conservative
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"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L12, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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EMBL; U34114; AAA91661.1; -.
EMBL; U34125; AAA91672.1; -.
EMBL; U34130; AAA91677.1; -.
EMBL; U34131; AAA91678.1; -.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Human papillomavirus.
Viruses, dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
VCBI_TaxID=10566;
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SEQUENCE 151 AA; 18292 MW; 35012A9Ë01993C35 CRC64;
                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 protein.
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SEQUENCE FROM N.A.
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NCBI_TaxID=10566;
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SEQUENCE FROM N.A.

MEDLINE-20112892; PubMed=10644829;

ANDLINE-20112892; PubMed=10644829;

A Wan Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

A van Duin M., Shijders P.J., Meijer C.J., Walboomers J.M.;

A Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

T. Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

J. Gen. Virol. 81:317-325 (2000).

R EMBL; AR465197; AAO15691.1;

R EMBL; AA388063; CAB4518.1;

R EMBL; AA388063; CAB4518.1;

R GO; GO:0042025; C:host cell nucleus; IEA.

R GO; GO:003677; F:DNA binding; IEA.

R niterProf. IPRO01334; E6.
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Q80966; 012650; O12651; 012652; 012925; 012926; 012927; Q80962;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                       Pfam; PF00518; E6; 1.
SEQUENCE 151 Aa; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
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SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
E6 oncoprotein (E6 protein).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL; AJ388056; CAB45104.1; -.
EMBL; AJ388061; CAB45114.1; -.
EMBL; AJ388066; CAB45124.1; -.
EQQ: GO:0041025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Best Local Similarity 100.
Matches 9; Conservative
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NCBI_TaxID=10581;
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MEDILIRE-20112882; PubMed=10644829;
A van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst.F.,
A van Duin M., Shijders P.J., Vossen M.T., Klaassen E., Voorhorst.F.,
Avan Duin M., Shijders P.J., Wossen M.T., Klaassen E., Voorhorst.F.,
Avan Duin M., Shijders P.J., Wossen M.T., Klaassen E., Voorhorst.F.,
Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
B EMBI, AR003014; AAB70731.1; -
B EMBI, AR003017; AAB70731.1; -
B EMBI, AAB70508, AA015697.1; -
B EMBI, AJ388068; CAB45128.1; -
B EMBI, AJ388068; CAB45128.1; -
B EMBI, AC003013; AAB70730.1; -
B EMBI, PRO03013; AAB70730.1; -
B EMBI, EF00030477; F:DNA binding; IEA.
B InterPro, IPR001334; E6.
SEQUENCE FROM N.A.
MEDLINE=97437474; PubMed=9292007;
MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and viral genomic state of human papillomavirus
Jeden. Virol. 78:2199-2208(1997).
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"Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: J034129; AAA91676.1; -.
EMBL: AF469198; AAO15693.1; -.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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SEQUENCE 151 Aa; 18292 MW; 35012A9E01993C35 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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EMBL; U34120; AAA91667.1; -.
EMBL; U34124; AAA91671.1; -.
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"Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments";
U. Virol. 69:7743-7753(1995).
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Yamada T., Wheeler C.M., Halpern'A.L., Stewart A.C., Hildesheim A.,
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100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels
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Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                                                                Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;
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SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Early transforming protein B6.
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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60; G0:0042025; C:host cell nucleus; IEA.
G0; G0:000367; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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MEDLINE=96079021; PubMed=7494284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
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EMBL; U34117; AAA91664.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 SLYGTTLEO 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 SLYGITLEQ 90
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Q89708;
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08975
1D 08975
AC 08975
DT 01-NO
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DE Early
OC Virus
OC Virus
CO VIRUS
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089708
0C Q89708
DT 01-NO
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DT 05-JU
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RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A., RA Jenison S.A.;

RY Joulations S.A.;

RT Tuly appillomavirus type 16 variant lineages in United States
RT E.Z. and Li coding segments.";

RI L2, and Li coding segments.";

RN 12]

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Run on:

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PRELIMINARY; PRT; 81 AA.

080886; Crewit of Created)

1 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

1 01-NOV-1996 (TrEMBLrel. 25, Last annotation update)

1 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

2 E6 protein (Pragment).

3 Human papillomavirus.

4 Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

8 Papillomavirus.

1 11 TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 47; DB 2; Length 81; 100.0%; Pred. No. 0.094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUB=Cervical tissue;
STRAIN=HPV16; TISSUB=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14515; AAB60569.2; -. Group Co., Go:004267; C.host call nucleus; IEA.
GO: GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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STRAIN=HPV16; TISSUE-Cervical;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14511; AAB60565.2; --
GO; GO:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
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                             Q8BB21
Q9W8C3
Q9W931
Q9WMP2
Q9WMP3
Q9WMP4
Q9WMP4
Q9WMP6
Q9WMP6
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Q8QHP5
Q8QHT0
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Q80882;
Q80882;
Q1-NOV-1996 (TEMBLrel. 01)
Q1-NOV-1996 (TEMBLrel. 02)
Q1-OCT-2003 (TEMBLrel. 25
E protein (Fragment)
Human papillomavirus.
Viruses; dsDNA viruses, no Papillomavirus.
Viruses; dsDNA viruses, no Papillomavirus.
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Les 9; Conservative
Pfam; PF00518; E6; 1.

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SEQUENCE 81 AA; 978
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                                                                                                                                                                                                                                                                                           1612378 seqs, 512079187 residues
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             GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Query Match
100.0%; Score 47; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels
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STRAIN=HPV16; TISSUE=Cervical tissue;
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14516; AAB60570.1; -.
GO; GO:000477; F. End to the EMBL/GenBank/DDBJ databases.
GO; GO:000177; F. End binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=HPV16; TISSUE=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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90 90
90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OOT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
                                                                                                                                                                                                             90 AA.
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GO; GO:0003677; F:DNA binding; IEA.
InterPro: PRO01334; E6.
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NCBI_TaxID=10566;
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NCBI_TaxID=10566;
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Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels
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STRAIN-HPVIG; TISSUE-Cervical tissue;
Haegert D.G., Galutira D.F., Younghueband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14513; AAB60567.2; -.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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STRAIN=HPV16; TISSUG=Cervical tissue;
Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U14512; AAB60566.1; -.
                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
E6 protein (Fragment).
Human papillomavirus.
Viruses; daDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
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84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
NON TER 84 84
SEQÜENCE 84 AA; 10177 MW; 5AB6B
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                                                                                                                                            Sequence 12, Application US/09359382

Patent No. 6306397

General No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRAZER, Ian

APPLICANT: FRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

ERALIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1999-09-22

EARLIER FILING DATE: 1999-12-20

EARLIER FILING DATE: 1994-12-20

EARLIER FILING DATE: 1994-112-20

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FRAZEK, INC.
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PNO157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 266
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ORGANISM: Human papillomavirus type 16
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
                                   35 QQYNKPLCD 43
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1 OQYNKPLCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12. Application US/08860165A

Patent No. 6004557

GENERAL INFORMATION:

APPLICANT: EDMARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: PRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS

FILE REFERENCE: 17227/130

CURRENT FILING DATE: 1995-09-22

EARLIER PILING DATE: 1995-09-22

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PAPENTING VARIANTS OF NO. 157

EARLIER PILING DATE: 1994-112-20

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 12

LENGTH: 172
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                                                                              STATE: v.A
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILING DATE: 30-SEP-1994
FILING DATE: 30-SEP-1994
***CATPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTREATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: 35,205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
              ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not releve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 QQYNKPLCD 105
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US-08-860-165-12
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 292;
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100.0%; Pred. No. 0.015;
                                 Sequence 4, Application US/09485885

Patent No. 6342224

GENERAL INFORMATION:

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Delisse, Anne-Marie Eva Fernande

APPLICANT: Delisse, Anne-Marie Ghislaine

APPLICANT: Lombardo-Bencheikh, Angela

APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENITON: Vaccine

TITLE OF INVENITON: Vaccine

FILE RFERENCE: B45107

CURRENT APPLICATION NUMBER: US/09/485,885

CURRENT APPLICATION NUMBER: GP17EP98/05285

PRIOR APPLICATION NUMBER: GP2-18

PRIOR FILING DATE: 1998-08-17

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Delises, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45.07
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 1990-08-17
FRIOR APPLICATION NUMBER: CT/EP98/05285
FRIOR APPLICATION NUMBER: GB 9717953.5
FRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ 1D NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
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US-09-485-885-6
; Sequence 6, Application US/09485885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapien
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                                                                                                                                                                                    | FATERIT NO. 6366397
| GENERAL INFORMATION:
| APPLICANT: EDMANDS, Stirling John
| APPLICANT: EDMANDS, Stirling John
| APPLICANT: COX, John Cooper
| APPLICANT: PRAZER, Ian
| APPLICANT: FRAZER, Ian
| TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
| FILLE REPRESENCE: 017227/0148
| CURRENT APPLICATION NUMBER: US/09/359,382
| CURRENT PILING DATE: 1999-07-23
| EARLIER PILING DATE: 1999-07-23
| EARLIER FILING DATE: 1999-09-22
| EARLIER FILING DATE: 1995-19-22
| EARLIER FILING DATE: 1995-12-20
| FARLIER FILING DATE: 1994-12-20
| SARLIER PILING DATE: 1994-12-20
| SEQ ID NO 10
| SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 10227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-00-11
PRIOR PELLING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1997-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Human papillomavirus type 16
US-09-359-382-10
                                                                                                                                                       Sequence 10, Application US/09359382
Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09367309A; Patent No. 6428807; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                        97 QOYNKPLCD 105
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1 QQYNKPLCD 9
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Best Local Similarity
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 54; DB 3; Length 390; 100.0%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: RestSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
GENERAL INFORMATION:
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PLILNG DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-17
PRIOR FILING DATE: 1997-08-2
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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; Sequence 164, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-485-885-14
; Sequence 14; Application US/09485885
; Patent No. 6342224
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                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QQYNKPLCD 9
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US-09-485-885-14
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LENGTH: 371
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APPLICANT: DILLNER, JOAKIM

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLCMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURFOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM: Windows 3.0
SOFTWREY: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FLING DATE: 25-SEP-1997
CLASSIFICATION NUMBER: 07/949,836
                         SYNTHETIC PEPTIDES OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QOYNKPLCN 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-934-915-164
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec

US-08-170-344-52 Perfect score: Title:

1 TTLEQQYNK 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	:	-	Wewless	protein E6 - human
7	36	76.6		7	A69484	ical
m	36	76.6	739	7	T21769	
4	36	9.9/		7	A12077	
S	36	9.9/	2541	~	S11661	− 00
9	34	72.3	27	7	E83900	2-hydroxyhepta-2,4
7	34	72.3		7	C45600	asparagine-rich bl
80	34	72.3		~	.T10487	glutamate dehydrog
6	34	72.3	526	~	T27581	hypothetical prote
10	34	72.3		~	869702	hypothetical prote
11	34	72.3		~	C70791	probable ponA' pro
. 12	33	70.2		7	AG1733	gp49 (Bacteriophag
13	33	70.2		~	AE1364	protein gp49 (Bact
14	33	70.2		~	T06825	ketol-acid reducto
15	33	70.2		-	S30145	ketol-acid reducto
16	33	70.2		~	T45681	ketol-acid reducto
17	33	70.2		Н	S17180	l-acid
18	33	70.2	1173	7	T43527	sp8 protein - fiss
19	33	70.2			A41622	ein-tyr
20	33	70.2		~	G64237	DNA-directed RNA p
21	33	70.2	1607	7	T13250	hypothetical prote
22	33	70.2		7	T39305	protein kinase - f
23	33	70.2		~	T50073	myosin-like coiled
. 24	32	68.1		7	AI2178	$\overline{}$
25	32	68.1		~	F84145	
56	32	68.1		7	H84149	transposase (27) B
27	32	68.1	27	7	AB0345	probable phosphate
28	32	68.1	292	~	S15269	post-translocation
53	32	68.1	419	0	T23666	hypothetical prote

hypothetical prote Similar to disease	penicillin binding	probable ATPase ch	Clp ATPase [import	penicillin-binding	protein kinase C (hypothetical prote	hypothetical prote	S-adenosylmethioni	homeodomain protei	SAM-dependent meth	probable aldo/keto	protein-tyrosine k	probable tpr prote	hypothetical prote
H96008 F86308	H87197	AE0179	AE0119	F83862	S35362	T33345	F96833	H97211	H85433	E96989	AF0083	A48073	E71379	AC1425
01 00	7	7	N	~	-	N	~	~	ď	~	~	N	N	~
538	803	880	882	886	988	194	201	208	217	272	277	359	398	427
68.1	68.1	68.1	68.1	68.1	68.1	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99
32	35	32	32	32	32	31	31	31	31	31	31	31	31	31
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: WIPROT: P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
A;Cross-references: UNIPROT: P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032
B;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Ritle: A negative element in the human poapillomavirus type 16 genome acts at the level
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Recession: T10427
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T10427
A;Residues: DNA
A;Residues: 1-158 <KEN>
A;Residues: L-158 <KEN>
C;Genetics:
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protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Accession: A01682; T1048; Heat Eevision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A01682; T1048; Murst, M.; Suhai, S.; Rowekamp, W.G.
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: papillomavirus E6 protein
Keywords: DNA binding; early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Best Local Similarity
Matches 9; Conserv
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RESULT 2 A69484

hypothetical protein AF1874 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Acsata
C;Accession: A6344
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F;Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woses, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor

N

2; Indels

5,

Score 36; DB Pred. No. 31; 0; Mismatches

76.6**%**; 77.8**%**;

7; Conservative

Query Match Best Local Similarity Matches 7; Conserv

77 TLLEDQYNK 85 TTLEQQYNK 9

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hypothetical protein F35E12.7 - Caenorhabditis elegans

Risteward, C.

Risteward, C.

Rubmitted to the EMBL Data Library, November 1996

A;Reference number: 219470

A;Accession: 721769

A;Status: preliminary; translated from GB/EMBL/DDBJ

Molecule type: DNA Residues: 1-739 <WIL>

A; Reference number: A69250; MUID:98049343; PMID:9389475 A; Accession: A69484

A, Molecule type: DNA

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C;Accession: E83900
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4311, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ç
A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:09KBC3; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB057; A;Experimental source: strain C-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :-hydroxyhepta-2,4-diene-1,7-dioate isomerase BH2005 [imported] - Bacillus halodurans (st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-2541 <REE>
A;Cross-references: UNIPROT:P26039; EMBL:X56123; NID:g54257; PIDN:CAA39588.1; PID:g54258
C;Keywords: cytoskeleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              asparagine-rich blood stage antigen (clone Pfa35-2) - Plasmodium falciparum (fragment) C; Species: Plasmodium falciparum (c; Species: Plasmodium falciparum (c; Species: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C; Accession: C45600; S27826 R; Nolte, D: Knapp, B. Mol. Biochem. Parasitol. 46, 319-321, 1991 Mol. Biochem. Parasitol. 46, 319-321, 1991 A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: Plasmod A; Title: 
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                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S11661
R;Rees, D.J.G.; Ades, S.E.; Singer, S.J.; Hynes, R.O.
Nature 347, 685-689, 1990
A;Title: Sequence and domain structure of talin.
A;Reference number: S11661; MUID:91015390; PMID:2120593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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Pred. No. 1.5e+02;
2; Mismatches 1; Indels
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Pred. No. 38;
4; Mismatches
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A;Status: nucleic acid sequence not shown
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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Matches 6; Conservative
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408 TLDQEYNK 415
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TTIEQEYHR
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A; Residues: 1-276 <STO>
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A,Status: preliminary
A,Molecule type: mRNA
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A;Status: preliminary
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                 A;Reaiduea: 1-546 <KLE>
A;Cross-references: UNIPROT:O28405; GB:AE000973; GB:AE000782; NID:g2689296; PIDN:AAB8938
C;Superfamily: Pyrococcus horikoshii probable helicase PH0917
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A;Cross-references: UNIPROT:Q8YV06; GB:BA000019; PIDN:BAB73874.1; PID:g17131266; GSPDB:G
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:002360; EMBL:Z81527; PIDN:CAB04275.1; GSFDB:GN00023; CESP:F3
A;Experimental source: clone F35E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: alr2175
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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A;Map position: 5
A;Introns: 26/1; 61/3; 92/2; 131/1; 164/3; 240/1; 295/3; 319/2; 428/2; 482/3; 704/3
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Length 739

Score 36; DB 2; Pred. No. 42; 3; Mismatches

76.6%;

6; Conservative

Best Local Similarity Matches 6; Conser

[||:::||| TTLDKKYNK 431

423

1 TTLEQQYNK 9

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0; Indels

Indels

Query Match 76.6%; Score 36; DB Best Local Similarity 75.0%; Pred. No. 50; Matches 6; Conservative 2; Mismatches

Status: preliminary Molecule type: DNA

Genetics:

2 TLEQQYNK 9

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A;Cross-references: UNIPROT:Q9KRP3; GB:AE004236; GB:AE003852; NID:g9656095; PIDN:AAF9474; A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: E72299
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-508 <ARN>
A;Cross-references: UNIPROT:Q9X0E8; GB:AE001766; GB:AE000512; NID:g4981600; PIDN:AAD3613!
                         RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seqn
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: E72299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamate synthase-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human homolog of Drosophila lethal discs large 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
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60;
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Pred. No. 72;
2; Mismatches 1; Indels
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A;Accession: G02165
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-585 <ALB>
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2
Pred. No. 60;
1; Mismatches
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R;Albertsen, H.
submitted to the EMBL Data Library, October 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain MSB8
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66.7%;
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85.7%;
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Best Local Similarity 66.7.,
6; Conservative
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Best Local Similarity 85.7-
Then 6; Conservative
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412 SKYGTTVEE 420
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372 SLYGTTI 378
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                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-429 <HEI>
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                                                                                                                                                                                                  A;Status: preliminary
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A:Gene: TM1058
                                                                                                                                                                                                                                                                                                                                                  A; Gene: VC1593
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E72299
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A,Residues: 1-148 <DEL>
A,Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAA52585.1; PID:g3970
C,Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding; early protein; nucleus; zinc finger
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R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 444-429, 1991
A;Title: Characterization of the complete RhPV 1 genomic sequence and an integration lod A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: A38503
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D82181
GGDEF family protein VC1593 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: rheeus papillomavirus
C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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Keywords: DNA binding; early protein; transforming protein; zinc finger
F;60-96/Region: zinc finger CCCC motif
F;133-169/Region: zinc finger CCCC motif
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
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                                                                                                                                               1; Indels
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Pred. No. 25;
2; Mismatches
                                                                                                  DB 2;
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                                                                                                  Score 36;
Pred. No.
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A;Molecule type: DNA
A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein
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77.8%;
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77.8%;
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Best Local Similarity 66.7%;
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Best Local Similarity 77.8.
7; Conservative
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Best·Local Similarity
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CiSpecies: Brachydanio rerio (zebra fish)
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CiSpecies: Brachydanio rerio
CiAccession: T18291
RiConcordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;
Development 122, 2815-2846, 1996
A;Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic
A;Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic
A;Title: Development T18291
A;Accession: T18291
A;Accession: T18291
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1220 cCON>
A;Cross-references: UNIPROT:Q98864; EMBL:X98883; PIDN:CAA67386.1
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C,Superfamily: Drosophila membrane protein patched
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A;Residues: 1-592 <LYE>
A;Cross-references: UNIPROT: P38009; EMBL: Z49273; NID: 9809577; PIDN: CAA89269.1; PID: 98095
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
CiAccession: T13952
Fixetopyama, J.; Takabatake, T.; Takeshima, K.; Hui, C.
Nature Genet. 18, 104-106, 1998
A; Title: Ptch2, a second mouse Patched gene is co-expressed with Sonic hedgehog. A; Reference number: Z17830; MUID:98122566; FMID:9462734
A; Accession: T13952
A; Ancession: T13952
A; Molecule type: mRNA
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A;Cross-references: SGD:S0004727; MIPS:YMR120C
A;Map position: 13h
C;Superfamily: purH bifunctional enzyme
C;Keywords: hydrolase; purine nucleotide biosynthesis; transferase
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Pred. No. 1.8e+02;
0; Mismatches 2; Indels
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                                                                                                                            73.3%; Score 33; DB 2; Length 585; 75.0%; Pred. No. 84;
                                                                                                                                                                                                                          0; Indels
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C;Superfamily: Drosophila membrane protein patched
C;Keywords: transmembrane protein
F;142-214/Domain: GLGF domain homology <GLG>F;386-573/Domain: guanylate kinase, homology <GKI>
                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%;
77.8%;
                                                                                         Query Match
Best Local Similarity 75.v-
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Best Local Similarity 77.8
Matches 7; Conservative
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460 NLYGTSLE 467
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700 SLYGATLVQ 708

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Sequence 16, Appli Sequence 2, Appli Sequence 157, App Sequence 158, App Sequence 160, App

Sequence 1, Appli Sequence 4, Appl

Sequence 4, Appl

US-10-484-063-20 US-10-848-063-27 US-10-367-057-16 US-10-751-845-157 US-10-751-845-157 US-10-751-845-150 US-10-751-845-160 US-09-367-309A-1 US-10-000-903-10 US-10-000-903-10 US-10-000-903-10 US-10-000-903-10 US-10-000-903-14 US-10-000-903-14 US-10-000-903-14 US-10-000-903-14 US-10-899-771-14 US-10-899-771-14 US-10-899-771-14 US-10-899-771-14 US-10-899-771-14

sequence 10, Appl Sequence 10, Appl Sequence 6, Appli Sequence 14, Appl Sequence 14, Appl Sequence 90, Appl Sequence 14, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 51, Appli Sequence 53, Appl Sequence 536, Appl Sequence 239661,

US-09-848-294-6

US-10-293-231-6 US-10-606-038-7 US-10-211-962-41 US-10-211-962-49 US-10-211-962-49 US-10-177-293-470 US-10-179-293-535 US-10-119-993-535 US-10-424-599-239661 US-10-424-599-239661

Sequence 265261

ALIGNMENTS

Sequence

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Sequence 73, Application US/10751845
; Sequence 73, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYBEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT FILING DATE: 2004-01-05
; FRIOR APPLICATION NUMBER: US/10/751,845
; FRIOR APPLICATION NUMBER: US 60/169,846
; FRIOR APPLICATION NUMBER: US 60/169,846
; FRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR APPLICATION NUMBER: US 60/159,846
; PRIOR PILING DATE: 1999-12-09
; RIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 47; DB 17;
.larity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
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 6
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9; Conserva
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76.
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US-10-751-845-73
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Best Local S
Matches 9
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                                                                                             29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: \cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT_MEW_PUB.pep:*
3: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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12: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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18: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
19: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
20: \cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-751-845-77
US-10-476-570-36
US-10-476-570-35
US-10-476-570-35
US-10-751-845-66
US-10-476-570-13
US-10-476-570-55
US-10-858-384-8
US-10-751-845-126
US-10-751-845-126
US-10-177-390-6
                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           1717557 seqs, 384547976 residues
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                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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Match Length
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Maximum DB e
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Length 9; Indels ~

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* OTHER INFORMATION: Description of the artificial sequence: peptide E6 89-103
US-10-476-570-36
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US-10-476-570-36

US-10-476-570-36

Sequence 36, Application US/10476570

Publication No. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MALLERE, BETTACT

APPLICANT: MALLERE, BETTACT

APPLICANT: BOUNGAULT-VILLADA, Isabelle

APPLICANT: POUVELLE-MORATILLE, Sandra

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

TITLE OF INVENTION: Mathematical proteins and uses thereof

TITLE REFERENCE: 45636-5071-US

CURRENT PILING DATE: 2003-11-04

PRIOR APPLICATION NUMBER: PCT/FR02/01533

PRIOR APPLICATION NUMBER: PC 01 05980
                    Sequence 77, Application US/10751845
Publication No. US20050100928A1
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Olicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PRIJNG DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
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TYPE: PRT
ORGANISM: Human Papilloma virus
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ORGANISM: artificial sequence
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SOFTWARE: PatentIn Ver. 2.1
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JS-10-751-845-77
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 93-107
US-10-476-570-37
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                                                                             JERUSTAND INCOMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLEBER, Mennard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: MUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: 10/416,570
CURRENT EILING DATE: 2003-11-04
PRIOR FILING DATE: 2003-11-04
PRIOR PELICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 37
LENGTH: 15
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COMMISSABLAT A L'ENERGIE ATONIQUE
APPLICANT: COMMISSABLAT A L'ENERGIE ATONIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6
TITLE REFERENCE: 45636-5071-US
CURRENT FILING DATE: 2003-11-04
PRIOR PAPLICATION NUMBER: PR 01 05980
PRIOR PAPLICATION NUMBER: FR 01 05980
PRIOR PILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 35
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Sequence 37, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
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; Sequence 35, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
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ORGANISM: artificial sequence
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ORGANISM: artificial sequence
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Best Local Similarity
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Best Local Similarity
Matches 9; Conserv
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Pred. No. 0.1;

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100.08;
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLER, BERTANT
APPLICANT: MAILLER, BERTANT
APPLICANT: BOURGAUT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: MAXLUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXLUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXLUE of peptides derived from E6 and/or E7
TITLE OF INVENTION: MAXLUE of peptides derived from E6
CURRENT APPLICATION NUMBER: PC1/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO. 33
                                                                                                                                                                                                           Sequence 66, Application US/10751845

Publication No. US20050100928A1

GENERAL INFORMATION:

APPLICANT: Hedley, Mary Lynne

APPLICANT: Hedley, Mary Lynne

APPLICANT: Chicz, Roman M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES

FILE REFERENCE: 08191-013001

CURRENT APPLICATION NUMBER: US/10/751,845

CURRENT APPLICATION NUMBER: US/09/664,225

PRIOR FILING DATE: 2000-08-18

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-12-09

PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 163

SOFTWARR: FastSEQ for Windows Version 4.0
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       0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
       9; Conservative
                                                                                 TTLEQQYNK 11
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                                                     TTLEOOYNK 9
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     Matches
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, OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108 US-10-476-570-55
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MALLEER, BELTANA,
APPLICANT: MALLEER, BELTANA,
APPLICANT: BOUVELLE-VILLADA,
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: POUVELLE MAKTURE OF ESPETIAN GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
APPLICANTION: WAKER: LOSS
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: RO 105980
PRIOR PELLING DATE: 2002-05-04
PRIOR PELLING DATE: 2002-05-04
PRIOR PELLING DATE: 2002-05-04
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR PLICATION NUMBER: PR 9907012
PRIOR PLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE PARENCE: PARENCE: 1999-06-03
SEQ ID NO 8
LENGTH: 29
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100.0%; Score 47; DB 16;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0;
Mismatches
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Publication No. US20050033025A1
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ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 29
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, ORGANISM: Human papillomavirus type 16
US-10-484-063-27
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ORGANISM: Human papillomavirus
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US-10-484-063-20
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US-10-484-063-27
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US-10-177-390-6

Sequence 6, Application US/1017390

Sequence 6, Application Wo. US20030143743A1

Sequence 70. US20030143743A1

SEQUENCE 71. USA CONTROL 10. US20030143743A1

SERENCE 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTROL 10. USA CONTRO
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APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
FAPPLICANT: Urban, Robert G.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 1999-00-16
PRIOR SPILING DATE: 1999-00-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
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100.0%; Score 47; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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                                                                                                           Query Match 100.0%; Score 47; DB 17; Length.29; Best Local Similarity 100.0%; Pred. No. 0.1; Matches 9; Conservative 0; Mismatches 0; Indels
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US-10-751-845-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Human papillomavirus type 16
US-10-177-390-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 126, Application US/10751845; Publication No. US20050100928A1; GENERAL INFORMATION:
; OTHER INFORMATION: for E6 of HPV US-10-858-384-8
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Sequence 27, Application US/10484063

Publication No. US20050048467A1

GENERAL INPORMATION:

APPLICANT: SASTRY, K. JAGANNADHA

APPLICANT: TORTOLERO-LUNA, GUILLERMO

TITLE OF INVENTION: METHODS AND CANCEROUS GROWTHS, INCLUDING CIN

FILE REFERENCE: UTSC:560US

CURRENT APPLICATION NUMBER: US/10/484,063

CURRENT FILING DATE: 2002-07-19

PRIOR PILING DATE: 2002-07-19

PRIOR FILING DATE: 2001-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 27
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: METHODS AND COMPOSITIONS GROWTHS, INCLUDING CIN
FILE REFERRINCE: UTSC:560US
CURRENT APPLICATION NUMBER: 02/10/484,063
CURRENT PILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR PILING DATE: 2002-07-19
PRIOR PELLING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PAGENETIN VET: 2.1
SOFTWARE: PAGENETIN VET: 2.1
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Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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Sequence 2, Application US/10858384

| Publication No. US20050033025A1
| GENERAL INFORMATION: US20050033025A1
| APPLICANT: CHOPPIN, JEANNINE
| APPLICANT: CHOPPIN, JEANNINE
| APPLICANT: GUILLET, JEAN-GERAD
| APPLICANT: GUILLET, JEAN-GERAD
| APPLICANT: GUILLET, JEAN-GERAD
| APPLICANT: GUILLET, JEAN-GERAD
| APPLICANT: CONNAN, FRANCINE
| APPLICANT: CONNAN, FRANCINE
| APPLICANT: CRITELIE
| TITLE OF INVENTION: PARTICULARLY IN VACCINATION
| TITLE OF INVENTION: PARTICULARLY IN VACCINATION
| TITLE OF INVENTION: PARTICULARLY IN VACCINATION
| TITLE REFERENCE: 0508-103-1
| CURRENT APPLICATION NUMBER: PR 9907012
| FRICH APPLICATION NUMBER: PR 9907012
| FRICH APPLICATION NUMBER: PR 9907012
| NUMBER OF SEQ ID NOS: 24
| SEQ ID NO 2
| LENGTH: 158
| TENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ool, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same;
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT APPLICATION NUMBER: 60/256,911
PRIOR APPLICATION WUMBER: 60/256,911
PRIOR PRILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 198
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 16
LEMICT HIS
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Best Local Similarity 100.0%; Pred. No.
Matches 9; Conservative 0; Mismatc
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Best Local Similarity 100.0%;
Matches 9; Conservative
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CORGANISM: Homo sapiens
US-10-367-057-16
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Search completed: June 29, 2005, 05:18:14 Job time : 116.15 secs

93 TTLEQOYNK 101

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 28, 2005, 21:28:02; Search time 11.05 Seconds (without alignments) 78.367 Million cell updates/sec Run on:

US-08-170-344-51 45 Title: Perfect score:

1 SLYGTTLEQ 9 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79: * 1: pir1: * 2: pir2: * 3: pir3: *

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			Corner	•
Result No.	Score	Query Match	Length	DB	ΙD	Description
-	4	TOO. 0	T	4	MOWLHS	
72	39	86.7	14	Н	W6WL58	E6 protein - human
٣	38	84.4	149	Н	W6WL31	E6 protein - human
4	37	82.2	149	Н	W6WL33	6 protein -
ß	37	82.2	151	Н	W6WL51	ı
ø	37	82.2	774	N	JC7265	neprilysin (EC 3.4
7	36	80.0	148	7	A61237	•
80	36	80.0	148	~	S36573	•
6	33	73.3	191	-	WGWLR1	E6 protein - rhesu
10	33	73.3	429	~	D82181	GGDEF family prote
11	33	73.3	508	~	E72299	glutamate synthase
12	33	73.3	585	N	G02165	human homolog of D
13	33	73.3	592	N	S54489	phosphoribosylamin
14	33	73.3	1182	~	T13952	membrane protein p
15	33	73.3		~	T18291	patched protein -
16	32	71.1	86	~	D71947	hypothetical prote
17	32	71.1		Н	W6WL35	E6 protein - human
18	32	71.1	150	~	S36544	E6 protein - human
19	32	71.1	155	~	W6WL56	E6 protein - human
20	32	71.1	155	~	A44890	E6 protein - human
21	32	71.1	158	-	W6WL18	E6 protein - human
22	32	71.1	158	~	S36561	E6 protein - human
23	32	71.1	255	~	S41690	cytochrome-c oxida
24	32	71.1		~	S28662	hypothetical prote
25	32	71.1		~	S19706	•
56	32	71.1	419	N	A86414	hypothetical prote
27	32	71.1	419	0	F82183	probable outer mem
28	32	71.1	421	7	T52033	19S proteosome sub
29	32	71.1	530	~	A87518	hypothetical prote

Eprotein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Réference number: A36779; MUID:92024102; PMID:1656594

RESULT 2

W6WL58

A;Status: translation not shown

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3-methylcrotonoyl-	probable acyl-CoA	hypothetical prote	hypothetical prote	hypothetical prote	E6 protein - human	E6 protein - human	E6 protein - human	hypothetical prote	21K protein precur	hypothetical prote	hypothetical prote	tryptophan synthas	tryptophan synthas	hypothetical prote	hypothetical prote
AE2984	B98299	T21072	T21073	T14633	S36515	W6WL39	W6WLPR	T12457	T09390	H82262	AG2085	E75162	T43928	T42936	C70675
~	N	N	~	N	~	Н	Н	~	N	~	~	~	~	~	N
533	537	624	965	1237	148	158	158	184	187	235	240	248	251	255	260
71.1	71.1	71.1	71.1	71.1	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.9	68.8	68.9
32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1-158 <SERS>
A; Residues: 1-158 <SERS>
A; Cross-references: UNTROT: P03126; GB: K02718; NID: 9333031; PIDN: AAA46939.1; PID: 9333032
B; Cross-references: UNTROT: Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A; Reference number: Z17014; MUID: 91162763; PMID: 1848319
A; Reference number: Applications T10427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Directin E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Species: 1003682; 110427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
N;rology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Robesidues: 1-158 <KEN>
A/SCOSS-references: EMBL:KO2718; NID:g333031; PIDN:AAA46939.1; PID:g333032
C/Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding: early protein; zinc finger
E;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 SLYGTTLEQ 97
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nes 9; Conserv
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Best Local S
Matches 9
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Eprotein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Accession: A61237
R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U. Int. J. Cancer 48, 516-552, 1991
A;Title: Cloning and characterization of human papillomavirus type 52 from cervical carc; A;Reference number: A61237
A;Reference number: A61237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Accession: 4540g-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: JC7265
R;Tanja, O; Facchinetti, P; Rose, C; Bonhomme, M.C; Gros, C; Schwartz, J.C.
Biochem. Biochem. Brophys. Res. Commun. 271, 565-570, 2000
A;Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and test A;Reference number: JC7265
                                                                                                                                                                                                                                                                   C;Accession: B40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
Virol. 65, 4216-4225; 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus tyr
A;Reference number: A40415; MUID:91303675; PMID:1649326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: neprilysin
C;Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis; trar
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                                                                                                                                                                                                                  A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.2%; Score 37; DB 1; Length 151;
87.5%; Pred. No. 2.9;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.2%; Score 37; DB 2; Length 774; 66.7%; Pred. No. 16; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-151 <LUN>
A;Cross-references: UNIPROT:P26554; GB:M62877
A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
                                                                                                                                                        E6 protein - human papillomavirus type 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                C, Species: human papillomavirus type 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: translation not shown
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           420 ALYGTIMEE 428
         82 SVYGNTLEQ 90
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82 SVYGTTLE 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: E40415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Accession: JC7265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                             W6WL51
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A,Molecule type: DNA
A,Residues: 1-149 <KIR>
A,Residues: 1-149 <KIR>
C,Superfamily: papillomavirus E6 protein
C,Superfamily: papillomavirus E6 protein
C,Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916 C;Comment: This protein may be involved in the oncogenic potential of this virus. C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;30-66/Region: zinc finger CCCC motif F;10-61789/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: A03683
R;Cole, S. T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh A;Reference number: A93020; MUID:86200464; PMID:3009902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc
A;Reference number: A94398; MUID:89299478; PMID:2545036
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C;Accession: A32444
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C;Species: human papillomavirus type 33
C;Date: 30-Jun_1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                    1; Indels
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                                                                                                                                                                                                                                       Score 39; DB 1
Pred. No. 1.1;
0; Mismatches
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C;Species: human papillomavirus type 31
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: host Homo sapiens (man)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity
7; Conserv?
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Best Local Similarity
Matches 7; Conserv
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A; Residues: 1-149 <COL>
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RESULT 4 W6WL33

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TELEX:
INFORMATION FOR SEQ ID NO: 78
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300
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Sequence 77, Appl
Sequence 45, Appl
Sequence 164, App
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Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1, Appli
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Sequence 1, Appli
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49, Appl
7826, Ap
1962, Ap
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14, Appl
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                                                                                                June 28, 2005, 21:33:36; Search time 17.05 Seconds (without alignments) 39.404 Million cell updates/sec
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Sequence 2, P
Sequence 3, P
Sequence 4, P
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-562-737-42
US-09-562-737-43
US-09-562-737-48
US-09-248-796A-16048
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US-08-159-339A-77
US-08-159-339A-77
US-08-934-915-164
US-09-980-523A-8
US-09-980-523A-8
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US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-08-316-239B-3
US-09-359-382-12
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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Sequence 33, Appl Sequence 27186, A Sequence 32262, A Sequence 24, Appl Sequence 26, Appl Sequence 19794, A Sequence 19794, A Sequence 15156, A Sequence 7294, Ap Sequence 7294, Ap Sequence 7294, Appl Sequence 26, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appli Sequence 21, Appli		
28 32 68.1 821 4 US-08-311-731A-33 29 31 66.0 134 4 US-09-248-796A-27186 30 31 66.0 137 4 US-09-270-767-32262 31 31 66.0 137 4 US-09-270-767-32262 33 31 66.0 661 4 US-09-575-081B-23 34 31 66.0 670 4 US-09-575-081B-24 35 31 66.0 684 4 US-09-575-081B-26 36 31 66.0 865 4 US-09-248-796A-19794 38 31 66.0 913 4 US-09-248-796A-15156 39 31 66.0 1024 4 US-09-248-796A-15156 40 31 66.0 1024 4 US-09-248-796A-15156 41 31 66.0 1024 4 US-09-914-259-24 42 31 66.0 1052 3 US-08-914-259-24 43 31 66.0 1052 3 US-08-911B-1 44 31 66.0 1052 3 US-08-863-11B-1 45 31 66.0 1053 3 US-08-863-11B-1 45 31 66.0 1053 3 US-08-863-11B-2	ALIGNMENTS	RESULT 1 US-08-159-339A-78 Sequence 78, Application US/08159339A Patent No. 6037135- GENERAL INFORMATION: APPLICANT: Kubo, Ralph T. APPLICANT: Grey, Howard M. APPLICANT: Celis, Esteban TITLE OF INVENTION: Uses NUMBER OF SEQUENCES: 1254 CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Their TITLE OF INVENTION: Uses NUMBER OF SEQUENCES: 1254 COUNTY: San Francisco STRRET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STRATE: CA COUNTY: USA COUNTY: USA COMPUTER: IBM Compatible OPERATION SYSTEM: DOS SOFTWARE: Fast ESQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/027,746 FILING DATE: 05-MAR-1993 ATTORNEY/AGENT INFORMATION: NAME: Weber, Ellen Lauver REGISTRATION NUMBER: US 08/103,396 FILING DATE: 07-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Weber, Ellen Lauver REGISTRATION NUMBER: 32,762 REFERENCE/DOCKET WUMBER: 32,762 REFERENCE/DOCKET WUMBER: 32,762 REFERENCE/DOCKET WUMBER: 32,762 REFERENCE/DOCKET WUMBER: 12,0200

78:

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APPLICANT: DILLINER, DENALUS
APPLICANT: DILLINER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHERIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPTILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL, IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSER: MASON & ASSOCIATES, P.A.
STREET: 1775 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                     CHENG, HWEE-MING
VENTION: SYNTHETIC PEPTIDES OF HUMAN
VENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 47; DB 2; 100.0%; Pred. No. 0.012;
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ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: 10.5.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
APPLICATION NUMBER: 07/949,836
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Patent No. 5932412
            Sequence 45, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37,133
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REGISTRATION NUMBER: 37,13.
REFERENCE/DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-08-934-915-45
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STATE:
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                                           100.0%; Score 47; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                 Sequence 77, Application US/08159339A
| Patent No. 6037135
| GENERAL INFORMATION:
| APPLICANT: Kubo, Ralph T. APPLICANT: Grey, Howard M. APPLICANT: Sette, Alessandro APPLICANT: Sette, Beteand TITLE OF INVENTION: HLA Binding peptides and Their TITLE OF INVENTION: Uses
| NUMBER OF SEQUENCES: 1254
| CORRESPONDENCE ADDRESS: ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CALL FIGHCISCO STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: CALL STATE: DOS SOFTWARE: FastERO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY, AGENT INFORMATION: NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
BREGISTRATION NUMBER: 33,762
BREGISTRATION NUMBER: BLION: NAME: Weber, Ellen Lauver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 018623-005030US TELECOMMUNICATION INFORMATION:
                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                 Query Match
Best Local Similarity 100.00
Pron 9; Conservative
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HOLECULE TYPE: peptide
US-08-159-339A-77
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US-08-159-339A-78
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Gaps

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Length 20; 0; Indels

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GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                APPLICANT: BOUGHAIT ULLADA, ISABELLE
APPLICANT: BOUGHAIT ULLADA, ISABELLE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THERR PRODUCTION AND THEIR USE
FILE REFERENCE: WOBI AO INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 47; DB 4; Length 158; Best Local Similarity 100.0%; Pred. No. 0.11; Matches 9; Conservative 0; Mismatches 0; Indels
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COUNTRY: USA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
TILING BATE: 30-SEP-1994
TLING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE ALFARMANE, MOSI TO INO 109/980,523A CURRENT PILING DATE: 2002-04-29 PRIOR APPLICATION NUMBER: 92/7FR00/01513 PRIOR FILING DATE: 2000-05-31 PRIOR PELING DATE: 1999-06-03 PRIOR FILING DATE: 1999-06-03 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENTIN VET. 2.1 SOFTWARE: PATENTIN VET. 2.1 SEQ ID NO 2: LENGTH: 158
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REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
                                                                                                                                                          Sequence 2, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08316239B Patent No. 5679509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 TTLEQOYNK 101
14 TTLEQQYNK 22
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APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 A0 INS
CURRENT FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-04-29
FRIOR PRICATION NUMBER: PCT/FR00/01513
FRIOR PLICATION NUMBER: PCT/FR00/01513
FRIOR PLICATION NUMBER: PS 99/07012
FRIOR PLICATION NUMBER: E7 99/07012
FRIOR PLICATION NUMBER: E7 99/07012
FRIOR PLICATION NUMBER: 24
SOFTWARE: PATENTING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 8
LENGTH: 29
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                                          CONDUTY: TO.S.A.
CONDUTY: TO.S.A.
CONDUTRE READABLE FORM:
MEDIUM TYPE: Floppy disk
CONDUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFFCATION: 435
PH.OR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09980523A Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                               37,133
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,13
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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; ORGANISM: Human Papillomavirus
US-09-980-523A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 813-538-3820
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CLEARWATER
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1 TTLEQOYNK 9

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, OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-12
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; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
    APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; TILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT APPLICATION NUMBER: US/09/22
; EARLIER PILING DATE: 1997-09-22
; EARLIER PILING DATE: 1997-09-22
; EARLIER PILING DATE: 1997-12-20
; RARLIER PILING DATE: 1995-12-20
; RARLIER PILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTHARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                     , SERLIER APPLICATION NUMBER: DATE 1995-12-20

FARLIER APPLICANT: EDWARDS, Stirling John

APPLICANT: WEBB, Elizabeth Ann

TITLE OF INVERTION: VARIANTS OF HUMAN PAPILLIOMA VIRUS ANTIGENS

FILE REFERENCE: 17227/130

CURRENT APPLICATION NUMBER: US/08/68

EARLIER PAPLICATION NUMBER: PCT/AU95/00868

EARLIER PAPLICATION NUMBER: AU PNO157

EARLIER PLING DATE: 1995-12-20

SARLIER PLING DATE: 1994-12-20

SOFTWARE: PATENTING DATE: 1994-12-20

SOFTWARE: PATENTING DATE: 194-12-20

SOFTWARE: PATENTING DATE: 1914-12-20

SOFTWARE: PATENTING DATE: 1914-12-20

SOFTWARE: PATENTING DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE: DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 47; DB 3; Length 172; 100.0%; Pred. No. 0.12;
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ORGANISM: Human papillomavirus type 16
                                                                                                                                                         Sequence 12, Application US/08860165A Patent No. 6004557 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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      93 TTLEQQYNK 101
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Matches 9; Conserv
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Matches 9; Conserv
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Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Parmenter, Cheryl A.
ITILE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and ITILE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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ZID: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILLING DATE: 30-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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STREET: 6126 Rocky Way Court
CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGIESTRATION NUMBER: 35,205
REFRENCE/DOCKET NUMBER: UNME
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
      TELEPHONE: (703) 817-512.
TELEPAX: (703) 803-9387
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENGTH: 162 amino acids
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
                                                                                                                                                                                                                        SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 TTLEQQYNK 101
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                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rel
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Matches 9; Conserv
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Query Match
100.0%; Score 47; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels
                               Sequence 1, Application US/09367309A

Patent No. 642807

GENERAL INOFMATION:

APPLICANT: MACFALLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 017227/0118

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PUT/AU98/00080

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cetard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
FRIOR APPLICATION NUMBER: PCT/FP98/05285
FRIOR APPLICATION NUMBER: GE 9717953.5
FRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Patent No. 6342224
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US-09-485-885-4
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US-08-860-165-10

i Sequence 10. Application US/08860165A
; Sequence 10. Application US/08860165A
; Patent NO. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
APPLICANT: EDWARDS, Stirling John
APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; TILE REFERENCE: 1722/12B
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT PILLING DATE: 1997-09-22
; EARLIER FILLING DATE: 1995-12-20
; EARLIER PILLING DATE: 1994-12-20
; EARLIER PILLING DATE: 1994-12-20
; BARLIER PILLING DATE: 1994-12-20
; SERLIER APPLICATION NUMBER: AU PN0157
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO S: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
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Sequence 10, Application US/09359382

Sequence 10, Application US/09359382

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: COX, John Cooper
APPLICANT: PRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REPRENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-09-22

EARLIER PILING DATE: 1997-09-22

EARLIER FILING DATE: 1997-12-20

EARLIER FILING DATE: 1994-112-20

SERLIER PILING DATE: 1994-112-20

SOFTWARE: PALENTH Ver. 2.0

SEQ ID NO 10

LENGTH: 266
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US-09-359-382-10
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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100.0%; Score 47; DB 3; Length 273; 100.0%; Pred. No. 0.19;
                                0; Indels
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Patent No. 6342224
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GENERAL INFORMATION:
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93 TTLEOOYNK 101

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Query Match

100.0%; Score 47; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Vaccine
FILE REPERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
CUNMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE BRT
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Search completed: June 28, 2005, 23:37:51 Job time: 18.05 secs

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Sequence 16, Appl
Sequence 2, Appli
Sequence 157, App
Sequence 158, App
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                                                                                                                              June 29, 2005, 04:19:44; Search time 116.15 Seconds (without alignments) 29.797 Million cell updates/sec
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Sequence 1
Sequence 1
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Sequence
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/ cgn2 6/ptocate 1/puppaa/USO9B PUBCOMB.pep: .
/ cgn2 6/ptocate 1/puppaa/USO9C PUBCOMB.pep: .
/ cgn2 6/ptocate 1/pubpaa 1/USO9 NEW PUB.pep: *
/ cgn2 6/ptocate 1/pubpaa 1/USIOB PUBCOMB.pep: *
/ cgn2 6/ptocate 1/pubpaa 1/USIOB PUBCOMB.pep: *
/ cgn2 6/ptocate 1/pubpaa 1/USIOC PUBCOMB.pep: *
/ cgn2 6/ptocate 1/pubpaa 1/USIOC PUBCOMB.pep: *
/ cgn2 6/ptocate 1/pubpaa 1/USIOC PUBCOMB.pep: *
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(gn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(gn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

(gn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(gn2_6/ptodata/1/pubpaa/US06_PUBGOMB.pep:*

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(gn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

(gn2_6/ptodata/1/pubpaa/PCTUS_PUBGOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                   1717557 seqs, 384547976 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Sequence 160, Apple Sequence 1, Appli Sequence 4, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 6, Appli Sequence 14, Appli Sequence 14, Appli Sequence 27, Appli Sequence 27, Appli Sequence 23, Appli Sequence 23, Appli Sequence 201912, Sequence 201912, Sequence 201912, Sequence 201912, Sequence 201912, Sequence 291, Appli Sequence 291, Appli Sequence 291, Appli Sequence 291, Appli Sequence 291, Appli Sequence 291, Appli Sequence 291, Appli Sequence 2, Appli	Sequence 257, App Sequence 14, Appl Sequence 33, Appl Sequence 12, Appl Sequence 12, Appl Sequence 219887, Sequence 219893, Sequence 2076, Ap Sequence 2089, Ap
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ALIGNMENTS

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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 84-98 US-10-476-570-34
                                                                                                                  JAPPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLEERE, Bernard
APPLICANT: BOUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: POUVELLE-MORATILLE, Sandra
TITLE OF INVENTION: MAXLURE of peptides derived from B6 and/or E7
TITLE OF INVENTION: MARENE: US
TITLE OF INVENTION: MAMBER: US
TITLE OF INVENTION NUMBER: US
CURRENT APPLICATION NUMBER: PR
PRIOR APPLICATION NUMBER: PR
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PARENTIN VET. 2.1
SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 45; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.025; Matches 9; Conservative 0; Mismatches 0; Indels
                      Sequence 34, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: artificial sequence
US-10-476-570-34
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Sequence 8, Application US/10858384 Publication No. US20050033025A1 GENERAL INFORMATION:
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ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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                                                                         11 SLYGYTLEO 19
                            1 SLYGTTLEQ 9
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                                                                                                                                                                                                                                     APPLICANT: COWNISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: CONVISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6
TITLE OF INVENTION: Mixture of peptides derived from E6
TITLE OF INVENTION: Mixture of peptides derived from E6
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR PLING DATE: 2002-05-04
NUMBER OF SEQ ID NOS: 63
SEQ ID NO 36
LENGTH: 15
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APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR FILING DATE: 2006-08-18
PRIOR PILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SSQ ID NO 66
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                                                                                                                                                                        Sequence 36, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
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ORGANISM: Human Papilloma virus
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Best Local Similarity 100.
                              1 SLYGTTLEQ 9
SLYGTTLEQ 9
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55
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US-10-858-384-8
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOUGGAULT VILLADA, ISABELLE
APPLICANT: BOUGGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REPERENCE: 2058-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT PILING DATE: 1999-06-03
FRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SEQ ID NOS: 24
SEQ ID NO 8
LENGTH: 29
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US-10-476-570-55
US-10-476-570-55
Sequence 55, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: INSTITUT NATIONAL
                                                                                                                                                                                                                       APPLICANT: MAILERE, Bernard

APPLICANT: BOUGRAULT: VILLADA, Isabelle
APPLICANT: BOUGRAULT: VILLADA, Isabelle
APPLICANT: BOUGRAULT: VILLADA, Isabelle
APPLICANT: BOUGRAULT: Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: 9apillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO S5
LENGTH: 29
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100.0%; Score 45; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels
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TYPE: PRT
CRCANISM: Homo sapiens
US-10-367-057-16
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                                                                                                          1 SLYGTTLEQ 9
Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPTTOPIC PROTEIN FRAGMENTS OF THE B6 PROTEIN
TITLE OF INVENTION: POLYEPTTOPIC PROTEIN PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 50504-1037-1
CURRENT APPLICATION NUMBER: 10510-1
FRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 117
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100.0%; Score 45; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels (
                   Query Match 100.0%; Score 45; DB 17; Length 29; Best Local Similarity 100.0%; Pred. No. 0.052; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Artificial fusion sequence
                                                                                                                                                                                                                                                                                            US-10-751-845-126
; Sequence 126, Application US/10751845
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US-10-858-384-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                 Publication No. US20050100928A1
GENERAL INFORMATION:
                                                                                                                                                                                  10 SLYGTTLEO 18
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LENGTH: 158
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APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Angel
APPLICANT: Cid-Arregui, Harald
APPLICANT: Sur Hausen, Harald
APPLICANT: Sur Hausen, Harald
TITLE OF INVERTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: EP 011072/1.7
PRIOR APPLICATION NUMBER: EP 011072/1.7
PRIOR PILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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100.0%; Score 45; DB 17; Length 158; ilarity 100.0%; Pred. No. 0.35; Conservative 0; Mismatches 0: Indela (
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100.0%; Score 45; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CUCHIII, SCOLT;
APPLICANT: Cuckson, Amanda;
APPLICANT: Lackson, Amanda;
APPLICANT: Lackson, Amanda;
APPLICANT: Lackson, Amanda;
APPLICANT: Lackson, Complexes and Methods of Using Same;
FILE REFERENCE: 21042-559
FILE REFERENCE: 21042-559;
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 198
SEQ ID NO 16
LENGTH: 158
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                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/10367057
Publication No. US20050100554A1
GENERAL INFORMATION:
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Publication No. US20040171806A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
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56 SLYGTTLEQ 64
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                                                                                             US-10-751-845-160
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US-09-367-309A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUBLICANT: Hedley, Mary Lynne
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/10/751,845
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-09-16
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 158
                                                                                                                                                              APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-10-09
PRIOR PILING DATE: 1999-10-06
PRIOR PILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 45; DB 17; Length 236; Best Local Similarity 100.0%; Pred. No. 0.55; Matches 9; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158
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; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
                                                                                                Sequence 157, Application US/10751845
Publication No. US20050100928A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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55 SLYGTTLEQ 63
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                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 236
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| Sequence 160, Application 19/10751945
| Publication No. USGOSGIOGRAN
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RESULT 14

Search completed: June 29, 2005, 05:18:14 Job time: 117.15 secs

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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Dalemans, Wilfried L.J.
TITLE OF INVENTION: Compositions Comptising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976
PRIOR PLILING DATE: 2004-07-27
PRIOR PLILING DATE: 1996-12-18
PRIOR PLILING DATE: 1996-12-18
PRIOR PLILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
SEQ ID NO
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CTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type CTHER INFORMATION: 16)
US-10-899-771-4
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100.0%; Score 45; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels (
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                                                                                                                      APPLICANT: Bruck, claudine
APPLICANT: Bruck, claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gombardo-Bencheikh, Angela
TILLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
Sequence 4, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
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; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapien
US-10-000-903-4
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Matches 9; Conserva
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1 SLYGITLEO 9

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TOPOLOGY: Linear
MOLECULE TYPE: peptide
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Sequence 8, Appli
Sequence 2, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 10, Appl
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14, Appl
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-980-523A-8

US-08-316-239A-2

US-08-116-239B-1

US-08-117-083-10

US-09-359-382-10

US-09-359-382-10

US-09-359-382-10

US-09-485-885-10

US-09-486-885-10

US-09-105-339A-563

US-08-159-339A-563

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US-08-159-339A-1771

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Maximum Match 100%
Listing first 45 summaries
                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps

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APPLICANT: Wheeler, Cosette M.
APPLICANT: Wheeler, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
TITLE OF INVENTION: Cervical Cancer
TITLE OF INVENTION: Cervical Cancer
TOWNESPECTOR ADDRESS:
ADDRESSEE: Jagtiani & Associates
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                                                                                                           Query Match 100.0%; Score 45; DB 4; Length 158; Best Local Similarity 100.0%; Pred. No. 0.15; Matches 9; Conservative 0; Mismatches 0; Indels
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~hes 0; Indels
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STATE: VA
COUNTRY: USA
COMPUTER: LOSA OLD COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC COMPATIBLE
SOFTWARE: PARCHIN REAGES #1.0, Version #1.30
SOFTWARE: PACHIN REAGES #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagitani, Ajay A.
REFERENCE/BOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
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6126 Rocky Way Court
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
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TYPE: amino acid
STRANDEDNESS: not releva
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                                                                                                                                                                                                                                                                                                            89 SLYGTTLEQ 97
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: PROTEBINE OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PRATICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: PCT/FR00/01513
FRIOR PLICATION NUMBER: PCT/FR00/01513
FRIOR PLICATION DATE: 2000-05-31
FRIOR APPLICATION NUMBER: FR 99/07012
FRIOR PLICATION DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHOPPIN,
APPLICANT: CHOPPIN,
APPLICANT: CHOPPIN,
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: GUINGERIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FROO/01513
PRIOR APPLICATION NUMBER: FF 99/07012
PRIOR APPLICATION NUMBER: FF 99/07012
PRIOR APPLICATION NUMBER: FF 99/07012
PRIOR APPLICATION NUMBER: FF 99/07012
SOUTHARE PECENTIN OF: 2.1
SEQ ID NO 8
LENGTH: 29
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                                                                                     100.0%; Score 45; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09980523A; Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09980523A; Patent No. 6783763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                              Query Match
Best Local Similarity 100.
Matches 9; Conservative
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              US-08-159-339A-230
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US-09-980-523A-8
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Gaps

Recombinant Virus Vectors Encoding Human

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                                                                                                                                                                      COUNTRY:
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TELEX: 9
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LENGTH: 266
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STATE:
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APPLICANT: OBJOG397

GENERAL INCORMATION:

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: PRAZER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOWA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER PILING DATE: 1995-12-20

EARLIER FILING DATE: 1995-12-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VOY: 2.0

SEQ ID NO 12

LENGTH: 172
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                                           VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 45; DB 3; Length 172; 100.0%; Pred. No. 0.17;
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                                    FILE OF INVENTION: VARIANTS OF HUMAN PAPILLO
FILE REFERENCE: 1722/7130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
SARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Patent No. 6306397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08117083
Patent No. 5719054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Bouranell, Michael B.
APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
WEBB, Elizabeth Ann
                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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Gaps
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APPLICANT: EDWARDS,
Blizabeth Ann
APPLICANT: COX, John Cooper
APPLICANT: WEBB. Blizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 1722/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER PILING DATE: 1997-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
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100.0%; Pred. No. 0.18;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
Papilloma Virus Proteins
               NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08860165A Patent No. 6004557 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                            ZLF: 341.7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Walter H. REGISTRATION NUMBER: 24,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-117-083-10
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100.0%; Score 45; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels
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                     0; Indels
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Patent No. 634224
GENERAL INFORMATION:
APPLICANT: Black, Claudine
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE OF INVENTION: Vaccine
FILE OF INVENTION: 08700-02-18
FILE APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/FP98/05285
FRIOR FILING DATE: 1998-08-17
FRIOR FILING DATE: 1997-08-22
NUMBER: FRASEC FOR MINDOWS VETSION 3.0
SCOTWARE: FRASEC FOR MINDOWS VETSION 3.0
                                                                                                                                                                                                    Sequence 4, Application US/09485885

Patent No. 634224

GRUERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Lombardo-Bencheikh, Angela
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
  100.0%; Pred. No. 0.28;
                     0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapien
                                                                1 SLYGTTLEQ
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LENGTH: 292
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                   ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion US-08-860-165-10
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                                                                             Query Match 100.0%; Score 45; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 9; Conservative 0; Mismatches 0; Indels
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GENERAL INCORMATION:
APPLICANT: MACFALAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: BY/AUJ8/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
SPRIOR FILING DATE: 1998-02-13
SPRIOR FILING DATE: 1998-02-13
SPRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTING OF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 45; DB 3; Length 266; Best Local Similarity 100.0%; Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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ORGANISM: Human papillomavirus type 16
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18-09-367-309A-1
: Sequence 1, Application US/09367309A
; Patent No. 6428807
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89 SLYGTTLEQ 97
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  FEATURE:
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LENGTH: 162 amino acids TYPE: amino acid
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Best Local Similarity 88.5
These 8; Conservative
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APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Guislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
TITLE OF INVENTION: Vaccine
TITLE OF THE BASIO?
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 390
                                                                                                                                                        APPLICANT: Cabezon Silva, Texesa
APPLICANT: Cabezon Silva, Texesa
APPLICANT: Cabezon Silva, Texesa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Lombardo-Bencheikh, Angela
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45.07
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT APPLICATION NUMBER: CT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                 Sequence 6, Application US/09485885
Patent No. 6342224
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Best Local Similarity 100.
214 SLYGITLEQ 222
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ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-09-485-885-14
                                                                                  US-09-485-885-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 6
LENGTH: 371
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214 SLYGTTLEQ 222

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RESULT 15

OBJUST 15

OBJUST 15

DESCRIPTION OF COMPANION:

PARENT NUMBER 15 (2019)

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Query Match 100.0%; Score 51; DB 16; Length 15; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 9; Conservative 0; Mismatches 0; Indels
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LENGTH: 15
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Sequence 67, Appl
Sequence 96, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 74, Appli
Sequence 74, Appl
Sequence 1, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
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64.268 Million cell updates/sec
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21: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-306-541-67
US-10-306-541-93
US-10-306-541-96
US-10-306-541-96
US-10-888-721-7
US-10-898-721-7
US-10-890-526-74
US-10-890-526-74
US-09-8220-765-4
US-09-8210-765-4
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Maximum Match 100%
Listing first 45 summaries
                                                                    protein search, using sw model
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seq length: 2000000000
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Perfect score:
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Sequence 26, M
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US-10-679-956-25
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ALIGNMENTS

US-10-476-570-16

Sequence 16, Application US/10476570

Sequence 16, Application US/10476570

PUBLICATION NO. US20040170644A1

GENERAL INFORMATION:

APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

APPLICANT: MAILLERE, Bernard

APPLICANT: MAILLERE, Bernard

APPLICANT: POUNCELLE-WORATILLE, Sandra

APPLICANT: POUNCELLE-WORATILLE, Sandra

APPLICANT: GUILLET, Jean-Gerard

TITLE OF INVENTION: Maxture of peptides derived from E6 and/or E7

TITLE OF INVENTION: papillomavirus proteins and uses thereof

TITLE OF INVENTION: papillomavirus proteins and uses thereof

CURRENT APPLICATION NUMBER: US/10/476,570

CURRENT FILING DATE: 2003-11-04

FRIOR FILING DATE: 2003-11-04

FRIOR FILING DATE: 2003-11-04

FRIOR FILING DATE: 2001-05-03

FRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 63

SOFUTANE. SEQ ID NOS: 63 E7 OTHER INFORMATION: Description of the artificial sequence: peptide TYPE: PRT ORGANISM: artificial sequence

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Gaps

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Gaps

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Sequence 7, Application US/0988721
; Sequence 7, Application US/0988721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Als, Pierre
APPLICANT: Als, Pierre
APPLICANT: Laurent, Olivier
APPLICANT: Alsewan, Daniel
TITLE OF INVENTION: BICENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
TITLE OF INVENTION: BILLVERY
FILE REPRENCE: 23611-4 MGA
CURRENT FILING DATE: 2001-06-25
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10668400
; Sequence 9, Application US/20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richaed
; TITLE OF INVENTION: WILTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: WACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REPERBNCE: 102.1664.1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-03-23
; PRIOR PILING DATE: 1998-03-27
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                                                                                                                                                                                                                                                                                                Length 15;
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FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/333,249
PRIOR FILING DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                             ; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-96
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ORGANISM: Human papillomavirus
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Best Local Similarity 100.v
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US-09-888-721-7
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US-10-306-541-93

SEQUENCE 93, Application US/10306541

Publication No. US20040171081A1

GENERAL INRORMATION:

APPLICANT: Mittelman, Abraham

APPLICANT: Kanduc, Darja

TITIE NF INFUTION: Improved Antigens

FILE REFERENCE: 12354/4

CURRENT APPLICATION NUMBER: US/10/306,541

CURRENT FILING DATE: 2003-11-25

PRIOR APPLICATION NUMBER: 60/333,249

PRIOR FILING DATE: 2001-11-23

NUMBER OF SEQ ID NOS: 108

SOFTWARE: WordPerfect 8.0 for Windows

SEQ ID NO 93
                                                                                                                                                                                                                                                   APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
FILE REFERENCE: 12354/4
CURRENT APPLICATION NUMBER: US/10/306,541
CURRENT FILING DATE: 2003-11-25
PRIOR PELISH DATE: 2001-11-23
NUMBER OF SEQ ID NOS: 108
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 67
ELENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mittelman, Abraham
APPLICANT: Kanduc, Darja
TITLE OF INVENTION: Improved Antigens
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                                                                                                                                                               Sequence 67, Application US/10306541
Publication No. US20040171081A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: human papillomavirus
US-10-306-541-67
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                                                                                                                                                                                                                                   APPLICANT: Mittelman, Abraham
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Best Local Similarity 100.
Matches 9; Conservative
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       KCDSTLRLC 9
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